

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 2, 2003, 15:59:55 ; Search time 104 Seconds
(without alignments)
1342.370 Million cell updates/sec

Title: US-10-039-770A-1

Perfect score: 541
Sequence: 1 MGLVGVQLVLVADCTIFA.....EAEENIRQGETHVEGEDY 541

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 830525 seqs, 258052604 residues

Word size: 0

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database:

SPTREMBL_23:*

1: sp_archaea:*

2: sp_bacteria:*

3: sp_fungi:*

4: sp_human:*

5: sp_invertebrate:*

6: sp_mammal:*

7: sp_mhc:*

8: sp_organelle:*

9: sp_phage:*

10: sp_plant:*

11: sp_todent:*

12: sp_virus:*

13: sp_vertebrate:*

14: sp_unclassified:*

15: sp_virus:*

16: sp_bacteriap:*

17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	541	100.0	541	5	015681 toxoplasma
2	9	1.7	280	13	073716 grus americana
3	9	1.7	387	16	09KG75 bacillus ha
4	9	1.7	401	16	09A9P5 caulobacter
5	9	1.7	923	16	08X7V7 escherichia
6	8	1.5	121	4	09BWR5
7	8	1.5	126	4	09BRT4
8	8	1.5	130	13	090230
9	8	1.5	133	5	09VNS5
10	8	1.5	133	5	08M221
11	8	1.5	145	4	08NCV9
12	8	1.5	199	2	08KX04
13	8	1.5	210	2	08GC96
14	8	1.5	256	4	09B336
15	8	1.5	256	4	096NG2
16	8	1.5	256	4	096IK7

17	8	1.5	257	11	09D1F4	09d1f4 mus musculus
18	8	1.5	284	16	09EWP8	09ewp8 streptomyces
19	8	1.5	346	7	079458	079458 ambystoma m
20	8	1.5	383	16	08YB66	08yeb6 bruceella me
21	8	1.5	383	16	08FXX9	08fxx9 bruceella su
22	8	1.5	396	16	08YYSO	08yyso anabaena sp
23	8	1.5	437	4	096QH1	096qh1 homo sapien
24	8	1.5	437	4	08N6Q3	08n6q3 homo sapien
25	8	1.5	437	4	09HDS5	09hds5 homo sapien
26	8	1.5	463	16	08ZFW8	08zfw8 yersinia pe
27	8	1.5	468	16	08G7P9	08g7p9 bifidobacte
28	8	1.5	476	12	08U736	08u736 west nile v
29	8	1.5	501	12	09W184	09w184 west nile v
30	8	1.5	501	12	091MB8	091mb8 west nile v
31	8	1.5	501	12	091MC1	091mc1 west nile v
32	8	1.5	501	12	091MB6	091mb6 west nile v
33	8	1.5	501	12	091MB5	091mb5 west nile v
34	8	1.5	501	12	091MB2	091mb2 west nile v
35	8	1.5	501	12	091MC2	091mc2 west nile v
36	8	1.5	501	12	08UT35	08ut35 west nile v
37	8	1.5	501	12	091MB7	091mb7 west nile v
38	8	1.5	501	12	091MB4	091mb4 west nile v
39	8	1.5	501	12	091MB3	091mb3 west nile v
40	8	1.5	501	12	091MC0	091mc0 west nile v
41	8	1.5	501	12	091MB9	091mb9 west nile v
42	8	1.5	502	12	08U740	08u740 west nile v
43	8	1.5	515	10	094CQ3	094cq3 oryza sativ
44	8	1.5	521	10	094CQ6	094cq6 oryza sativ
45	8	1.5	532	10	094CQ5	094cq5 oryza sativ
46	8	1.5	535	11	063314	063314 ratulus norv
47	8	1.5	556	10	094CQ2	094cq2 oryza sativ
48	8	1.5	558	4	096D88	096d88 homo sapien
49	8	1.5	585	4	09BWN1	09bwn1 homo sapien
50	8	1.5	585	4	08WYX2	08wrx2 homo sapien
51	8	1.5	608	11	08K153	08k153 mus musculus
52	8	1.5	637	10	094CQ4	094cq4 oryza sativ
53	8	1.5	640	10	08S6R0	08s6r0 oryza sativ
54	8	1.5	773	12	09WHD2	09whd2 west nile v
55	8	1.5	773	12	09WHD1	09whd1 west nile v
56	8	1.5	813	12	09J5R9	09j5r9 west nile v
57	8	1.5	1126	10	064605	064605 arabidopsis
58	8	1.5	1266	4	081WK6	081wk6 homo sapien
59	8	1.5	1314	12	08U2J7	08u2j7 cercopithec
60	8	1.5	2189	5	09B105	09b105 etemera ten
61	8	1.5	3433	12	09EWM6	09ewm6 west nile v
62	8	1.5	3433	12	09EX21	09ex21 west nile v
63	8	1.5	3433	12	08QRN6	08qrn6 west nile v
64	8	1.5	3433	12	08JU45	08ju45 west nile v
65	8	1.5	3433	12	09Q519	09q519 west nile v
66	8	1.5	3433	12	099P37	099p37 west nile v
67	8	1.5	3433	12	08JU44	08ju44 west nile v
68	8	1.5	3433	12	08JU43	08ju43 west nile v
69	8	1.5	3433	12	08JU42	08ju42 west nile v
70	8	1.5	3433	12	09Q6P4	09q6p4 west nile v
71	8	1.5	3433	12	09EWM5	09ewm5 west nile v
72	8	1.5	3433	12	09Q3G9	09q3g9 west nile v
73	8	1.5	3433	12	08A273	08a273 west nile v
74	8	1.5	3434	10	09Q9F7	09q9f7 murray vall
75	8	1.5	3658	10	09M7K6	09m7k6 arabidopsis
76	7	1.3	25	4	09UL44	09ul44 homo sapien
77	7	1.3	53	16	08E102	08e102 streptococ
78	7	1.3	68	10	08RYJ4	08ryj4 oryza sativ
79	7	1.3	79	17	08RYJ3	08ryj3 mechanopyru
80	7	1.3	80	11	09EON2	09eon2 mus musculus
81	7	1.3	94	2	09S6G6	09s6g6 streptococ
82	7	1.3	111	16	08XNA3	08xna3 clostridium
83	7	1.3	115	16	09J210	09j210 streptococ
84	7	1.3	120	8	035710	035710 rivulus cyl
85	7	1.3	120	10	08LJ10	08lj10 oryza sativ
86	7	1.3	120	17	08ZUY6	08zuy6 pyrobaculum
87	7	1.3	122	3	09P3K5	09p3k5 neurospora
88	7	1.3	133	16	08XDM8	08xdm8 escherichia
89	7	1.3	133	16	08CW47	08cw47 escherichia

90	1.3	137	11	Q9EQN1	Q9eqn1 mus musculu	163	7	1.3	255	16	Q8Y6E0	Q8y6e0 listeria mo
91	1.3	137	11	Q8K160	Q8k160 mus musculu	164	7	1.3	256	16	Q8NMM3	Q8nm3 corynebacte
92	1.3	140	17	Q8TWR8	Q8twr8 methanopyru	165	7	1.3	258	16	Q8HUY6	Q8huy6 pseudomonas
93	1.3	141	16	Q8FTY7	Q8fty7 corynebacte	166	7	1.3	260	16	Q8DHM4	Q8dhm4 synchococc
94	1.3	151	2	Q8RQ98	Q8rq98 uncultured	167	7	1.3	264	16	Q8B693	Q8b693 streptomyce
95	1.3	151	2	Q9F096	Q9f096 nitrosomona	168	7	1.3	267	10	Q8O989	Q8o989 arabidopsis
96	1.3	151	2	Q8R085	Q8rq85 uncultured	169	7	1.3	269	10	Q94A83	Q94a83 arabidopsis
97	1.3	151	2	Q8E251	Q8e251 unidentified	170	7	1.3	269	16	Q34A06	Q34a06 bacillus su
98	1.3	151	2	Q9F046	Q9f046 unidentified	171	7	1.3	271	16	Q9ZFP8	Q9zfp8 bacillus me
99	1.3	151	2	Q9E2T5	Q9e2t5 unidentified	172	7	1.3	271	16	Q98MCO	Q98mco rhizobium l
100	1.3	151	2	Q9E2S2	Q9e2s2 unidentified	173	7	1.3	272	4	Q8N750	Q8n750 homo sapien
101	1.3	151	16	Q8YX85	Q8yx85 anabaena sp	174	7	1.3	276	16	Q8X6Z6	Q8x6z6 escherichia
102	1.3	154	16	Q8D8C8	Q8dec8 vibrio vuln	175	7	1.3	276	16	Q8FC55	Q8fc55 escherichia
103	1.3	156	16	Q8DXH2	Q8dxh2 streptococc	176	7	1.3	277	16	Q97J80	Q97j80 clostridium
104	1.3	159	8	Q8SIL6	Q8sil6 scaphidura	177	7	1.3	277	16	Q8G5L3	Q8g5l3 bifidobacte
105	1.3	159	8	Q8SIL8	Q8sil8 scaphidura	178	7	1.3	277	16	Q8E5R7	Q8e5r7 streptococc
106	1.3	160	16	Q3J255	Q3j255 mycobacteri	179	7	1.3	277	16	Q8DY51	Q8dy51 streptococc
107	1.3	161	16	Q9KUS6	Q9kus6 vibrio chol	180	7	1.3	278	11	Q61350	Q61350 mus musculu
108	1.3	169	16	Q9AAR2	Q9aar2 caulobacter	181	7	1.3	278	11	Q99232	Q99232 mus musculu
109	1.3	171	3	P87069	P87069 laccaria bi	182	7	1.3	280	2	Q9KIB5	Q9kib5 azotobacter
110	1.3	171	16	Q8VUP9	Q8vjp9 mycobacteri	183	7	1.3	282	4	Q8WY42	Q8wy42 homo sapien
111	1.3	173	16	Q8HMI4	Q8hmi4 catapus ber	184	7	1.3	282	13	Q90Y79	Q90y79 elaphe clim
112	1.3	175	8	Q9I2M8	Q9i2m8 pseudomonas	185	7	1.3	286	10	Q94KS6	Q94ks6 zea mays (m
113	1.3	178	2	Q93SM6	Q93sw6 anabaena va	186	7	1.3	291	16	Q92DQ2	Q92dq2 listeria in
114	1.3	178	16	Q93SW8	Q93sw8 anabaena sp	187	7	1.3	291	16	Q8Y6X5	Q8y6x5 listeria mo
115	1.3	179	16	Q8D7C7	Q8d7c7 vibrio vuln	188	7	1.3	291	17	Q8TL00	Q8tl00 methanocarc
116	1.3	182	5	Q20866	Q20866 caenorhabdi	189	7	1.3	292	3	Q96WP1	Q96wp1 agarcus bi
117	1.3	185	16	Q9S2A7	Q9s2a7 streptomyce	190	7	1.3	293	16	Q9HY65	Q9hy65 pseudomonas
118	1.3	188	16	Q9KLE1	Q9kle1 neisseria m	191	7	1.3	295	4	Q9H746	Q9h746 homo sapien
119	1.3	190	11	Q89083	Q89083 mus musculu	192	7	1.3	298	8	Q9G811	Q9g811 emberiza sc
120	1.3	193	10	Q8W492	Q8w492 arabidopsis	193	7	1.3	300	5	Q9N8B3	Q9n8b3 trypanosoma
121	1.3	194	10	Q8G239	Q8g239 arabidopsis	194	7	1.3	305	4	Q75308	Q75308 homo sapien
122	1.3	195	16	Q9RKD9	Q9rkd9 streptomyce	195	7	1.3	305	4	Q15287	Q15287 homo sapien
123	1.3	201	11	Q9E0N0	Q9eqn0 mus musculu	196	7	1.3	305	11	Q99W28	Q99w28 mus musculu
124	1.3	204	16	Q910Z8	Q910z8 pseudomonas	197	7	1.3	307	2	Q9ZAV8	Q9zav8 yersinia en
125	1.3	205	2	Q9APC1	Q9apc1 synchococc	198	7	1.3	308	16	Q916Z4	Q916z4 pseudomonas
126	1.3	206	16	Q03679	Q03679 mus musculu	199	7	1.3	314	16	Q9CFM1	Q9cfm1 lactococcus
127	1.3	206	16	Q9HTL7	Q9htl7 pseudomonas	200	7	1.3	315	16	Q8PIT6	Q8pit6 xanthomonas
128	1.3	207	10	P78939	P78939 schizosacch	201	7	1.3	317	10	Q9LRS4	Q9lrs4 arabidopsis
129	1.3	207	10	Q9ZPX0	Q9zpx0 arabidopsis	202	7	1.3	324	2	Q05581	Q05581 streptomyce
130	1.3	215	16	Q9WX74	Q9wx74 acetobacter	203	7	1.3	327	16	Q34480	Q34480 bacillus su
131	1.3	216	16	Q8P1B7	Q8p1b7 streptococc	204	7	1.3	330	16	Q9ACY1	Q9acy1 streptomyce
132	1.3	216	16	Q8K7V0	Q8k7v0 streptococc	205	7	1.3	331	2	Q9PDD3	Q9pdd3 brucella ab
133	1.3	218	16	Q8XBC6	Q8xbc6 escherichia	206	7	1.3	332	2	Q8KIM3	Q8kim3 rhizobium e
134	1.3	220	5	Q20008	Q20008 caenorhabdi	207	7	1.3	333	5	Q8TIL4	Q8til4 dictyosteli
135	1.3	220	16	Q9RZ00	Q9rz00 deinococcus	208	7	1.3	336	5	Q8IR04	Q8ir04 anopheles g
136	1.3	221	4	Q8N5H1	Q8n5h1 homo sapien	209	7	1.3	338	5	Q8SRM1	Q8srw1 encephalito
137	1.3	222	16	Q8PD41	Q8pd41 xanthomonas	210	7	1.3	338	16	Q9RRAS	Q9rras yersinia en
138	1.3	226	10	Q9EGU7	Q9egu7 arabidopsis	211	7	1.3	339	3	Q96V05	Q96v05 magnaporthe
139	1.3	227	2	Q9JRA1	Q9jral hydrogenoba	212	7	1.3	341	11	Q61354	Q61354 mus musculu
140	1.3	228	10	Q8H6L6	Q8h6l6 capsicum an	213	7	1.3	344	12	Q89563	Q89563 varicola vir
141	1.3	228	10	Q8H6L5	Q8h6l5 capsicum an	214	7	1.3	344	13	Q98T08	Q98t08 gallus gall
142	1.3	228	10	Q8GSF9	Q8gsf9 capsicum an	215	7	1.3	347	8	Q9G139	Q9g139 motus baesa
143	1.3	229	4	Q8NA43	Q8na43 homo sapien	216	7	1.3	349	5	Q9B1J3	Q9b1j3 sarcocystis
144	1.3	231	10	Q9M4R8	Q9m4r8 lycopersico	217	7	1.3	350	5	Q96501	Q96501 supella jon
145	1.3	232	16	Q8FPD0	Q8fpd0 corynebacte	218	7	1.3	351	12	Q9DM14	Q9dm14 plurella xy
146	1.3	234	16	Q8U7M2	Q8u7m2 agrobacteri	219	7	1.3	355	10	Q9SBG7	Q9sbg7 arabidopsis
147	1.3	235	16	Q9KQ09	Q9kq09 vibrio chol	220	7	1.3	355	10	Q81242	Q81242 arabidopsis
148	1.3	237	16	Q8RB91	Q8rb91 thermomane	221	7	1.3	355	12	Q00906	Q00906 hepatitis c
149	1.3	244	16	Q8P6B3	Q8p6b3 xanthomonas	222	7	1.3	360	11	Q8R4S8	Q8r4s8 raltus norv
150	1.3	246	16	Q8ZB86	Q8zb86 yersinia pe	223	7	1.3	368	8	Q8W6E1	Q8w6e1 emberiza sc
151	1.3	247	11	Q8BXP1	Q8bxp1 mus musculu	224	7	1.3	372	2	Q9XCVO	Q9xcvo coxiella bu
152	1.3	247	16	Q97MD5	Q97md5 clostridium	225	7	1.3	372	17	Q9YAM9	Q9yam9 aeropyrum p
153	1.3	247	16	Q929V8	Q929v8 listeria in	226	7	1.3	373	16	Q8FWM1	Q8fwm1 xanthomonas
154	1.3	247	16	Q8Y5K1	Q8y5k1 listeria mo	227	7	1.3	377	9	Q9G1W6	Q9g1w6 ictalurus p
155	1.3	248	10	Q81858	Q81858 arabidopsis	228	7	1.3	379	5	Q45528	Q45528 caenorhabdi
156	1.3	249	16	Q8P8E7	Q8p8e7 leptospira	229	7	1.3	381	16	Q8CV92	Q8cv92 oceanobacti
157	1.3	251	12	Q84603	Q84603 paramecium	230	7	1.3	384	2	Q8KZ77	Q8kz77 uncultured
158	1.3	253	4	Q8N6N0	Q8n6n0 homo sapien	231	7	1.3	386	16	Q8D175	Q8d175 yersinia pe
159	1.3	253	11	Q9CWM5	Q9cwm5 mus musculu	232	7	1.3	387	16	Q8EJL3	Q8ejl3 shewanella
160	1.3	254	16	Q8BXV2	Q8bxv2 mus musculu	233	7	1.3	387	17	Q9YAB0	Q9yab0 aeropyrum p
161	1.3	254	16	Q8PB90	Q8pb90 xanthomonas	234	7	1.3	390	5	Q9VID2	Q9vid2 drosophila
162	1.3	255	16	Q92AR1	Q92arl listeria in	235	7	1.3	390	5	Q9VID2	Q9vid2 drosophila

236	7	1.3	392	5	Q9B110	Q9b110 anopheles g	309	7	1.3	518	16	Q9RVW8	Q9rvw8 deinococcus
237	7	1.3	392	16	Q9KMG6	Q9kmg6 vibrio chol	310	7	1.3	518	16	Q8U6U9	Q8u6u9 agrobacteri
238	7	1.3	392	16	Q8EM15	Q8em15 oceanobacil	311	7	1.3	521	11	Q61352	Q61352 mus musculu
239	7	1.3	394	10	Q24091	Q24091 medicago tr	312	7	1.3	521	11	Q925P3	Q925p3 mus musculu
240	7	1.3	395	16	Q8PFI3	Q8pfi3 xanthomonas	313	7	1.3	521	16	Q8P3U4	Q8p3u4 xanthomonas
241	7	1.3	395	16	Q8P403	Q8p403 xanthomonas	314	7	1.3	525	4	Q8IX15	Q8ix15 homo sapien
242	7	1.3	399	16	Q8XMD0	Q8xmd0 clostridium	315	7	1.3	530	16	Q9AC16	Q9ac16 caulobacter
243	7	1.3	401	16	Q32891	Q32891 mycobacteri	316	7	1.3	539	11	Q8ROD9	Q8rod9 mus musculu
244	7	1.3	401	16	Q9XAK0	Q9xak0 streptomyc	317	7	1.3	541	16	Q9KUB4	Q9kub4 vibrio chol
245	7	1.3	403	17	Q29358	Q29358 archaeoglob	318	7	1.3	541	16	Q8FWE7	Q8fwe7 bruceella su
246	7	1.3	405	16	Q69546	Q69546 mycobacteri	319	7	1.3	542	3	Q05379	Q05379 saccharomyc
247	7	1.3	409	16	Q8UBD7	Q8ubd7 agrobacteri	320	7	1.3	550	10	Q65335	Q65335 pisum sativ
248	7	1.3	409	16	Q8PBY3	Q8pby3 xanthomonas	321	7	1.3	554	5	Q9VPX9	Q9vpix9 drosophila
249	7	1.3	412	16	Q8P273	Q8p273 xanthomonas	322	7	1.3	554	16	Q8Z0B3	Q8z0b3 anabena sp
250	7	1.3	412	16	Q92Y26	Q92y26 rhizobium m	323	7	1.3	555	2	Q9JMW8	Q9jmw8 bradyrhizob
251	7	1.3	415	16	Q8DIC6	Q8dic6 synecchococc	324	7	1.3	557	5	Q8MSB5	Q8msb5 drosophila
252	7	1.3	417	16	Q911G1	Q911g1 pseudomonas	325	7	1.3	563	10	Q04553	Q04553 arabidopsis
253	7	1.3	423	5	Q61532	Q61532 drosophila	326	7	1.3	566	17	Q976Q3	Q976q3 bulfolobus
254	7	1.3	424	16	Q915K2	Q915k2 pseudomonas	327	7	1.3	567	10	Q8VYE4	Q8vye4 arabidopsis
255	7	1.3	426	16	Q9A6K4	Q9a6k4 caulobacter	328	7	1.3	570	4	Q9H6M6	Q9h6m6 homo sapien
256	7	1.3	427	17	Q8U1G8	Q8u1g8 pyrococcus	329	7	1.3	570	4	Q81Z22	Q81z22 homo sapien
257	7	1.3	429	2	Q8RNM2	Q8rnm2 legionella	330	7	1.3	572	11	Q8CAL5	Q8cal5 mus musculu
258	7	1.3	442	13	Q9W622	Q9w622 xenopus lae	331	7	1.3	573	4	Q9P2A5	Q9p2a5 homo sapien
259	7	1.3	444	17	Q28453	Q28453 archaeoglob	332	7	1.3	578	16	Q8YBX4	Q8ybx4 bruceella me
260	7	1.3	449	10	Q9LXQ3	Q9lxq3 arabidopsis	333	7	1.3	579	10	Q8W0V5	Q8w0v5 lolium pere
261	7	1.3	449	16	Q8ZJU4	Q8zju4 salmonella	334	7	1.3	581	16	Q8DTZ7	Q8dtz7 streptococc
262	7	1.3	449	16	Q8Z0T0	Q8z0t0 salmonella	335	7	1.3	583	5	Q21007	Q21007 caenorhabdi
263	7	1.3	454	11	Q91W54	Q91w54 mus musculu	336	7	1.3	585	10	Q81393	Q81393 arabidopsis
264	7	1.3	456	11	Q92N77	Q92n77 pseudomonas	337	7	1.3	585	10	Q8W4N9	Q8w4n9 arabidopsis
265	7	1.3	457	2	Q5E076	Q5e076 spalingomona	338	7	1.3	585	10	Q8H157	Q8h157 arabidopsis
266	7	1.3	458	10	Q9XE15	Q9xel15 zea mays (m	339	7	1.3	586	3	Q9URE1	Q9ure1 saccharomyc
267	7	1.3	458	11	Q61351	Q61351 mus musculu	340	7	1.3	589	5	Q8SY18	Q8sy18 drosophila
268	7	1.3	459	16	Q9S4U0	Q9s4u0 streptococc	341	7	1.3	592	16	Q67937	Q67937 aquifex aeo
269	7	1.3	462	10	Q8D0S2	Q8d0s2 streptococc	342	7	1.3	593	5	Q9TX05	Q9tx05 drosophila
270	7	1.3	462	10	Q94DP6	Q94dp6 oryza sativ	343	7	1.3	600	5	Q8T2G2	Q8t2g2 dictyosteli
271	7	1.3	466	5	Q8T0P5	Q8t0p5 lycopodium	344	7	1.3	600	10	Q9CAR8	Q9car8 arabidopsis
272	7	1.3	466	16	Q35266	Q35266 lycopodium	345	7	1.3	602	16	Q8CJP2	Q8cjp2 streptomyc
273	7	1.3	469	16	Q92LZ9	Q92l29 rhizobium m	346	7	1.3	605	10	Q8H9F2	Q8h9f2 oryza sativ
274	7	1.3	473	2	Q9JRK0	Q9jrk0 neisseria m	347	7	1.3	606	16	Q9WXM8	Q9wxm8 thermotoga
275	7	1.3	473	10	Q9KJVL	Q9kjl1 lactobacill	348	7	1.3	610	16	Q9KXG9	Q9kxg9 bacillus ha
276	7	1.3	473	10	Q9JML8	Q9jml8 arabidopsis	349	7	1.3	611	16	Q8DKF5	Q8dkf5 synecchococc
277	7	1.3	474	16	Q9X929	Q9x929 streptomyc	350	7	1.3	612	16	Q8FQU0	Q8fqu0 corynebacte
278	7	1.3	476	10	Q9SXR2	Q9sxr2 scutellaria	351	7	1.3	631	10	Q9XED8	Q9xed8 arabidopsis
279	7	1.3	476	16	Q9AAR2	Q9aar2 caulobacter	352	7	1.3	641	10	Q94GM3	Q94gm3 oryza sativ
280	7	1.3	480	2	Q93F90	Q93f90 streptomyc	353	7	1.3	645	10	Q9FMZ8	Q9fmz8 arabidopsi
281	7	1.3	480	16	Q9JKNM0	Q9jknm0 vibrio chol	354	7	1.3	647	5	Q21573	Q21573 caenorhabdi
282	7	1.3	482	2	Q9APV8	Q9apv8 pseudomonas	355	7	1.3	651	4	Q9NX19	Q9nx19 homo sapien
283	7	1.3	482	10	Q8LB19	Q8lb19 arabidopsis	356	7	1.3	651	4	Q9NX86	Q9nx86 homo sapien
284	7	1.3	482	10	Q8VZ15	Q8vz15 arabidopsis	357	7	1.3	651	10	Q8VXS1	Q8vxs1 solanum tub
285	7	1.3	484	16	Q8Y1J5	Q8y1j5 ralsonia s	358	7	1.3	656	16	Q8D4W4	Q8d4w4 vibrio vuln
286	7	1.3	484	16	Q8EMC2	Q8emc2 oceanobacil	359	7	1.3	658	2	Q8GPT3	Q8gpt3 citrobacter
287	7	1.3	487	2	P72269	P72269 rhodococcus	360	7	1.3	658	16	Q9KMG2	Q9kmg2 arabidopsi
288	7	1.3	488	3	Q96U74	Q96u74 neurospora	361	7	1.3	660	16	Q8FL17	Q8fl17 escherichia
289	7	1.3	492	4	Q9H784	Q9h784 homo sapien	362	7	1.3	669	5	Q8SXS8	Q8sxs8 drosophila
290	7	1.3	492	11	Q8R3T2	Q8r3ct mus musculu	363	7	1.3	669	5	Q9VYE6	Q9vye6 drosophila
291	7	1.3	492	11	Q8BH98	Q8bh98 mus musculu	364	7	1.3	671	16	Q9BDY9	Q9bdy9 rhizobium 1
292	7	1.3	493	5	Q8UN07	Q8un07 apis mellif	365	7	1.3	676	10	Q8VXS2	Q8vxs2 solanum tub
293	7	1.3	493	5	Q9U8X5	Q9u8x5 apis mellif	366	7	1.3	676	10	Q8VXS2	Q8vxs2 solanum tub
294	7	1.3	495	2	Q46252	Q46252 clostridium	367	7	1.3	685	16	Q8PXR3	Q8pxr3 xanthomonas
295	7	1.3	495	16	Q8XP02	Q8xp02 xanthomonas	368	7	1.3	705	10	Q9LKB0	Q9lkb0 arabidopsis
296	7	1.3	495	16	Q8P6M5	Q8p6m5 xanthomonas	369	7	1.3	706	3	Q12039	Q12039 saccharomyc
297	7	1.3	496	13	Q8JFQ5	Q8jfg5 oncorhynch	370	7	1.3	708	4	Q9UGU9	Q9ugu9 homo sapien
298	7	1.3	497	10	Q22991	Q22991 arabidopsis	371	7	1.3	714	4	Q96G17	Q96g17 homo sapien
299	7	1.3	498	11	Q8BNB0	Q8bnb0 mus musculu	372	7	1.3	721	10	Q22208	Q22208 arabidopsi
300	7	1.3	498	16	Q98KQ0	Q98kq0 rhizobium 1	373	7	1.3	721	10	Q8L7E7	Q8l7e7 arabidopsi
301	7	1.3	501	2	Q9LAL1	Q9lal1 pseudomonas	374	7	1.3	723	2	Q9EWC1	Q9ewc1 streptomyc
302	7	1.3	503	5	Q8WQM9	Q8wqm9 anopheles g	375	7	1.3	731	16	Q91664	Q91664 pseudomonas
303	7	1.3	503	17	Q28026	Q28026 archaeoglob	376	7	1.3	743	16	Q9RWS7	Q9rws7 deinococcus
304	7	1.3	505	10	Q8W032	Q8w032 arabidopsis	377	7	1.3	744	2	Q8KTP4	Q8ktp4 listeria mo
305	7	1.3	510	16	Q8EMZ5	Q8emz5 leptospira	378	7	1.3	745	3	Q944C4	Q944c4 schizosacch
306	7	1.3	512	16	Q9HVA7	Q9hva7 pseudomonas	379	7	1.3	755	3	Q8NIU6	Q8niu6 neurospora
307	7	1.3	517	2	Q9ZGB6	Q9zgb6 streptomyc	380	7	1.3	755	16	Q9RTB1	Q9rtb1 deinococcus
308	7	1.3	518	5	Q9V6K8	Q9v6k8 drosophila	381	7	1.3	766	10	Q8H6B0	Q8h6b0 zea mays (m

382	1.3	773	16	08YVD2	08Yvd2 anabaena sp	455	7	1.3	2064	5	09VP19	09vp19 drosophila
383	1.3	774	4	09SE941	09se941 homo sapien	456	7	1.3	2138	5	09XZE3	09xez3 ameoba prot
384	1.3	778	5	09SX07	09sx07 pernaeus mon	457	7	1.3	2492	12	08JTW9	08jtw9 sweet potat
385	1.3	782	10	09L2A0	09l2a0 arabidopsis	458	7	1.3	3177	5	09NA13	09na13 drosophila
386	1.3	794	16	09X212	09x212 thermotoga	459	7	1.3	3257	5	09VT36	09vt36 drosophila
387	1.3	802	4	08TDA0	08tda0 homo sapien	460	6	1.1	22	6	09TRC4	09trc4 canis famli
388	1.3	802	10	08L4U4	08l4u4 oryza sativ	461	6	1.1	24	2	005421	005421 mycobacteri
389	1.3	816	11	08BRS5	08brs5 mus musculu	462	6	1.1	27	2	056139	056139 streptococ
390	1.3	830	16	09H2V6	09h2v6 pseudomonas	463	6	1.1	31	2	053411	053411 bacillus mu
391	1.3	839	9	064076	064076 bacteriophia	464	6	1.1	34	6	0951A4	0951a4 macaca mula
392	1.3	839	16	09RX57	09rx57 delinococcus	465	6	1.1	34	6	0951A6	0951a6 sus scrofa
393	1.3	839	16	031945	031945 bacillus su	466	6	1.1	34	11	0912X2	0912x2 cavia porce
394	1.3	845	4	09HAU3	09ha3 homo sapien	467	6	1.1	38	2	09REY8	09rey8 carnobacter
395	1.3	845	4	09HBB8	09hbb8 homo sapien	468	6	1.1	42	2	09ZPA2	09zfaz rhodobacter
396	1.3	845	4	09HBB5	09hbb5 homo sapien	469	6	1.1	43	16	09X131	09x131 thermotoga
397	1.3	884	11	08BN06	08bnq6 mus musculu	470	6	1.1	46	12	092581	092581 hepatitis c
398	1.3	894	4	08NSL2	08ns12 homo sapien	471	6	1.1	46	16	034568	034568 bacillus su
399	1.3	911	4	09H330	09h330 homo sapien	472	6	1.1	47	11	09OWS6	09ow6 mus musculu
400	1.3	942	5	018298	018298 caenorhabdi	473	6	1.1	47	16	09PUR2	09pur2 chlamydia m
401	1.3	944	12	09DM96	09dm96 rat cytomeg	474	6	1.1	48	5	09V942	09v942 drosophila
402	1.3	962	5	08IGQ1	08igq1 drosophila	475	6	1.1	48	5	09V942	09v942 drosophila
403	1.3	968	3	09Y7J9	09y7j9 schizosacch	476	6	1.1	48	12	091FP9	091fp9 chilo iride
404	1.3	971	4	060337	060337 homo sapien	477	6	1.1	48	16	09KLD0	09kld0 vibrio chol
405	1.3	1010	3	09USN1	09usn1 schizosacch	478	6	1.1	49	12	09WANO	09wano hepatitis c
406	1.3	1013	3	09HPE4	09hpe4 ashyba goss	479	6	1.1	49	12	09W9E1	09w9e1 hepatitis c
407	1.3	1014	5	018016	018016 caenorhabdi	480	6	1.1	50	12	09WAM6	09wam6 human echov
408	1.3	1043	5	08SSW7	08ssw7 dictyosteli	481	6	1.1	50	12	0966E5	0966e5 human echov
409	1.3	1050	16	08FN18	08fn18 corynebacte	482	6	1.1	53	16	09K6C3	09k6c3 bacillus ha
410	1.3	1052	3	09PE63	09pe63 schizosacch	483	6	1.1	54	16	08U5A8	08u5a8 agrobacteri
411	1.3	1061	5	08WRF4	08wrf4 monosiga br	484	6	1.1	56	2	08GAJ3	08gaj3 escherichia
412	1.3	1068	10	09AXF7	09axf7 chlamydomon	485	6	1.1	56	6	029276	029276 sus scrofa
413	1.3	1078	5	09V460	09v460 drosophila	486	6	1.1	56	11	091ZS5	091zas mus musculu
414	1.3	1081	2	068831	068831 bacterioides	487	6	1.1	58	16	09CFI7	09cf17 laccococcus
415	1.3	1090	16	0928J2	0928j2 listeria in	488	6	1.1	58	16	08ERU9	08eru9 oceanobacil
416	1.3	1091	16	08Y4J2	08y4j2 listeria mo	489	6	1.1	60	9	08W630	08w630 bacteriophia
417	1.3	1092	5	0964R2	0964r2 theileria t	490	6	1.1	61	6	097974	097974 equus cabal
418	1.3	1151	5	096593	096593 heterodera	491	6	1.1	61	6	09TUP2	09tup2 equus cabal
419	1.3	1174	16	082P89	082p89 salmoneila	492	6	1.1	61	10	08S9E5	08s9e5 oryza sativ
420	1.3	1174	16	082781	082781 salmoneila	493	6	1.1	62	2	050163	050163 mycobacteri
421	1.3	1174	16	08X9Q3	08x9q3 escherichia	494	6	1.1	62	2	09C8I9	09c8i9 mus musculu
422	1.3	1174	16	08FHP2	08fhp2 escherichia	495	6	1.1	62	11	09CSJ9	09csj9 halobacteri
423	1.3	1177	16	08ZES0	08zes0 yersinia pe	496	6	1.1	62	17	09HSJ9	09hsj9 oryza sativ
424	1.3	1185	16	08KC02	08kc02 chlorobium	497	6	1.1	63	10	09SPN4	09spn4 oryza sativ
425	1.3	1187	16	08YVR3	08yvr3 anabaena sp	498	6	1.1	63	16	09RTW3	09rtw3 deinococcus
426	1.3	1201	4	08N3V0	08n3v0 homo sapien	499	6	1.1	63	16	098P59	098p59 rhizobium l
427	1.3	1204	4	08NDG4	08ndg4 homo sapien	500	6	1.1	64	5	09VY10	09vy10 drosophila
428	1.3	1208	5	018023	018023 caenorhabdi	501	6	1.1	64	12	08U2N1	08u2n1 garlic late
429	1.3	1234	4	094983	094983 homo sapien	502	6	1.1	64	12	091UW7	091uw7 hepatitis c
430	1.3	1241	5	09U144	09u144 leishmania	503	6	1.1	65	10	08S755	08s755 oryza sativ
431	1.3	1250	4	09UCJ4	09ucj4 homo sapien	504	6	1.1	65	16	099UR9	099ur9 staphylococ
432	1.3	1251	4	09UBZ9	09ubz9 homo sapien	505	6	1.1	66	10	08L1V5	08l1v5 hordeum vul
433	1.3	1253	11	061810	061810 mus musculu	506	6	1.1	67	2	09S4D2	09s4d2 staphylococ
434	1.3	1256	13	090WJ3	090wj3 xenopus lae	507	6	1.1	67	12	0842E4	0842e4 european el
435	1.3	1271	5	09V8K6	09v8k6 drosophila	508	6	1.1	67	16	08XWJ3	08xwj3 ralsiconia s
436	1.3	1276	13	090X22	090x22 brachydanio	509	6	1.1	68	5	09N6Z6	09n6z6 mytilus edu
437	1.3	1298	5	09XZ32	09xz32 drosophila	510	6	1.1	68	15	09N1D5	09n1d5 human immun
438	1.3	1346	2	04S996	04s996 clostridium	511	6	1.1	71	3	09WMD5	09wmd5 agrobacteri
439	1.3	1611	2	033957	033957 streptomyce	512	6	1.1	71	3	09UWDC	09uwc8 mytilus edu
440	1.3	1616	2	093HMO	093hmo streptococ	513	6	1.1	72	8	09NAT8	09nat8 mytilus edu
441	1.3	1659	16	097S90	097s90 streptococ	514	6	1.1	73	12	091FP8	091fp8 chilo iride
442	1.3	1659	16	08C252	08c252 streptococ	515	6	1.1	73	12	0950A6	0950a6 mycobacteri
443	1.3	1661	6	09GKPI	09gkpi sus scrofa	516	6	1.1	73	16	0950A6	0950a6 mycobacteri
444	1.3	1730	13	08UVY7	08uvy7 xenopus lae	517	6	1.1	74	16	0930R4	0930r4 streptomyce
445	1.3	1734	4	09Y6Y1	09y6y1 homo sapien	518	6	1.1	75	2	0546E1	0546e1 streptococ
446	1.3	1742	16	08P377	08p377 xanthomonas	519	6	1.1	75	2	09P8I0	09p8i0 xyella fas
447	1.3	1792	10	08LSR5	08lsr5 oryza sativ	520	6	1.1	75	16	08CSP3	08csp3 archaeglob
448	1.3	1795	5	076894	076894 drosophila	521	6	1.1	75	17	034839	034839 archaeglob
449	1.3	1858	3	P78615	P78615 emericella	522	6	1.1	76	3	09Y8F5	09y8f5 glomus moss
450	1.3	1910	16	08Z8Y3	08z8y3 yersinia pe	523	6	1.1	76	11	09Y8F5	09y8f5 glomus moss
451	1.3	1916	5	09VKG8	09vkg8 drosophila	524	6	1.1	77	2	054671	054671 streptococ
452	1.3	1980	5	09VHD1	09vhd1 drosophila	525	6	1.1	77	2	027725	027725 methanobac
453	1.3	2051	4	09P2F2	09p2f2 homo sapien	526	6	1.1	77	17	09N241	09n241 saimiri bol
454	1.3	2062	4	09H231	09h231 homo sapien	527	6	1.1	78	6	09N241	09n241 saimiri bol

528	6	1.1	79	5	09W312	09W312 drosophila	601	6	1.1	95	6	097520	097520 pongo pygma
529	6	1.1	79	16	08ZIR4	08ZIR4 yersinia pe	602	6	1.1	95	6	097519	097519 pongo pygma
530	6	1.1	80	3	08JW3	08JW3 colletoctic	603	6	1.1	95	16	08ZLS4	08ZLS4 salmonella
531	6	1.1	80	11	08CF36	08CF36 mus musculu	604	6	1.1	95	16	08Z3G9	08Z3G9 salmonella
532	6	1.1	81	2	044114	044114 bynechococ	605	6	1.1	96	5	06106	06106 reticuliter
533	6	1.1	81	8	08MA07	08MA07 chaetosphae	606	6	1.1	96	5	0908X4	0908X4 reticuliter
534	6	1.1	81	10	08RU61	08RU61 atropa bell	607	6	1.1	96	12	09QTY5	09QTY5 tt virus. o
535	6	1.1	81	10	09LHB8	09LHB8 arabidopsis	608	6	1.1	96	12	09QU12	09QU12 tt virus. o
536	6	1.1	82	8	09TL14	09TL14 nephroselm	609	6	1.1	96	12	09QU18	09QU18 tt virus. o
537	6	1.1	83	2	08LIC4	08LIC4 pasteurella	610	6	1.1	96	12	09QU09	09QU09 tt virus. o
538	6	1.1	84	4	09P183	09P183 homo sapien	611	6	1.1	96	12	09QU24	09QU24 tt virus. o
539	6	1.1	84	10	094AQ4	094AQ4 arabidopsis	612	6	1.1	96	12	09QU28	09QU28 tt virus. o
540	6	1.1	84	10	08HM9	08HM9 gossypium h	613	6	1.1	96	13	09AVT7	09AVT7 xenopus lae
541	6	1.1	84	16	09XW7	09XW7 bacillus ha	614	6	1.1	96	15	08JAT5	08JAT5 human immun
542	6	1.1	85	4	08TES9	08TES9 homo sapien	615	6	1.1	96	16	08URE2	08URE2 agrobacteri
543	6	1.1	85	10	08W2B2	08W2B2 capsicum an	616	6	1.1	97	16	08PE65	08PE65 xanthomonas
544	6	1.1	85	10	08LAF8	08LAF8 oryza sativ	617	6	1.1	98	4	016303	016303 homo sapien
545	6	1.1	86	4	09BY16	09BY16 homo sapien	618	6	1.1	98	4	016303	016303 homo sapien
546	6	1.1	86	8	020482	020482 andropadu	619	6	1.1	98	5	09BK59	09BK59 caenorhadi
547	6	1.1	86	10	09M1K8	09M1K8 arabidopsis	620	6	1.1	98	8	094X19	094X19 neoceratodu
548	6	1.1	86	10	09CAJ1	09CAJ1 arabidopsis	621	6	1.1	98	10	09FH20	09FH20 arabidopsis
549	6	1.1	87	5	08IC09	08IC09 plasmodium	622	6	1.1	98	10	P93347	P93347 nicotiana t
550	6	1.1	87	6	09W242	09W242 ateles sp.	623	6	1.1	99	2	08VLJ0	08VLJ0 escherichia
551	6	1.1	87	10	040441	040441 nicotiana g	624	6	1.1	99	2	08GEM3	08GEM3 erwinia pyr
552	6	1.1	87	11	035366	035366 mus musculu	625	6	1.1	99	4	08N6X9	08N6X9 homo sapien
553	6	1.1	87	11	035365	035365 mus musculu	626	6	1.1	99	4	09UG68	09UG68 homo sapien
554	6	1.1	87	12	08V2T4	08V2T4 camelopx vi	627	6	1.1	99	6	097518	097518 pongo pygma
555	6	1.1	87	16	08XH57	08XH57 clostridium	628	6	1.1	99	8	08SKR4	08SKR4 orthomyx te
556	6	1.1	87	16	08E795	08E795 streptococ	629	6	1.1	99	10	08W537	08W537 retama taet
557	6	1.1	87	16	08E1T1	08E1T1 streptococ	630	6	1.1	99	10	08GYN2	08GYN2 arabidopsis
558	6	1.1	87	17	08ZY17	08ZY17 pyrobaculum	631	6	1.1	99	16	097R38	097R38 streptococ
559	6	1.1	88	4	099587	099587 homo sapien	632	6	1.1	99	16	08ZWN6	08ZWN6 salmonella
560	6	1.1	88	8	020506	020506 andropadu	633	6	1.1	99	16	08CLH2	08CLH2 yersinia pe
561	6	1.1	88	13	09PSY9	09PSY9 sparus aura	634	6	1.1	100	2	09X625	09X625 coxiella bu
562	6	1.1	89	16	09K8S2	09K8S2 bacillus ha	635	6	1.1	100	8	08HHT2	08HHT2 poecile atr
563	6	1.1	89	16	08P1V3	08P1V3 xanthomonas	636	6	1.1	100	12	08QRH3	08QRH3 hepatitis c
564	6	1.1	90	4	096GH6	096GH6 homo sapien	637	6	1.1	100	12	08QCR7	08QCR7 hepatitis c
565	6	1.1	90	10	09MW2	09MW2 arabidopsis	638	6	1.1	100	12	08OR12	08OR12 hepatitis c
566	6	1.1	90	11	08CSJ6	08CSJ6 mus musculu	639	6	1.1	100	12	08OR68	08OR68 hepatitis c
567	6	1.1	90	13	09DD49	09DD49 oryzias lat	640	6	1.1	100	12	08QRH8	08QRH8 hepatitis c
568	6	1.1	90	13	08UT03	08UT03 oryzias lat	641	6	1.1	100	12	08QRH4	08QRH4 hepatitis c
569	6	1.1	90	13	08AWF6	08AWF6 oreochromis	642	6	1.1	100	15	040277	040277 human immun
570	6	1.1	90	16	097MR2	097MR2 clostridium	643	6	1.1	100	15	091132	091132 human immun
571	6	1.1	91	6	09N244	09N244 naealis lar	644	6	1.1	100	16	08DPK7	08DPK7 vibrio vuln
572	6	1.1	91	6	09N245	09N245 macaca mula	645	6	1.1	101	4	09BX24	09BX24 homo sapien
573	6	1.1	91	6	097517	097517 gorilla gor	646	6	1.1	101	16	09XZ49	09XZ49 thermotoga
574	6	1.1	91	6	097515	097515 pan paniscu	647	6	1.1	102	2	09AFR3	09AFR3 shigella fl
575	6	1.1	91	6	097521	097521 pongo pygma	648	6	1.1	102	8	08WCI6	08WCI6 parus atric
576	6	1.1	91	6	09N243	09N243 presbytis c	649	6	1.1	102	8	08WC17	08WC17 parus carol
577	6	1.1	91	6	09N246	09N246 papio hamad	650	6	1.1	102	11	08CGR7	08CGR7 mus musculu
578	6	1.1	91	12	09NM23	09NM23 hepatitis c	651	6	1.1	102	11	08BRD6	08BRD6 mus musculu
579	6	1.1	91	12	09M9K2	09M9K2 hepatitis c	652	6	1.1	102	16	09CFR3	09CFR3 lactococcus
580	6	1.1	91	13	098TB2	098TB2 ambloplites	653	6	1.1	102	17	09UWX1	09UWX1 sulfolobus
581	6	1.1	91	16	08YG26	08YG26 bruceia me	654	6	1.1	103	2	049825	049825 mycobacteri
582	6	1.1	91	16	09CHV2	09CHV2 lactococcus	655	6	1.1	103	11	08GQ80	08GQ80 pseudomonas
583	6	1.1	91	16	08GOW3	08GOW3 bruceia su	656	6	1.1	103	11	08VDP22	08VDP22 mus musculu
584	6	1.1	91	16	08DLD7	08DLD7 yersinia pe	657	6	1.1	103	13	09PSE1	09PSE1 torpedo cal
585	6	1.1	92	4	08NHM4	08NHM4 homo sapien	658	6	1.1	103	15	040324	040324 human immun
586	6	1.1	92	12	08ULZ1	08ULZ1 mamestra co	659	6	1.1	103	15	0992T8	0992T8 human immun
587	6	1.1	92	12	08V501	08V501 monkeypox v	660	6	1.1	104	8	08SLI8	08SLI8 dunaliella
588	6	1.1	92	12	08OL70	08OL70 mamestra co	661	6	1.1	104	16	08B9P1	08B9P1 shewanella
589	6	1.1	93	16	08XPB6	08XPB6 clostridium	662	6	1.1	105	5	09V941	09V941 drosophila
590	6	1.1	93	6	09N247	09N247 hylobates s	663	6	1.1	105	10	094FC5	094FC5 gossypium a
591	6	1.1	94	2	09P1P0	09P1P0 shewanella	664	6	1.1	105	10	094FC4	094FC4 gossypium b
592	6	1.1	94	2	054670	054670 streptococ	665	6	1.1	105	10	094FC3	094FC3 gossypium l
593	6	1.1	94	6	097950	097950 equus cabal	666	6	1.1	105	10	094FC1	094FC1 oryza sativ
594	6	1.1	94	6	08HYN2	08HYN2 macaca mula	667	6	1.1	105	10	094FC1	094FC1 kokia dryna
595	6	1.1	94	16	08P9Q8	08P9Q8 xanthomonas	668	6	1.1	105	10	094FC2	094FC2 gossypium b
596	6	1.1	95	4	099586	099586 homo sapien	669	6	1.1	105	15	09M695	09M695 gossypioide
597	6	1.1	95	6	097514	097514 pan troglod	670	6	1.1	105	15	P88188	P88188 human immun
598	6	1.1	95	6	09N249	09N249 hylobates x	671	6	1.1	105	16	092079	092079 rhizobium m
599	6	1.1	95	6	09N248	09N248 hylobates l	672	6	1.1	106	2	09F6W6	09F6W6 chloroflexu
600	6	1.1	95	6	097516	097516 gorilla gor	673	6	1.1	106	2	08GM40	08GM40 legionella

674	6	1.1	106	5	08SRV8	08SRV8 encephalito	747	6	1.1	114	6	097534	097534 aotus vocif
675	6	1.1	106	6	08HXF5	08HXF5 macaca fasc	748	6	1.1	114	10	08LJ57	08LJ57 oryza sativ
676	6	1.1	106	11	08CG35	08CG35 ratuus norv	749	6	1.1	114	15	08G511	08G511 human immun
677	6	1.1	106	16	08Z018	08Z018 anabena sp	750	6	1.1	114	15	09WN14	09WN14 human immun
678	6	1.1	106	16	08EE21	08EE21 shewanelia	751	6	1.1	114	15	08Q618	08Q618 human immun
679	6	1.1	106	16	08EE03	08EE03 shewanelia	752	6	1.1	114	15	08Q6E1	08Q6E1 human immun
680	6	1.1	107	10	08O374	08O374 aeter tripo	753	6	1.1	114	15	08Q6D7	08Q6D7 human immun
681	6	1.1	107	10	08O371	08O371 aeter tripo	754	6	1.1	114	15	08Q6S1	08Q6S1 human immun
682	6	1.1	107	10	08O375	08O375 aeter tripo	755	6	1.1	114	15	08Q6E3	08Q6E3 human immun
683	6	1.1	107	11	08CCU5	08CCU5 mus musculu	756	6	1.1	114	15	09O452	09O452 human immun
684	6	1.1	107	16	09PAR7	09PAR7 xyliella fas	757	6	1.1	114	15	08Q6L9	08Q6L9 human immun
685	6	1.1	107	16	09KEC3	09KEC3 bacillus ha	758	6	1.1	114	15	08Q6R5	08Q6R5 human immun
686	6	1.1	107	16	092TK9	092TK9 rhizobium ha	759	6	1.1	114	15	09WNQ0	09WNQ0 human immun
687	6	1.1	108	16	08YGR7	08YGR7 bruceella me	760	6	1.1	114	15	07O164	07O164 human immun
688	6	1.1	108	16	08G147	08G147 bruceella su	761	6	1.1	114	15	09WNR0	09WNR0 human immun
689	6	1.1	108	16	08CKC1	08CKC1 yersinia pe	762	6	1.1	114	15	08Q6O5	08Q6O5 human immun
690	6	1.1	109	2	09XDM3	09XDM3 rhodopseudo	763	6	1.1	114	16	09BLU0	09BLU0 human immun
691	6	1.1	109	2	03O535	03O535 pseudomonas	764	6	1.1	114	16	09K9N3	09K9N3 human immun
692	6	1.1	109	2	09R7F9	09R7F9 unidentified	765	6	1.1	114	16	08PC77	08PC77 xanthomonas
693	6	1.1	109	3	093910	093910 neurospora	766	6	1.1	114	16	08NNE0	08NNE0 corynebacte
694	6	1.1	109	3	08T785	08T785 cryptospori	767	6	1.1	115	10	043762	043762 hordium vul
695	6	1.1	109	5	08T785	08T785 cryptospori	767	6	1.1	115	11	08CS47	08CS47 mus musculu
696	6	1.1	109	15	09J0M9	09J0M9 human immun	768	6	1.1	115	11	09QDL3	09QDL3 human immun
697	6	1.1	109	16	025421	025421 helicobacte	769	6	1.1	115	15	09Q0L3	09Q0L3 human immun
698	6	1.1	109	16	091328	091328 pseudomonas	770	6	1.1	115	15	09O429	09O429 human immun
699	6	1.1	109	16	08Z4U7	08Z4U7 salmonella	771	6	1.1	115	15	09O469	09O469 human immun
700	6	1.1	109	17	08TVZ7	08TVZ7 methanopyru	772	6	1.1	115	16	09RVA4	09RVA4 human immun
701	6	1.1	110	2	08KKD9	08KKD9 helicobacte	773	6	1.1	115	16	08EE35	08EE35 shewanelia
702	6	1.1	110	2	093EB6	093EB6 rhizobium l	774	6	1.1	116	2	09F817	09F817 carboxydoth
703	6	1.1	110	2	087801	087801 pseudomonas	775	6	1.1	116	2	08KKAO	08KKAO proteus vul
704	6	1.1	110	2	08G1O7	08G1O7 streptomyce	776	6	1.1	116	5	09BNF4	09BNF4 chthonius t
705	6	1.1	110	10	041975	041975 arabidopsis	777	6	1.1	116	8	09ME13	09ME13 lama guanac
706	6	1.1	110	11	091X13	091X13 spermophilu	778	6	1.1	116	8	08HKU3	08HKU3 petrosiote
707	6	1.1	110	16	08PIE7	08PIE7 xanthomonas	779	6	1.1	116	9	08SC58	08SC58 stx2 conver
708	6	1.1	110	16	08P733	08P733 xanthomonas	780	6	1.1	116	10	094DK4	094DK4 oryza sativ
709	6	1.1	111	3	012243	012243 saccharomyc	781	6	1.1	116	11	09CT65	09CT65 mus musculu
710	6	1.1	111	4	09H2B5	09H2B5 homo sapien	782	6	1.1	116	15	08Q6N8	08Q6N8 human immun
711	6	1.1	111	10	041951	041951 arabidopsis	783	6	1.1	116	16	0915Q6	0915Q6 pseudomonas
712	6	1.1	111	10	09SCA7	09SCA7 arabidopsis	784	6	1.1	117	2	P71212	P71212 escherichia
713	6	1.1	111	11	09EBQ7	09EBQ7 ratuus norv	785	6	1.1	117	2	08VMT3	08VMT3 pseudomonas
714	6	1.1	111	15	08ATH0	08ATH0 human immun	786	6	1.1	117	4	09UFL7	09UFL7 homo sapien
715	6	1.1	111	16	08YC74	08YC74 bruceella me	787	6	1.1	117	4	09POQ4	09POQ4 homo sapien
716	6	1.1	111	16	08PDT5	08PDT5 xanthomonas	788	6	1.1	117	5	09XXE7	09XXE7 caenorhabdi
717	6	1.1	111	16	09X8N1	09X8N1 streptomyce	789	6	1.1	117	10	094DK6	094DK6 oryza sativ
718	6	1.1	111	16	09EXK3	09EXK3 streptomyce	790	6	1.1	118	5	09NCS1	09NCS1 cryptospori
719	6	1.1	112	11	08UZX1	08UZX1 mus musculu	791	6	1.1	118	9	09G081	09G081 bacterioph
720	6	1.1	112	11	08RIE9	08RIE9 mus musculu	792	6	1.1	118	16	09ISEK3	09ISEK3 pseudomonas
721	6	1.1	112	15	037376	037376 human immun	793	6	1.1	119	4	09WSK7	09WSK7 homo sapien
722	6	1.1	112	15	08ATH7	08ATH7 human immun	794	6	1.1	119	16	08ZKL5	08ZKL5 salmonella
723	6	1.1	112	15	08ATH5	08ATH5 human immun	795	6	1.1	119	16	08Z312	08Z312 salmonella
724	6	1.1	112	15	08ATH4	08ATH4 human immun	796	6	1.1	120	2	09SS57	09SS57 pseudomonas
725	6	1.1	112	15	08ATH3	08ATH3 human immun	797	6	1.1	120	2	093HP8	093HP8 streptomyce
726	6	1.1	112	15	08ATH2	08ATH2 human immun	798	6	1.1	120	2	09KWX3	09KWX3 pseudomonas
727	6	1.1	112	15	08ATH1	08ATH1 human immun	799	6	1.1	120	5	09WSB0	09WSB0 caenorhabdi
728	6	1.1	112	15	08ATG8	08ATG8 human immun	800	6	1.1	120	10	042049	042049 arabidopsis
729	6	1.1	112	15	08ATG5	08ATG5 human immun	801	6	1.1	120	16	09SS65	09SS65 pseudomonas
730	6	1.1	112	15	08ATG3	08ATG3 human immun	802	6	1.1	120	16	08FRP4	08FRP4 corynebacte
731	6	1.1	112	15	08ATG2	08ATG2 human immun	803	6	1.1	120	17	08TKG0	08TKG0 methanosarc
732	6	1.1	112	15	08ATG1	08ATG1 human immun	804	6	1.1	121	8	09SEB7	09SEB7 rana sylvat
733	6	1.1	113	5	08DC00	08DC00 vibrio vuln	805	6	1.1	121	8	09SBW0	09SBW0 rana cateeb
734	6	1.1	113	5	09VZ24	09VZ24 drosophila	806	6	1.1	121	10	08GZV1	08GZV1 oryza sativ
735	6	1.1	113	10	09AS11	09AS11 oryza sativ	808	6	1.1	121	12	072197	072197 hepatitis c
736	6	1.1	113	15	08UAV6	08UAV6 human immun	809	6	1.1	121	12	072200	072200 hepatitis c
737	6	1.1	113	15	08UAT6	08UAT6 human immun	810	6	1.1	121	12	072201	072201 hepatitis c
738	6	1.1	113	15	08ATG7	08ATG7 human immun	811	6	1.1	121	12	072203	072203 hepatitis c
739	6	1.1	113	15	08ATG6	08ATG6 human immun	812	6	1.1	121	12	072198	072198 hepatitis c
740	6	1.1	113	15	08ATG4	08ATG4 human immun	813	6	1.1	121	16	08UBU7	08UBU7 agrobacteri
741	6	1.1	113	17	09HQV3	09HQV3 halobacteri	814	6	1.1	121	16	08FW52	08FW52 bruceella su
742	6	1.1	113	17	08TWG8	08TWG8 methanopyru	815	6	1.1	122	5	046063	046063 drosophila
743	6	1.1	114	4	09UPB9	09UPB9 homo sapien	816	6	1.1	122	16	08ZNB5	08ZNB5 salmonella
744	6	1.1	114	4	09UTN5	09UTN5 aotus lemur	817	6	1.1	122	16	08Z4Z6	08Z4Z6 salmonella
745	6	1.1	114	6	09TTH6	09TTH6 aotus nigri	818	6	1.1	122	16	08VJK5	08VJK5 mycobacteri
746	6	1.1	114	6	097539	097539 aotus nancy	819	6	1.1	123	12	08JKA9	08JKA9 hepatitis c

820	6	1.1	123	16	Q926M4	Q926M4 listeria in	893	6	1.1	138	11	Q99J91	Q99J91 marmota mon
821	6	1.1	123	16	Q8D359	Q8D359 wigleswort	894	6	1.1	138	12	Q83421	Q83421 pseudorabie
822	6	1.1	123	17	Q8Y9H3	Q8Y9H3 aeropyrum p	895	6	1.1	138	16	Q9PW49	Q9PW49 campylobac
823	6	1.1	124	10	Q9SXX4	Q9SXX4 oryza sativ	896	6	1.1	138	16	Q9PR48	Q9PR48 xylella fas
824	6	1.1	124	17	Q9YEM1	Q9YEM1 aeropyrum p	897	6	1.1	139	5	Q18272	Q18272 caenorhabdi
825	6	1.1	125	2	Q93DY1	Q93DY1 magnetospir	898	6	1.1	139	15	Q8AKW4	Q8AKW4 human immun
826	6	1.1	125	5	Q962D8	Q962D8 dirosophila	899	6	1.1	139	15	Q8AKU3	Q8AKU3 human immun
827	6	1.1	125	16	Q8FQ59	Q8FQ59 corynebacte	900	6	1.1	139	15	Q8AKT5	Q8AKT5 human immun
828	6	1.1	125	17	Q974A1	Q974A1 sulfolobus	901	6	1.1	139	16	Q8PJ76	Q8PJ76 xanthomonas
829	6	1.1	125	17	Q8TOYO	Q8TOYO methanocarc	902	6	1.1	139	16	Q8EZJ9	Q8EZJ9 leprospira
830	6	1.1	126	4	Q81VT3	Q81VT3 homo sapien	903	6	1.1	139	16	Q8BAK5	Q8BAK5 shewanella
831	6	1.1	126	11	Q9D288	Q9D288 mus musculu	904	6	1.1	140	1	Q9Y8U9	Q9Y8U9 halobacteri
832	6	1.1	126	16	Q9J2U4	Q9J2U4 neisseria m	905	6	1.1	140	2	Q9JN80	Q9JN80 myxococcu
833	6	1.1	126	16	Q97T41	Q97T41 streptococc	906	6	1.1	140	5	Q9W569	Q9W569 dirosophila
834	6	1.1	126	16	Q8YE28	Q8YE28 brucella me	907	6	1.1	140	8	Q9XKW1	Q9XKW1 paragonimus
835	6	1.1	126	16	Q8FY14	Q8FY14 brucella su	908	6	1.1	140	10	Q8S7D5	Q8S7D5 oryza sativ
836	6	1.1	126	16	Q8CXB2	Q8CXB2 streptococc	909	6	1.1	140	12	Q9D1W9	Q9D1W9 hepatitis c
837	6	1.1	127	16	Q9RSB5	Q9RSB5 deinococcus	910	6	1.1	140	12	Q99A23	Q99A23 bovine vira
838	6	1.1	128	11	Q9DA35	Q9DA35 mus musculu	911	6	1.1	140	15	Q75101	Q75101 human immun
839	6	1.1	128	11	Q8CD36	Q8CD36 mus musculu	912	6	1.1	140	16	Q8YX23	Q8YX23 anabaena sp
840	6	1.1	128	11	Q8C320	Q8C320 mus musculu	913	6	1.1	140	16	Q8XOD4	Q8XOD4 ralatonia s
841	6	1.1	128	12	Q99C39	Q99C39 bovine herp	914	6	1.1	140	16	Q9ZLC3	Q9ZLC3 helicobacte
842	6	1.1	128	16	Q9JZZ9	Q9JZZ9 neisseria m	915	6	1.1	140	16	Q8ZJ23	Q8ZJ23 yersinia pe
843	6	1.1	128	16	Q8YJ61	Q8YJ61 anabaena sp	916	6	1.1	140	16	Q8ECY0	Q8ECY0 shewanella
844	6	1.1	129	16	Q8XGMO	Q8XGMO salmoneila	917	6	1.1	141	2	Q06689	Q06689 treponema p
845	6	1.1	129	16	Q8RIL0	Q8RIL0 fusobacteri	918	6	1.1	141	4	Q9WFK5	Q9WFK5 synechococc
846	6	1.1	129	16	Q8PJ32	Q8PJ32 xanthomonas	919	6	1.1	141	4	Q8N2E8	Q8N2E8 homo sapien
847	6	1.1	130	2	Q8KM22	Q8KM22 paracoccus	920	6	1.1	141	9	Q38066	Q38066 bacterioph
848	6	1.1	130	4	Q8N827	Q8N827 homo sapien	921	6	1.1	141	11	Q9QY70	Q9QY70 mus musculu
849	6	1.1	130	10	Q8S3P7	Q8S3P7 oryza sativ	922	6	1.1	141	11	Q61692	Q61692 mus musculu
850	6	1.1	130	16	Q8E2X5	Q8E2X5 streptococc	923	6	1.1	141	16	Q911S8	Q911S8 pseudomonas
851	6	1.1	130	16	Q8DX28	Q8DX28 streptococc	924	6	1.1	141	16	Q91166	Q91166 pseudomonas
852	6	1.1	131	16	P73579	P73579 synechocyst	925	6	1.1	141	16	Q8NSE7	Q8NSE7 corynebacte
853	6	1.1	131	16	Q8XW33	Q8XW33 ralatonia s	926	6	1.1	142	1	Q8N667	Q8N667 homo sapien
854	6	1.1	131	17	Q9Y9G2	Q9Y9G2 aeropyrum p	927	6	1.1	143	6	Q9N056	Q9N056 bos taurus
855	6	1.1	132	3	Q9P656	Q9P656 schizosacch	928	6	1.1	143	10	Q8S363	Q8S363 antioecarpus
856	6	1.1	132	3	P78948	P78948 schizosacch	929	6	1.1	143	10	Q8W024	Q8W024 antirrhinum
857	6	1.1	132	5	Q81079	Q81079 dirosophila	930	6	1.1	143	17	Q9HMT1	Q9HMT1 halobacteri
858	6	1.1	132	10	Q8S070	Q8S070 oryza sativ	931	6	1.1	144	2	Q9ZNG5	Q9ZNG5 wolbachia s
859	6	1.1	132	16	Q97H58	Q97H58 clostridium	932	6	1.1	144	2	P78000	P78000 kingella de
860	6	1.1	132	16	Q8PR58	Q8PR58 xanthomonas	933	6	1.1	144	6	Q9GL44	Q9GL44 macaca mula
861	6	1.1	132	16	Q8PE50	Q8PE50 xanthomonas	934	6	1.1	144	10	Q8VXT0	Q8VXT0 beta vulgar
862	6	1.1	133	2	Q9R489	Q9R489 agrobacteri	935	6	1.1	144	11	Q8BMJ3	Q8BMJ3 mus musculu
863	6	1.1	133	2	Q66170	Q66170 agrobacteri	936	6	1.1	144	11	Q8BMH8	Q8BMH8 mus musculu
864	6	1.1	133	5	Q9VCZ4	Q9VCZ4 dirosophila	937	6	1.1	144	11	Q8BJZ2	Q8BJZ2 mus musculu
865	6	1.1	133	15	Q8AEP1	Q8AEP1 human immun	938	6	1.1	144	16	Q9RTS8	Q9RTS8 deinococcus
866	6	1.1	133	16	Q9RU77	Q9RU77 deinococcus	939	6	1.1	144	17	P95921	P95921 sulfolobus
867	6	1.1	133	16	Q8YML1	Q8YML1 anabaena sp	940	6	1.1	145	8	P92685	P92685 parus ater
868	6	1.1	134	2	Q55063	Q55063 synechocyst	941	6	1.1	145	8	P92684	P92684 parus ater
869	6	1.1	134	2	Q9LAV0	Q9LAV0 caulobacter	942	6	1.1	145	10	Q9FKI2	Q9FKI2 arabidopsis
870	6	1.1	134	2	Q8LTR9	Q8LTR9 uncultured	943	6	1.1	145	10	Q8W027	Q8W027 arabidopsis
871	6	1.1	134	2	Q9AIS6	Q9AIS6 chlamydomo	944	6	1.1	145	10	Q9S0B9	Q9S0B9 arabidopsis
872	6	1.1	134	16	Q8CYU8	Q8CYU8 streptococc	945	6	1.1	145	10	Q9JVF1	Q9JVF1 arabidopsis
873	6	1.1	135	11	Q63317	Q63317 rattus norv	946	6	1.1	145	10	Q8WVK5	Q8WVK5 antirrhinum
874	6	1.1	135	16	Q9A6E3	Q9A6E3 caulobacter	947	6	1.1	145	14	Q991U2	Q991U2 uncultured
875	6	1.1	135	16	Q8LK17	Q8LK17 vicia faba	948	6	1.1	145	16	Q9RT39	Q9RT39 deinococcus
876	6	1.1	137	5	Q96335	Q96335 brugia mala	949	6	1.1	146	2	Q9RE93	Q9RE93 enterococcu
877	6	1.1	137	8	Q8HIG1	Q8HIG1 schistosoma	950	6	1.1	146	6	Q8MJ96	Q8MJ96 equus cabal
878	6	1.1	137	11	Q8C442	Q8C442 mus musculu	951	6	1.1	146	8	P92702	P92702 parus carol
879	6	1.1	137	11	Q8BN67	Q8BN67 mus musculu	952	6	1.1	146	8	P92686	P92686 parus atric
880	6	1.1	137	16	Q9HYV4	Q9HYV4 pseudomonas	953	6	1.1	146	10	Q8LSM4	Q8LSM4 triticum ae
881	6	1.1	137	16	Q988H6	Q988H6 rhizobium 1	954	6	1.1	146	12	Q8JSM1	Q8JSM1 bovine papl
882	6	1.1	137	16	Q8U693	Q8U693 agrobacteri	955	6	1.1	146	13	Q8QCG0	Q8QCG0 bovine papl
883	6	1.1	137	16	Q8PIW8	Q8PIW8 xanthomonas	956	6	1.1	147	4	Q9BRJ5	Q9BRJ5 homo sapien
884	6	1.1	138	2	Q8RK71	Q8RK71 nitrosomona	957	6	1.1	147	6	Q8MIT3	Q8MIT3 bos taurus
885	6	1.1	138	2	Q8RK79	Q8RK79 nitrosomona	958	6	1.1	147	10	Q9JN60	Q9JN60 arabidopsis
886	6	1.1	138	2	Q8RK75	Q8RK75 nitrosomona	959	6	1.1	147	11	Q8VHG9	Q8VHG9 notomys ale
887	6	1.1	138	2	Q8KMP4	Q8KMP4 lactococcus	960	6	1.1	147	12	Q8UJ44	Q8UJ44 virus phich
888	6	1.1	138	2	Q8RK63	Q8RK63 nitrosospir	961	6	1.1	147	12	Q98S06	Q98S06 paramectum
889	6	1.1	138	2	Q8RK61	Q8RK61 nitrosomona	962	6	1.1	148	2	Q9ERT0	Q9ERT0 envitroment
890	6	1.1	138	2	Q8GC85	Q8GC85 enterobacte	963	6	1.1	148	2	Q9LAK5	Q9LAK5 uncultured
891	6	1.1	138	5	Q8T957	Q8T957 dirosophila	964	6	1.1	148	2	Q9F9A3	Q9F9A3 uncultured
892	6	1.1	138	5	Q8MLE1	Q8MLE1 dirosophila	965	6	1.1	148	2	Q9F9A6	Q9F9A6 uncultured

966	6	1.1	148	2	Q8RMP3	Q8RMP3 uncultured
967	6	1.1	148	2	Q8ETL8	Q8ETL8 environment
968	6	1.1	148	2	Q9F9A5	Q9F9A5 uncultured
969	6	1.1	148	2	Q9EUA3	Q9EUA3 environment
970	6	1.1	148	2	Q9ETR1	Q9ETR1 environment
971	6	1.1	148	2	Q9F9A1	Q9F9A1 uncultured
972	6	1.1	148	2	Q9F9A8	Q9F9A8 uncultured
973	6	1.1	148	2	Q9F9A4	Q9F9A4 uncultured
974	6	1.1	148	2	Q9EUD8	Q9EUD8 environment
975	6	1.1	148	5	Q9VEA1	Q9VEA1 drosophila
976	6	1.1	148	5	Q9NUB4	Q9NUB4 drosophila
977	6	1.1	148	5	Q9U9L3	Q9U9L3 anophelis 9
978	6	1.1	148	5	Q8J544	Q8J544 human immun
979	6	1.1	149	2	Q9K4P6	Q9K4P6 unidentifite
980	6	1.1	149	2	Q9K4Q0	Q9K4Q0 unidentifite
981	6	1.1	149	2	Q9K4P7	Q9K4P7 unidentifite
982	6	1.1	149	2	Q9K4N5	Q9K4N5 nitrosomona
983	6	1.1	149	2	Q9K4P2	Q9K4P2 unidentifite
984	6	1.1	149	2	Q9K4P8	Q9K4P8 unidentifite
985	6	1.1	149	2	Q9K2W9	Q9K2W9 unidentifite
986	6	1.1	149	2	Q9K4Q1	Q9K4Q1 unidentifite
987	6	1.1	149	2	Q9K4P9	Q9K4P9 unidentifite
988	6	1.1	149	2	Q9K4P3	Q9K4P3 unidentifite
989	6	1.1	149	2	Q9K4N6	Q9K4N6 nitrosomona
990	6	1.1	149	2	Q9K4N3	Q9K4N3 nitrosomona
991	6	1.1	149	2	Q9K4P5	Q9K4P5 unidentifite
992	6	1.1	149	2	Q9K4N4	Q9K4N4 nitrosomona
993	6	1.1	149	2	Q9K4Q2	Q9K4Q2 unidentifite
994	6	1.1	149	5	Q02582	Q02582 inciliaria f
995	6	1.1	149	8	Q9MD22	Q9MD22 schistosoma
996	6	1.1	149	9	Q80313	Q80313 bacteriophya
997	6	1.1	149	12	Q9IHK7	Q9IHK7 human polio
998	6	1.1	149	12	Q9IHK6	Q9IHK6 human polio
999	6	1.1	149	12	Q9IHK5	Q9IHK5 human polio
1000	6	1.1	149	12	Q9IHL0	Q9IHL0 human polio

ALIGNMENTS

RESULT 1
015681 PRELIMINARY; PRT; 541 AA.
AC 015681;
DT 01-JAN-1998 (TREMBLrel. 05, Created)
DT 01-JAN-1998 (TREMBLrel. 05, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE Apical membrane antigen 1 homolog.
GN AMAING.
OS Toxoplasma gondii;
OC Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;
OC Toxoplasma.
OX NCBI_TaxID=5811;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ME49; PubMed=11083833;
RC MEDLINE=20536458; PubMed=11083833;
RA Hehl A.B., Lekutis C., Grigg M.E., Bradley P.J., Dubremetz J.F.,
RA Ortega-Barria E., Boochroy J.C.;
RT "Toxoplasma gondii Homologue of Plasmodium Apical Membrane Antigen 1
RT Is Involved in Invasion of Host Cells";
RL Infect. Immun. 68:7078-7086(2000).
DR EMBL; AF010264; AAB65410.1; -
DR InterPro; IPR003298; Apmem_Ag1.
DR Pfam; PFO2430; AMA-1; 1.
DR PRINTS; PRO1361; MEROZOITESA.
SQ SEQUENCE 541 AA; 59978 MW; DD38EF3A0F258E27 CRC64;

Query Match 100.0%; Score 541; DB 5; Length 541;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGVLGVQLLVLVADCTIFASGLSSSTRRESQTLASLSTSGNFQANVEMKTFMERFNL 60

Db		1	MGVLGVQLLVLVADCTIFASGLSSSTRRESQTLASLSTSGNFQANVEMKTFMERFNL 60
QY	HHHSGIYVVDIGQDKEVDGTYREBPAGLCPIWGHIELOQBDRLPYNNFLEDPTEKEY 120	61	
Db	HHHSGIYVVDIGQDKEVDGTYREBPAGLCPIWGHIELOQBDRLPYNNFLEDPTEKEY 120	61	
QY	KQSGNPLPGGNLNFVTPSGORTSPFMELEKSNIKASDGLGRCAEPAFTVAMDKN 180	121	
Db	KQSGNPLPGGNLNFVTPSGORTSPFMELEKSNIKASDGLGRCAEPAFTVAMDKN 180	121	
QY	KATKRRYPFYVDSKKRLCHILYVSMQMEGKKYCSVAGEPDLTWYCFKPKSVTENHL 240	181	
Db	KATKRRYPFYVDSKKRLCHILYVSMQMEGKKYCSVAGEPDLTWYCFKPKSVTENHL 240	181	
QY	IYSAVYGENPDATISKCPNOLAGYRQVWKKRCIDYTLTPTVIERVSKAQCWKT 300	241	
Db	IYSAVYGENPDATISKCPNOLAGYRQVWKKRCIDYTLTPTVIERVSKAQCWKT 300	241	
QY	FENDGVASDOPHTYPLTQASWMDWPLHOSDOPHSGVGRNRYVYVDTTGEGKALSD 360	301	
Db	FENDGVASDOPHTYPLTQASWMDWPLHOSDOPHSGVGRNRYVYVDTTGEGKALSD 360	301	
QY	QVPDCLVSDSAVSYTAGSLSEETPNFIIPSNBSVTPPTETALQCTADKFPDSGACD 420	361	
Db	QVPDCLVSDSAVSYTAGSLSEETPNFIIPSNBSVTPPTETALQCTADKFPDSGACD 420	361	
QY	VOACKRQKTSVCGVQIGSTVDTCTADNDEGSGNTALAGLVGVLLALLGGGCVFAK 480	421	
Db	VOACKRQKTSVCGVQIGSTVDTCTADNDEGSGNTALAGLVGVLLALLGGGCVFAK 480	421	
QY	RLDNRKGVQAAHHEHFEPSDRGARKRPSDLMQEAEPFMEAEENIEQDETHVMVGD 540	481	
Db	RLDNRKGVQAAHHEHFEPSDRGARKRPSDLMQEAEPFMEAEENIEQDETHVMVGD 540	481	
QY	541 Y 541		
Db	541 Y 541		

RESULT 2
073716 PRELIMINARY; PRT; 280 AA.
AC 073716;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE B-G-1-like protein.
GN BG2.
OS Grus americana (whooping crane).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Gruiformes; Gruidae; Grus.
OX NCBI_TaxID=9117;
RN [1]
RP SEQUENCE FROM N.A.
RA Javri S.I., Goto R.M., Gee G.F., Briles W.E., Miller M.M.;
RT "Identification, inheritance and linkage of B-G-1-like and MHC class I
RT genes in cranes";
RL J. Hered. 0:0-0(1998).
DR EMBL; AF031107; AAC23712.1; -
DR InterPro; IPR007110; IG-1like.
DR InterPro; IPR003006; IG_MHC.
DR InterPro; IPR003596; IG_v.
DR Pfam; PFO0047; ig_1.
DR SMART; SM00406; IGv_1.
DR PROSITE; PS50835; IG_LIKE; 2.
SQ SEQUENCE 280 AA; 31411 MW; C379DE8A61C52DD0 CRC64;

Query Match 1.7%; Score 9; DB 13; Length 280;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 VGVQVLVL 12

Db 249 VGVGVLLVL 257

RESULT 3

ID 09KG75 PRELIMINARY; PRT; 387 AA.

AC 09KG75;
DT 01-OCT-2000 (TRENBLrel. 15, Created)
DT 01-OCT-2000 (TRENBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Multidrug-efflux transporter.
GN BH0237.

OS Bacillus halodurans.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=86665;

RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=C-125 / JCM 9153;
RX MEDLINE=20512582; PubMed=11058132;
RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
RA Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
RA Horikoshi K.,
RT "Complete genome sequence of the alkaliphilic bacterium Bacillus
RT halodurans and genomic sequence comparison with Bacillus subtilis.";
RL Nucleic Acids Res. 28:4317-4331(2000).

DR EMBL; AP001507; BAB03956.1; -

DR InterPro; IPR007114; MFS.

DR InterPro; IPR005828; Sub_transporter.

DR InterPro; IPR003829; Sug_transporter.

DR InterPro; IPR001958; TCR_Teta.

DR Pfam; PF00083; Sugar_tr_1.

DR PRINTS; PR01035; TCRTETA.

DR PROSITE; PS00850; MFS; 1.

DR PROSITE; PS00216; SUGAR_TRANSPORT_1; 1.

KM Complete proteome.

SO SEQUENCE 387 AA; 41096 MW; 611247A4EA854BC8 CRC64;

Query Match 1.7%; Score 9; DB 16; Length 387;
Best Local Similarity 100.0%; Pred. No. 2.3;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 461 LAVGVLL 469

Db 73 LAVGVLL 81

RESULT 4

ID 09A9P5 PRELIMINARY; PRT; 401 AA.

AC 09A9P5;
DT 01-JUN-2001 (TRENBLrel. 17, Created)
DT 01-JUN-2001 (TRENBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TRENBLrel. 20, Last annotation update)
DE Hypothetical protein CC0931.

GN CC0931.

OS Caulobacter crescentus.

OC Bacteria; Proteobacteria; Alphaproteobacteria; Caulobacteriales;

OC Caulobacteraceae; Caulobacter.

OX NCBI_TaxID=155892;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=ATCC 19089 / CB15;

RX MEDLINE=21173698; PubMed=11259647;

RA Nieman W.C., Feldblum T.V., Laub M.T., Paulsen I.T., Nelson K.E.,

RA Eichen J., Heidelberg J.F., Alley M.R.K., Ohta N., Maddock J.R.,

RA Potocka I., Nelson W.C., Newton A.S., Stephens C., Phadke N.D., Ely B.,

RA DeJoy R.T., Dodson R.J., Durkin A.S., Gwin M.L., Haft D.H.,

RA Kojanay J.F., Smit J., Craven M.B., Khouri H., Shetty J., Berry K.,

RA Uterback T., Tran K., Wolf A., Vamathavan J., Smolava M., White O.,

RA Salzberg S.L., Venter J.C., Shapiro H., Fraser C.M.,

RA "Complete genome sequence of Caulobacter crescentus.";

RT Proc. Natl. Acad. Sci. U.S.A. 98:4136-4141(2001).

DR EMBL; AE005770; AAK22915.1; -
DR TIGR; CC0931; -
DR InterPro; IPR003838; DUF214.
DR Pfam; PF02687; DUF214; 1.
KM Hypothetical protein; Complete proteome.
SO SEQUENCE 401 AA; 42438 MW; 13A40D0ACBCE8CA CRC64;

Query Match 1.7%; Score 9; DB 16; Length 401;
Best Local Similarity 100.0%; Pred. No. 2.3;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 455 TALAGLAV 463

Db 36 TALAGLAV 44

RESULT 5

ID 08X7V7 PRELIMINARY; PRT; 923 AA.

AC 08X7V7;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-JUN-2002 (TRENBLrel. 21, Last annotation update)
DE Putative protease (putative ATP-dependent Clp protease ATP-binding
DE chain).

GN 20254 OR ECS0223.

OS Escherichia coli O157:H7.

OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;

OC Enterobacteriaceae; Escherichia.

OX NCBI_TaxID=83334;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN=O157:H7 / EDL933 / ATCC 700927;

RX MEDLINE=21074935; PubMed=11206551;

RA Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

RA Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

RA Postel G., Hackel J., Klink S., Boutin A., Shao Y., Miller L.,

RA Grobeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

RA Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

RA Welch R.A., Blattner F.R.,

RT "Genome sequence of enterohaemorrhagic Escherichia coli O157:H7.";

RL Nature 409:529-533(2001).

RN [2]

RP SEQUENCE FROM N.A.

RC STRAIN=O157:H7 / RIMD 0509952;

RX MEDLINE=21156231; PubMed=11258796;

RA Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K.,

RA Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T.,

RA Iida T., Takami H., Honda T., Sasaki K., Ogasawara N., Yasunaga T.,

RA Kuhara S., Shiba T., Hattori M., Shinagawa H.,

RT "Complete genome sequence of enterohaemorrhagic Escherichia coli

RT O157:H7 and genomic comparison with a laboratory strain K-12.";

RL DNA Res. 8:11-22(2001).

DR EMBL; AE005198; AAG54523.1; -

DR EMBL; AP002550; BAB33646.1; -

DR InterPro; IPR003593; AAA_ATPase.

DR InterPro; IPR003959; AAA_ATPase_cent.

DR InterPro; IPR001270; Chaprinin_c1pA/B.

DR Pfam; PF00004; AAA; 1.

DR PRINTS; PR00300; CLPPTERSEA.

DR SMART; SM00382; AAA; 2.

DR PROSITE; PS00870; CLPAB_1; 1.

KM Protease; Complete proteome.

SO SEQUENCE 923 AA; 101229 MW; 0D1465A573031035 CRC64;

Query Match 1.7%; Score 9; DB 16; Length 923;
Best Local Similarity 100.0%; Pred. No. 5.1;

Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 464 GGVLLALL 472

Db 114 GGVLLALL 122

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RESULT 6
Q9BWR5 PRELIMINARY; PRT; 121 AA.
ID Q9BWR5;
AC Q9BWR5;
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE Hypothetical protein (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RA Strausberg R.;
RL Submitted (NOV-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC000031; AA00031.1; -.
KM Hypothetical protein.
FT NON_TER
SQ SEQUENCE 121 AA; 13233 MW; 8BD9FB4B56E478D8 CRC64;

Query Match 1.5%; Score 8; DB 4; Length 121;
Best Local Similarity 100.0%; Pred. No. 8.9;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 379 GSLSEETP 386
DB 19 GSLSEETP 26

RESULT 7
Q96BI4 PRELIMINARY; PRT; 126 AA.
ID Q96BI4;
AC Q96BI4;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Similar to hypothetical protein MG2865.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homindae; Homo.
CX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Skin;
RA Strausberg R.;
RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC015562; AA015562.1; -.
KM Hypothetical protein.
SQ SEQUENCE 126 AA; 13807 MW; 2E34744BBEFC1E9 CRC64;

Query Match 1.5%; Score 8; DB 4; Length 126;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 379 GSLSEETP 386
DB 24 GSLSEETP 31

RESULT 8
Q90230 PRELIMINARY; PRT; 130 AA.
ID Q90230;
AC Q90230;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
DE ASK1 transcription factor (Fragment).
OS Ambystoma mexicanum (Axolotl).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Caudata; Salamandroidae; Ambystomatidae;

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OC Ambystoma.
OX NCBI_TaxID=82296;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=95092782; PubMed=7999783;
RA Ludolph D.C., Neff A.W., Parker M.A., Mescher A.L., Smith R.C.,
RA Malachuk G.M.;
RT "Cloning and expression of the axolotl proto-oncogene skt.";
RL Biochim. Biophys. Acta 1260:102-104(1995).
DR EMBL: D28907; BA018908.1; -.
DR EMBL: X77994; CA54956.1; -.
DR InterPro: IPR003380; TransForm_Skt.
DR Pfam: PF02437; Skt_Sno; 1.
KM DNA-binding.
FT NON_TER
FT NON_TER
SQ SEQUENCE 130 AA; 14107 MW; DEB17C02D4C0CF46 CRC64;

Query Match 1.5%; Score 8; DB 13; Length 130;
Best Local Similarity 100.0%; Pred. No. 9.5;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 470 ALLGGGCV 477
DB 36 ALLGGGCV 43

RESULT 9
Q9VNS5 PRELIMINARY; PRT; 133 AA.
ID Q9VNS5;
AC Q9VNS5;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
DE CG14453 protein.
GN CG14453.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BERKELEY;
RX MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champagne M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abail J.F., Agbayani A., An H.-J., Andrews-Franko C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Broctier P.,
RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrera S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodex A., Gong P., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibesam C.,
RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kethum K.A.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA Mewlrow G., Mishina N.V., Modyar C., Morris J., Moshrefi A.,
RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA Nelson D.R., Nelson K.A., Nixon K., Nussekn D.R., Paiebo J.M.,
RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

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RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skipski M.P., Smith T.,
 RA Spler E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Wolley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yen R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Glibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 DR EMBL; AF003598; AAF51845.1;
 DR FlyBase; FBgn0037179; CG14453.
 SQ SEQUENCE 133 AA; 14796 MW; 07BA825ABCEAEF CRC64;
 QY Query Match 1.5%; Score 8; DB 5; Length 133;
 Best Local Similarity 100.0%; Pred. No. 9.7;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 466 VLLALLG 473
 6 VLLALLG 13

RESULT 10
 Q8M221 PRELIMINARY; PRT; 133 AA.
 AC Q8M221 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE RE13473P.
 GN BCDNA:RE13473.
 OS *Drosophila melanogaster* (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkely;
 RA Stapleton M., Brokstein P., Hong L., Agbayan A., Carlson J.,
 RA Champe M., Chavez C., Dorset H., Dresnek D., Farfan D., Frise E.,
 RA George R., Gonzalez M., Guertin V., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Ceinlier S.;
 RL Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY113408; AAM29413.1;
 DR FlyBase; FBgn0063060; BCDNA:RE13473.
 SQ SEQUENCE 133 AA; 14822 MW; 2530B376B8666957 CRC64;
 QY Query Match 1.5%; Score 8; DB 5; Length 133;
 Best Local Similarity 100.0%; Pred. No. 9.7;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 466 VLLALLG 473
 6 VLLALLG 13

RESULT 11
 Q8NCV9 PRELIMINARY; PRT; 145 AA.
 AC Q8NCV9 01-OCT-2002 (TrEMBLrel. 22, Created).
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Glycoprotein NBI precursor.
 GN NBI.
 OS *Homo sapiens* (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22006006; PubMed=12010833;
 RA Kissel K., Scheffler S., Kerowgan M., Bux J.;
 RT "Molecular basis of NBI (HNA-2a, CDI177) deficiency.";
 RL Blood 99:4231-4233(2002).
 DR EMBL; AJ305326; CAC83758.1;
 KW Signal.
 FT SIGNAL 1 21
 FT CHAIN 22 145 GLYCOPROTEIN NBI.
 SQ SEQUENCE 145 AA; 15709 MW; EF7FB498AB839053 CRC64;
 QY Query Match 1.5%; Score 8; DB 4; Length 145;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 466 VLLALLG 473
 4 VLLALLG 11

RESULT 12
 Q8KX04 PRELIMINARY; PRT; 199 AA.
 AC Q8KX04 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
 DE Hypothetical protein.
 GN SL11486.
 OS *Synechococcus* sp. (strain PCC 7002) (Agmenellum quadruplicatum).
 OC Bacteria; Cyanobacteria; Chroococcales; Synechococcus.
 OX NCBI_TaxID=32049;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Nomura C.T., Persson S., Zhao J., Bryant D.A.;
 RT "An Analysis of Forty Genes Encoding Electron Transport Proteins from
 RT *Synechococcus* sp. PCC 7002: A Comparative Study of Electron Transport
 RT Proteins from Cyanobacteria and Chloroplasts.";
 RL Submitted (May-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF81049; AAN03589.1;
 KW Hypothetical protein.
 SQ SEQUENCE 199 AA; 22445 MW; 454000D4949067F4 CRC64;
 QY Query Match 1.5%; Score 8; DB 2; Length 199;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Db 464 GGVLALL 471
 119 GGVLALL 126

RESULT 13
 Q8GC96 PRELIMINARY; PRT; 210 AA.
 AC Q8GC96 01-MAR-2003 (TrEMBLrel. 23, Created)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE Putative regulatory protein.
 GN F1M2 GENE.
 OS *Citrobacter freundii*.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Citrobacter.
 OX NCBI_TaxID=546;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=3009;
 RA Oelschlaeger T.A.;
 RT "Cloning, sequencing and expression of an invasion determinant from
 RT *Citrobacter freundii* strain 3009.";

RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AJ508060; CAD56976.1; -
 SQ SEQUENCE 210 AA; 23624 MW; CDDDE380BF594F57 CRC64;

Query Match 1.5%; Score 8; DB 2; Length 210;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 150 LLEKXSN1 157
 |||||
 DB 22 LLEKXSN1 29

RESULT 14

O96B36 PRELIMINARY; PRT; 256 AA.
 AC O96B36;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Hypothetical protein.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Tissue=Eye;
 RA Strausberg R.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL, BC016043; AAH16043.1; -
 DR InterPro; IPR002965; P_Rich_extensn.
 DR PRINTS; PRO1217; PRICHEXTENSN.
 DR Hypothetical protein.
 SQ SEQUENCE 256 AA; 27383 MW; FC6C195CBB54326C CRC64;

Query Match 1.5%; Score 8; DB 4; Length 256;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 379 GSLSEETP 386
 |||||
 DB 154 GSLSEETP 161

RESULT 15

O96NG2 PRELIMINARY; PRT; 256 AA.
 AC O96NG2;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Hypothetical protein FLJ10949.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Tissue=Eye;
 RA Ishihashi T., Kanehori K., Yosida M., Watanabe S., Ishida S., Ono Y.,
 Houtura T., Hirooka S., Murakawa K., Takiguchi S., Kusano J.,
 Watanabe M., Fujimori K., Tanai H., Ishida M., Yamashita H., Chiba Y.,
 RA Sugiyama T., Irie R., Otsuki T., Sato H., Wakamatsu A., Ishii S.,
 RA Yamamoto J., Isono Y., Kawai-Hio Y., Saito K., Nishikawa T.,
 RA Kimura K., Matsuo K., Nakamura Y., Sekine M., Kikuchi H., Kanda K.,
 RA Magatsuna M., Takahashi-Fujii A., Oshima A., Sugiyama A., Kawakami B.,
 RA Suzuki Y., Sugano S., Nagahari K., Masuno Y., Negai K., Isega T.;
 RT "NEO human cDNA sequencing project";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL, AK055511; BAB70937.1; -
 DR InterPro; IPR002965; P_Rich_extensn.
 DR PRINTS; PRO1217; PRICHEXTENSN.
 DR Hypothetical protein.

SQ SEQUENCE 256 AA; 27298 MW; 312E1A6C8F0F931C CRC64;

Query Match 1.5%; Score 8; DB 4; Length 256;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 379 GSLSEETP 386
 |||||
 DB 154 GSLSEETP 161

RESULT 16

O96IK7 PRELIMINARY; PRT; 256 AA.
 AC O96IK7;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Similar to RIKEN cDNA 1110012J22 gene.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
 NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Tissue=Skin;
 RA Strausberg R.;
 RL Submitted (MAY-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL, BC007416; AAH07416.1; -
 DR InterPro; IPR002965; P_Rich_extensn.
 DR PRINTS; PRO1217; PRICHEXTENSN.
 SQ SEQUENCE 256 AA; 27409 MW; A7D6794DA6385271 CRC64;

Query Match 1.5%; Score 8; DB 4; Length 256;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 379 GSLSEETP 386
 |||||
 DB 154 GSLSEETP 161

RESULT 17

O9DIF4 PRELIMINARY; PRT; 257 AA.
 AC O9DIF4;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE 1110012J22RIK protein.
 GN 1110012J22RIK.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Embryo;
 RC MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Kawata T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamazaki I.,
 RA Saito T., Okazaki Y., Gojibori T., Bono H., Kanakawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Baturov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
 RA Schiml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bona M.F.,
 RA Brownstein M.J., Bull C., Fletcher C., Fujita N., Gariboldi M.,
 RA Gustinich S., Hall D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momberts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,

RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wyszewski A., Yoshida K., Haegawa Y., Kawaji H., Kohlschütter S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection";
 RL Nature 403:685-690(2001).
 DR EMBL: AK003638; BAB22905.1; -;
 DR MGI: 1914855; 1110012J22R1K.
 DR InterPro: IPR002965; P rich extenstn.
 DR PRINTS: PR01217; PRICHECKTENS.
 SQ SEQUENCE 257 AA; 27483 MW; 4BFCC630DBA5EC CRC64;

Query Match 1.5%; Score 8; DB 11; Length 257;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 379 GSLSETP 386
 Db 155 GSLSETP 162

RESULT 18

O9EMP8 PRELIMINARY; PRT; 284 AA.
 AC O9EMP8;
 DT 01-MAR-2001 (TREMBLrel. 16, Created)
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Putative transport system integral membrane protein.
 GN SC07679 OR SC4C2.14.
 OS Streptomyces coelicolor.
 OC Bacteria; Actinobacteria; Actinomycetales; Actinomycetaceae;
 OC Streptomycinae; Streptomycetaceae; Streptomycetes.
 OX NCBI_TaxID=1902;

RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=A3(2) / M145;
 RX MEDLINE=2196410; PubMed=12000953;
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kleeer T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorek A., Woodward J., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 DR EMBL: AL939132; CAC17496.1; -;
 DR InterPro: IPR000515; BPD_transp.
 DR Pfam: PF00528; BPD_transp; 1.
 KW Complete proteome.
 SQ SEQUENCE 284 AA; 28595 MW; A4C45F8E795E6F83 CRC64;

Query Match 1.5%; Score 8; DB 16; Length 284;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 466 LLLALLG 473
 Db 34 LLLALLG 41

RESULT 19

ID P79458 PRELIMINARY; PRT; 346 AA.
 AC P79458;
 DT 01-MAY-1997 (TREMBLrel. 03, Created)
 DT 01-MAY-1997 (TREMBLrel. 03, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE MHC class IA alpha chain.

OS Ambystoma mexicanum (Axolotl).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Caudata; Salamandridae; Ambystomidae;
 OC Ambystoma.
 OX NCBI_TaxID=8296;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=97190244; PubMed=9038100;
 RA Sammut B., Laurens V., Tounetier A.;
 RT "Isolation of Mhc class I cDNAs from the axolotl Ambystoma
 mexicanum";
 RL Immunogenetics 45:285-294(1997).
 CC -I- FUNCTION: INVOLVED IN THE PRESENTATION OF FOREIGN ANTIGENS TO THE
 CC IMMUNE SYSTEM (BY SIMILARITY).
 CC -I- SUBUNIT: DIMER OF ALPHA CHAIN AND A BETA CHAIN (BETA-2-
 CC MICROGLOBULIN) (BY SIMILARITY).
 DR EMBL: U83137; AAC60108.1; -;
 DR HSSP: P01887; ICD1.
 DR InterPro: IPR007110; I9-1like.
 DR InterPro: IPR003597; I9_c1.
 DR InterPro: IPR003006; I9_MHC.
 DR InterPro: IPR001039; MHC_I.
 DR Pfam: PF00047; I9; 1.
 DR Pfam: PF00129; MHC_I; 1.
 DR PRINTS: PR01638; MHCCLASSI.
 DR ProDom: PD000050; MHC_I; 1.
 DR SMART: SMO0407; IGC1; 1.
 DR PROSITE: PS50835; I9-LIKE; 1.
 DR PROSITE: PS00290; I9_MHC; 1.
 KW Glycoprotein; Transmembrane.
 SQ SEQUENCE 346 AA; 39057 MW; B659876CEA15954 CRC64;

Query Match 1.5%; Score 8; DB 7; Length 346;
 Best Local Similarity 100.0%; Pred. No. 24;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 467 LLLALLG 474
 Db 6 LLLALLG 13

RESULT 20

O8YE66 PRELIMINARY; PRT; 383 AA.
 AC O8YE66;
 DT 01-MAR-2002 (TREMBLrel. 20, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Benzoyl membrane transport protein.
 GN BMR12012.
 OS Brucella melitensis.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Brucellaceae; Brucella.
 OX NCBI_TaxID=29459;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=15M / ATCC 23456 / Biotype 1;
 RX MEDLINE=20020109; PubMed=11756688;
 RA DelVecchio V.G., Kapatalai V., Redkar R.J., Patra G., Mujer C., Los T.,
 RA Ivanova N., Anderson I., Bhattacharya A., Lykide A., Reznik G.,
 RA Jablonski L., Larsen N., D'Souza M., Bernal A., Mazur M., Goldstein E.,
 RA Selkov E., Elizer P.H., Hagius S., O'Callaghan D., Leeseon J.-J.,
 RA Haselkorn R., Kyriades N., Overbeek R.;
 RT "The genome sequence of the facultative intracellular pathogen
 Brucella melitensis";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:443-448(2002).
 DR EMBL: AE009634; AAL53193.1; -;
 DR InterPro: IPR004711; Bene.
 DR Pfam: PF03594; Bene; 1.
 DR TIGRFAMs: TIGR00843; Bene; 1.
 KW Complete proteome.
 SQ SEQUENCE 383 AA; 39296 MW; 7920480702F49F3E CRC64;

Query Match 1.5%; Score 8; DB 16; Length 383;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 456 ALIAGLAV 463
 |||||
 Db 364 ALIAGLAV 371

RESULT 21

Q8FXX9 PRELIMINARY; PRT; 383 AA.

DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Benzocate transport protein, putative.
 GN BR2115.
 OS Brucella suis.
 OC Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
 OC Brucellaceae; Brucella.
 OX NCBI_TaxID=29461;
 RN [1]

SEQUENCE FROM N.A.
 RC STRAIN=1330 / Biovar 1;
 RX MEDLINE=22247741; PubMed=12271122;
 RA Paulsen I.T., Seshadri R., Nelson K.E., Eisen J.A., Heidelberg J.F.,
 Read T.D., Dodson R.J., Umayam L., Brinkac L.M., Beanan M.J.,
 Daugherty S.C., Debroy R.T., Durkin A.S., Kolonay J.F., Madupu R.,
 Nelson W.C., Ayodeji B., Kraul M., Shetty J., Malek J., Van Aken S.E.,
 Riedmuller S., Treitel H., Gill S.R., White O., Salzberg S.L.,
 Hoover D.L., Lindler L.E., Halling S.M., Boyle S.M., Fraser C.M.,
 RT "The Brucella suis genome reveals fundamental similarities between
 animal and plant pathogens and symbionts."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:13148-13153(2002).
 DR EMBL; AE014498; AAN31005.1; -.
 KW TIGR; BR2115; -.
 SO Complete proteome.
 QY SEQUENCE 383 AA; 39371 MW; F7A9D502B71ED2F7 CRC64;

Query Match 1.5%; Score 8; DB 16; Length 383;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 456 ALIAGLAV 463
 |||||
 Db 364 ALIAGLAV 371

RESULT 22

Q8YYS0 PRELIMINARY; PRT; 396 AA.

AC Q8YYS0;
 DT 01-MAR-2002 (TREMBlrel. 20, Created)
 DT 01-MAR-2002 (TREMBlrel. 20, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Hypothetical protein AI10776.
 GN ALR0776.
 OS Anabaena sp. (strain PCC 7120).
 OC Bacteria; Cyanobacteria; Nostocales; Nostocaceae; Nostoc.
 OX NCBI_TaxID=103690;
 RN [1]

SEQUENCE FROM N.A.
 RC MEDLINE=21595285; PubMed=11759440;
 RA Kaneko T., Nakamura Y., Wolk C.P., Kuritz T., Sasamoto S.,
 Watanabe A., Iriguchi M., Ishikawa A., Kawashima K., Kimura T.,
 Kishida Y., Kohara M., Matsumoto M., Matsuno A., Muraki A.,
 Nakazaki N., Shimo S., Sugimoto M., Takazawa M., Yamada M.,
 Yasuda M., Tabata S.;
 RT "Complete genomic sequence of the filamentous nitrogen-fixing
 cyanobacterium Anabaena sp. strain PCC 7120."
 RL DNA Res. 8:205-213(2001).
 DR EMBL; AP003583; BAB72733.1; -.

DR InterPro; IPR001173; Glyco trans 2.
 DR Pfam; PF00535; Glycos transf 2; 1.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 396 AA; 44424 MW; BEB3E0B541D39CA CRC64;

Query Match 1.5%; Score 8; DB 16; Length 396;
 Best Local Similarity 100.0%; Pred. No. 27;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 GLSSSTRS 29
 |||||
 Db 266 GLSSSTRS 273

RESULT 23

Q96QH1 PRELIMINARY; PRT; 437 AA.

AC Q96QH1;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE NBI glycoprotein precursor.
 GN NBI.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]

SEQUENCE FROM N.A.
 RX MEDLINE=21357611; PubMed=11465086;
 RA Kiesel K., Santoso S., Hofmann C., Stroncek D., Bux J.,
 RT "Molecular basis of the neutrophil glycoprotein NBI (CD177) involved
 in the pathogenesis of immunoneutropenia and transfusion reactions."
 RL Eur. J. Immunol. 31:1301-1309(2001).
 DR EMBL; AJ290452; CAC44458.1; -.
 KW Signal.
 FT SIGNAL.
 FT CHAIN.
 SQ SEQUENCE 437 AA; 46335 MW; 823DAF784986A42F CRC64;

Query Match 1.5%; Score 8; DB 4; Length 437;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 466 VLLTALLG 473
 |||||
 Db 4 VLLTALLG 11

RESULT 24

Q8N6Q3 PRELIMINARY; PRT; 437 AA.

AC Q8N6Q3;
 DT 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-OCT-2002 (TREMBlrel. 22, Last annotation update)
 DE Polychemia rubra vera 1, cell surface receptor.
 GN Homo sapiens (Human).
 OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]

SEQUENCE FROM N.A.
 RC TISSUE=Colon, and Kidney;
 RA Strussberg R.;
 RT Submitted (May-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC029167; AAH29167.1; -.
 KW Receptor.
 SQ SEQUENCE 437 AA; 46419 MW; CC4DAECLIE7CFC4B CRC64;

Query Match 1.5%; Score 8; DB 4; Length 437;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy      466 VLLALLG 473
      |||||
Db      4 VLLALLG 11

RESULT 25
Q9HDA5 PRELIMINARY; PRT; 437 AA.
ID Q9HDA5;
AC Q9HDA5;
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
DT 01-MAR-2001 (TRENBLrel. 16, Last sequence update)
GN Cell surface receptor.
DE PRV1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Temerinac S., Klippel S., Roeder S., Luebbert M., Lange W., Azemar M.,
RA Meinhardt G., Pahl H.L.;
RT "Cloning of PRV-1, a novel member of the UPAR receptor superfamily.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF146747; AAC00895.1; -
KW Receptor.
SQ SEQUENCE 437 AA; 46363 MW; 3D40648723E43B65 CRC64;

Query Match 1.5%; Score 8; DB 4; Length 437;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      466 VLLALLG 473
      |||||
Db      4 VLLALLG 11

RESULT 26
Q8ZFW8 PRELIMINARY; PRT; 463 AA.
ID Q8ZFW8;
AC Q8ZFW8;
DT 01-MAR-2002 (TRENBLrel. 20, Created)
DT 01-MAR-2002 (TRENBLrel. 20, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Amino acid permease (Putative symporter).
GN YPO1557 OR Y2612.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=CO-92 / Biovar Orientalis;
RC MEDLINE=21470413; PubMed=11586360;
RA Parkhill J., Wren B.W., Thomson N.R.,
RA Prentice M.B., Sebatia M., James K.D., Churcher C., Mungall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cereno-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Feltwell T., Hamlin N., Holtroyd S., Jagsels K., Karlyshev A.V.,
RA Leather S., Moulé S., Oyston P.C.F., Quail M., Rutherford A.K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrett B.G.;
RT "Genome sequence of Yersinia pestis, the causative agent of plague.";
RL Nature 413:523-527(2001).
RN [2]
RP SEQUENCE FROM N.A.
RA STRAIN=KIMS / Biovar Mediaevalis;
RC MEDLINE=22137863; PubMed=12142430;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Niles W.L., Mason J.S., Blattner F.R.,
RA Perry R.D.;

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RT      "Genome sequence of Yersinia pestis KIM.";
RL J. Bacteriol. 184:4601-4611(2002).
DR EMBL; AJ414149; CAC90379.1; -
DR EMBL; AB013863; AAM6167.1; -
DR InterPro; IPR002293; AA/rel_permease1.
DR InterPro; IPR004841; Permease.
DR Pfam; PF00324; aa_permeases; 1.
KW Complete proteome.
SQ SEQUENCE 463 AA; 50183 MW; D0BD3747147F9226 CRC64;

Query Match 1.5%; Score 8; DB 16; Length 463;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      380 SLSETPN 387
      |||||
Db      230 SLSETPN 237

RESULT 27
Q8G7P9 PRELIMINARY; PRT; 468 AA.
ID Q8G7P9;
AC Q8G7P9;
DT 01-MAR-2003 (TRENBLrel. 23, Created)
DT 01-MAR-2003 (TRENBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Hypothetical membrane protein with unknown function.
GN B10198.
OS Bifidobacterium longum.
OC Bacteria; Actinobacteria; Actinobacteridae; Bifidobacteriales;
OC Bifidobacteriaceae; Bifidobacterium.
OX NCBI_TaxID=216816;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=NCC 2705;
RC MEDLINE=22294977; PubMed=12381787;
RA Schell M.A., Karmilantzu M., Snel B., Vilanova D., Berger B.,
RA Pessi G., Zehren M.-C., Desiere F., Bork P., Delley M.,
RA Pridmore R.D., Arigoni F.;
RT "The genome sequence of Bifidobacterium longum reflects its adaptation
RT to the human gastrointestinal tract.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:14422-14427(2002).
DR EMBL; AE014637; AAN24052.1; -
KW Hypothetical protein; Complete proteome.
SQ SEQUENCE 468 AA; 49486 MW; 24D405F0F6530A1 CRC64;

Query Match 1.5%; Score 8; DB 16; Length 468;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy      462 AVGGVLL 469
      |||||
Db      328 AVGGVLL 335

RESULT 28
Q8JZ36 PRELIMINARY; PRT; 476 AA.
ID Q8JZ36;
AC Q8JZ36;
DT 01-OCT-2002 (TRENBLrel. 22, Created)
DT 01-OCT-2002 (TRENBLrel. 22, Last sequence update)
DT 01-MAR-2003 (TRENBLrel. 23, Last annotation update)
DE Polypeptide (Fragment).
OS West Nile virus (WNV).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus.
OX NCBI_TaxID=11082;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=B956;
RC MEDLINE=21992730; PubMed=11996693;
RA Briese T., Rambaut A., Pattnayek M., Bishara J., Weinberger M.,
RA Pflük S., Lipkin W.I.;

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RT "Phylogenetic analysis of a human isolate from the 2000 Israel West
RT Nile virus epidemic."
RL EMBL; AF394221; AAM21944.1; -.
DR InterPro; IPR000336; Flavi_glycoprote.
DR InterPro; IPR001157; Flavi_NSI.
DR Pfam; PF00869; Flavi_glycoprote; 1.
DR Pfam; PF02832; Flavi_glycop_C; 1.
DR Pfam; PF00948; Flavi_NSI; 1.
DR ProDom; PD001556; Flavi_glycoprote; 1.
DR ProDom; PD001496; Flavi_NSI; 1.
FT NON_TER 1
FT CHAIN 1 >414 ENVELOPE GLYCOPROTEIN E.
FT NON_TER 415 >476 NONSTRUCTURAL PROTEIN 1.
FT NON_TER 476
SQ SEQUENCE 476 AA; 51129 MW; D27018C7E6FE15F CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 32; Length 476;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 461 LAVGVLL 468
DB 399 LAVGVLL 406

RESULT 29
Q9WI84 PRELIMINARY; PRT; 501 AA.
ID Q9WI84;
AC Q9WI84;
DT 01-NOV-1999 (TREMBLrel. 12, Created)
DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN E.
OS West Nile virus (WN).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus.
OX NCB1_TaxID=11082;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=KN3829;
RA Miller B.R., Nasri R.S., Godsey M.S., Savage H.M., Luewama J.J.,
RA Lanciotti R.S., Peters C.J., Gubler D.J.;
RT "First field evidence for natural vertical transmission of West Nile
RT virus in Culex univittatus mosquitoes from Rift Valley Province,
RT Kenya."
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF146082; AAD31720.1; -.
DR HSP; P14336; ISVB.
DR InterPro; IPR000336; Flavi_glycoprote.
DR Pfam; PF00869; Flavi_glycoprote; 1.
DR Pfam; PF02832; Flavi_glycop_C; 1.
DR ProDom; PD001556; Flavi_glycoprote; 1.
FT NON_TER 1
FT NON_TER 501
FT NON_TER 501
SQ SEQUENCE 501 AA; 53622 MW; D2A9C827F71C00D5 CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 33; Length 501;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 461 LAVGVLL 468
DB 486 LAVGVLL 493

RESULT 30
Q9IMB8 PRELIMINARY; PRT; 501 AA.
ID Q9IMB8;
AC Q9IMB8;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)

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DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS West Nile virus (WN).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus.
OX NCB1_TaxID=11082;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3000622;
RA Ebel G.D., Dupuis A.P., II, Ngo K., Nicholas D., Kauffman E.B.,
RA Jones S.A., Young D., Maffei J., Shi P.-Y., Bernard K., Kramer L.D.;
RT "Partial Genetic Characterization of West Nile Virus Strains, New York
RT State, 2000."
RL Emerging Infect. Dis. 7:0-0(2001).
DR EMBL; AF346313; AAK62760.1; -.
DR InterPro; IPR000336; Flavi_glycoprote.
DR Pfam; PF00869; Flavi_glycoprote; 1.
DR Pfam; PF02832; Flavi_glycop_C; 1.
DR ProDom; PD001556; Flavi_glycoprote; 1.
FT NON_TER 1
FT NON_TER 501
FT NON_TER 501
SQ SEQUENCE 501 AA; 53620 MW; FFAF78F09DCD089B CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 33; Length 501;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 461 LAVGVLL 468
DB 486 LAVGVLL 493

RESULT 31
Q9IMC1 PRELIMINARY; PRT; 501 AA.
ID Q9IMC1;
AC Q9IMC1;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS West Nile virus (WN).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus.
OX NCB1_TaxID=11082;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3000365;
RA Ebel G.D., Dupuis A.P., II, Ngo K., Nicholas D., Kauffman E.B.,
RA Jones S.A., Young D., Maffei J., Shi P.-Y., Bernard K., Kramer L.D.;
RT "Partial Genetic Characterization of West Nile Virus Strains, New York
RT State, 2000."
RL Emerging Infect. Dis. 7:0-0(2001).
DR EMBL; AF346310; AAK62757.1; -.
DR InterPro; IPR000336; Flavi_glycoprote.
DR Pfam; PF00869; Flavi_glycoprote; 1.
DR Pfam; PF02832; Flavi_glycop_C; 1.
DR ProDom; PD001556; Flavi_glycoprote; 1.
FT NON_TER 1
FT NON_TER 501
FT NON_TER 501
SQ SEQUENCE 501 AA; 53620 MW; FFAF78F09DCD089B CRC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 33; Length 501;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 461 LAVGVLL 468
DB 486 LAVGVLL 493

RESULT 32

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Q91MB6 PRELIMINARY; PRT; 501 AA.
AC Q91MB6;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS West Nile virus (WN).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus.
OX NCBI_TaxID=11082;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=00-2741;
RA Ebel G.D., Dupuis A.P. II, Ngo K., Nicholas D., Kauffman E.B.,
RA Jones S.A., Young D., Maffei J., Shi P.-Y., Bernard K., Kramer L.D.;
RT "Partial Genetic Characterization of West Nile Virus Strains, New York
RT State, 2000."
RL Emerging Infect. Dis. 7:0-0(2001).
DR EMBL; AF346315; AAK62762.1; -
DR InterPro; IPR000336; Flavi_glycoprote.
DR Pfam; PF00869; Flavi_glycoprot; 1.
DR Pfam; PF02832; Flavi_glycoprot; 1.
DR ProDom; PD001556; Flavi_glycoprote; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 501 AA; 53620 MW; FF4F78F09DCD089B CRC64;

Query Match 1.5%; Score 8; DB 12; Length 501;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 461 LAVGVLL 468
Db 486 LAVGVLL 493

RESULT 33
Q91MB5 PRELIMINARY; PRT; 501 AA.
AC Q91MB5;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS West Nile virus (WN).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus.
OX NCBI_TaxID=11082;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3000259;
RA Ebel G.D., Dupuis A.P. II, Ngo K., Nicholas D., Kauffman E.B.,
RA Jones S.A., Young D., Maffei J., Shi P.-Y., Bernard K., Kramer L.D.;
RT "Partial Genetic Characterization of West Nile Virus Strains, New York
RT State, 2000."
RL Emerging Infect. Dis. 7:0-0(2001).
DR EMBL; AF346316; AAK62763.1; -
DR InterPro; IPR000336; Flavi_glycoprote.
DR Pfam; PF00869; Flavi_glycoprot; 1.
DR Pfam; PF02832; Flavi_glycoprot; 1.
DR ProDom; PD001556; Flavi_glycoprote; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 501 AA; 53620 MW; FF4F78F09DCD089B CRC64;

Query Match 1.5%; Score 8; DB 12; Length 501;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 461 LAVGVLL 468

Db 486 LAVGVLL 493

RESULT 34
Q91MB2 PRELIMINARY; PRT; 501 AA.
AC Q91MB2;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS West Nile virus (WN).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus.
OX NCBI_TaxID=11082;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=00-3282;
RA Ebel G.D., Dupuis A.P. II, Ngo K., Nicholas D., Kauffman E.B.,
RA Jones S.A., Young D., Maffei J., Shi P.-Y., Bernard K., Kramer L.D.;
RT "Partial Genetic Characterization of West Nile Virus Strains, New York
RT State, 2000."
RL Emerging Infect. Dis. 7:0-0(2001).
DR EMBL; AF346319; AAK62766.1; -
DR InterPro; IPR000336; Flavi_glycoprote.
DR Pfam; PF00869; Flavi_glycoprot; 1.
DR Pfam; PF02832; Flavi_glycoprot; 1.
DR ProDom; PD001556; Flavi_glycoprote; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 501 AA; 53620 MW; FF4F78F09DCD089B CRC64;

Query Match 1.5%; Score 8; DB 12; Length 501;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 461 LAVGVLL 468
Db 486 LAVGVLL 493

RESULT 35
Q91MC2 PRELIMINARY; PRT; 501 AA.
AC Q91MC2;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
DE Envelope glycoprotein (Fragment).
GN ENV.
OS West Nile virus (WN).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
OC Flavivirus.
OX NCBI_TaxID=11082;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=3000017;
RA Ebel G.D., Dupuis A.P. II, Ngo K., Nicholas D., Kauffman E.B.,
RA Jones S.A., Young D., Maffei J., Shi P.-Y., Bernard K., Kramer L.D.;
RT "Partial Genetic Characterization of West Nile Virus Strains, New York
RT State, 2000."
RL Emerging Infect. Dis. 7:0-0(2001).
DR EMBL; AF346309; AAK62756.1; -
DR InterPro; IPR000336; Flavi_glycoprote.
DR Pfam; PF00869; Flavi_glycoprot; 1.
DR Pfam; PF02832; Flavi_glycoprot; 1.
DR ProDom; PD001556; Flavi_glycoprote; 1.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 501 AA; 53620 MW; FF4F78F09DCD089B CRC64;

Query Match 1.5%; Score 8; DB 12; Length 501;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 461 LAVGVL 468
 |||||
 DB 486 LAVGVL 493

RESULT 36

08JTB5 PRELIMINARY; PRT; 501 AA.

AC 08JTB5: 01-OCT-2002 (TREMBlrel. 22, Created)
 DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Envelope protein (Fragment).
 GN E.
 OS West Nile virus (WN).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Flavivirus.
 OX NCBI_TaxID=11082;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H-442;
 RX MEDLINE=2203387; PubMed=12036314;
 RA Beasley D.W., Li L., Suderman M.T., Barrett A.D.;
 RT "Mouse neuroinvasive phenotype of West Nile virus strains varies
 depending upon virus genotype.";
 RL Virology 296:17-23(2002).
 DR EMBL, AF459403; AAM70028.3; -
 DR InterPro; IPR000336; Flav1_glycoprote.
 DR Pfam; PF00869; Flav1_glycoprot; 1.
 DR Pfam; PF02832; Flav1_glycoprot; 1.
 DR Prodom; PD001556; Flav1_glycoprote; 1.
 FT NON_TER 1 1
 FT NON_TER 501 501
 SQ SEQUENCE 501 AA; 53659 MW; 9899F74E90347286 CRC64;

Query Match 1.5%; Score 8; DB 12; Length 501;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 461 LAVGVL 468
 |||||
 DB 486 LAVGVL 493

RESULT 37

091MB7 PRELIMINARY; PRT; 501 AA.

AC 091MB7: 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.
 OS West Nile virus (WN).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Flavivirus.
 OX NCBI_TaxID=11082;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=3000352;
 RA Ebel G.D., Dupuis A.P. II, Ngo K., Nicholas D., Kauffman E.B.,
 RA Jones S.A., Young D., Maffei J., Shi P.-Y., Bernard K., Kramer L.D.;
 RT "Partial Genetic Characterization of West Nile Virus Strains, New York
 State, 2000.";
 RL Emerging Infect. Dis. 7:0-0(2001).
 DR EMBL, AF346314; AAK62761.1; -
 DR InterPro; IPR000336; Flav1_glycoprote.
 DR Pfam; PF00869; Flav1_glycoprot; 1.
 DR Pfam; PF02832; Flav1_glycoprot; 1.

DR Prodom; PD001556; Flav1_glycoprote; 1.
 FT NON_TER 1 1
 FT NON_TER 501 501
 SQ SEQUENCE 501 AA; 53620 MW; FF4F78F09DCD089B CRC64;

Query Match 1.5%; Score 8; DB 12; Length 501;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 461 LAVGVL 468
 |||||
 DB 486 LAVGVL 493

RESULT 38

091MB4 PRELIMINARY; PRT; 501 AA.

AC 091MB4: 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.
 OS West Nile virus (WN).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Flavivirus.
 OX NCBI_TaxID=11082;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=00-824;
 RA Ebel G.D., Dupuis A.P. II, Ngo K., Nicholas D., Kauffman E.B.,
 RA Jones S.A., Young D., Maffei J., Shi P.-Y., Bernard K., Kramer L.D.;
 RT "Partial Genetic Characterization of West Nile Virus Strains, New York
 State, 2000.";
 RL Emerging Infect. Dis. 7:0-0(2001).
 DR EMBL, AF346317; AAK62764.1; -
 DR InterPro; IPR000336; Flav1_glycoprote.
 DR Pfam; PF00869; Flav1_glycoprot; 1.
 DR Pfam; PF02832; Flav1_glycoprot; 1.
 DR Prodom; PD001556; Flav1_glycoprote; 1.
 FT NON_TER 1 1
 FT NON_TER 501 501
 SQ SEQUENCE 501 AA; 53606 MW; FF4F78EE6C22089B CRC64;

Query Match 1.5%; Score 8; DB 12; Length 501;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 461 LAVGVL 468
 |||||
 DB 486 LAVGVL 493

RESULT 39

091MB3 PRELIMINARY; PRT; 501 AA.

AC 091MB3: 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.
 OS West Nile virus (WN).
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC Flavivirus.
 OX NCBI_TaxID=11082;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=00-3356;
 RA Ebel G.D., Dupuis A.P. II, Ngo K., Nicholas D., Kauffman E.B.,
 RA Jones S.A., Young D., Maffei J., Shi P.-Y., Bernard K., Kramer L.D.;
 RT "Partial Genetic Characterization of West Nile Virus Strains, New York
 State, 2000.";

RL Emerging Infect. Dis. 7:0-0(2001).
 DR EMBL; AF346318; AK62765.1; -
 DR InterPro; IPR000336; Flavi_glycoprote.
 DR Pfam; PF00869; Flavi_glycoprot; 1.
 DR Pfam; PF02832; Flavi_glycop_C; 1.
 DR ProDom; PD001556; Flavi_glycoprote; 1.
 FT NON_TER 1
 FT NON_TER 501
 SO SEQUENCE 501 AA; 53646 MW; FF58739D3C1D089B CRC64;

Query Match 1.5%; Score 8; DB 12; Length 501;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 461 LAVGCVLL 468
 |||||
 Db 486 LAVGCVLL 493

RESULT 40

Q91MCO PRELIMINARY; PRT; 501 AA.
 ID Q91MCO
 AC Q91MCO:
 DT 01-DEC-2001 (TrEMBLrel. 19, Created)
 DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
 DE Envelope glycoprotein (Fragment).
 GN ENV.
 OS West Nile virus (WN).
 CC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 CC Flavivirus.
 OX NCBI_TaxID=11082;
 OX RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=3000548;
 RA Edel G.D., Dupuis A.P. II, Ngo K., Nicholas D., Kaufman E.B.,
 RA Jones S.A., Young D., Maftel J., Shi P.-Y., Bernard K., Kramer L.D.;
 RT "Partial Genetic Characterization of West Nile Virus Strains, New York
 State, 2000."
 RL Emerging Infect. Dis. 7:0-0(2001).
 DR EMBL; AF346311; AK62758.1; -
 DR InterPro; IPR000336; Flavi_glycoprote.
 DR Pfam; PF00869; Flavi_glycoprot; 1.
 DR Pfam; PF02832; Flavi_glycop_C; 1.
 DR ProDom; PD001556; Flavi_glycoprote; 1.
 FT NON_TER 1
 FT NON_TER 501
 SO SEQUENCE 501 AA; 53620 MW; FF4F78F09DCD089B CRC64;

Query Match 1.5%; Score 8; DB 12; Length 501;
 Best Local Similarity 100.0%; Pred. No. 33;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 461 LAVGCVLL 468
 |||||
 Db 486 LAVGCVLL 493

Search completed: October 2, 2003, 16:05:55
 Job time : 140 secs

2000

DEC

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: October 2, 2003, 15:47:54 ; Search time 29 Seconds

(without alignment)
789.316 Million cell updates/sec

Title: US-10-039-770A-1

Perfect score: 2922

Sequence: 1 MGWGVQLVLVADCTIFA.....EAEENIQDGETHVEGDY 541

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5 ,

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents, AA:
1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCITUS_COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/backfilltest.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	417.5	14.3	628	1	US-08-257-073-9
2	120	4.1	1507	3	US-08-929-329-5
3	107.5	3.7	1104	2	US-08-327-832-5
4	107.5	3.7	1104	2	US-08-828-584-5
5	104	3.6	1255	2	US-08-484-438-8
6	104	3.6	1255	2	US-08-625-101-2
7	104	3.6	1255	2	US-08-356-786-2
8	103	3.5	1255	1	US-08-467-083-68
9	103	3.5	1255	1	US-08-414-417B-68
10	103	3.5	1255	2	US-08-486-348A-68
11	103	3.5	1255	2	US-08-468-545B-68
12	103	3.5	1255	3	US-08-466-680B-68
13	103	3.5	1255	4	US-09-527-487-2
14	102.5	3.5	934	3	US-08-929-329-6
15	101.5	3.5	467	3	US-09-086-483A-6
16	101.5	3.5	467	4	US-09-580-212-6
17	101.5	3.5	468	4	US-09-013-895A-2
18	101.5	3.5	468	4	US-09-565-918-2
19	101.5	3.5	468	4	US-09-448-868-2
20	101.5	3.5	468	4	US-10-039-785-1
21	97.5	3.3	571	4	US-09-216-393B-327
22	97	3.3	484	4	US-08-252-493C-9
23	97	3.3	484	3	US-09-276-197-9
24	96	3.3	652	4	US-09-310-463-4
25	96	3.3	652	4	US-08-842-248A-4
26	95.5	3.3	454	3	US-08-929-329-8
27	94.5	3.2	724	1	US-08-121-713D-62

28	94.5	3.2	724	1	US-08-835-268-62	Sequence 62, Appl
29	94.5	3.2	724	2	US-09-060-692-62	Sequence 62, Appl
30	94.5	3.2	724	3	US-08-833-391-62	Sequence 62, Appl
31	94.5	3.2	724	4	US-09-060-610-62	Sequence 62, Appl
32	94.5	3.2	724	5	PCT-US94-10151A-62	Sequence 62, Appl
33	94.5	3.2	702	4	US-09-107-532A-5645	Sequence 5645, Ap
34	93.5	3.2	593	5	PCT-US93-07923-11	Sequence 11, Appl
35	93.5	3.2	650	4	US-09-310-463-2	Sequence 2, Appl
36	93.5	3.2	650	3	US-08-842-248A-2	Sequence 22, Appl
37	93.5	3.2	651	4	US-08-985-950-22	Sequence 22, Appl
38	93.5	3.2	651	4	US-09-546-049-22	Sequence 22, Appl
39	93.5	3.2	766	1	US-08-230-491A-3	Sequence 3, Appl
40	93.5	3.2	766	1	US-08-619-280A-3	Sequence 3, Appl
41	93.5	3.2	766	2	US-08-940-391-3	Sequence 1, Appl
42	93.5	3.2	766	4	US-09-794-236-1	Sequence 6, Appl
43	93.5	3.2	766	4	US-10-002-593-6	Sequence 6, Appl
44	93	3.2	487	4	US-09-685-462-8	Sequence 2, Appl
45	92.5	3.2	611	3	US-09-370-807-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-08-257-073-9
; Sequence 9, Application US/08257073
; Patent No. 5766597
; GENERAL INFORMATION:
; APPLICANT: Paoletti, Enzo
; APPLICANT: de Talamo, Charles
; APPLICANT: Tine, John A.
; TITLE OF INVENTION: MALARIA RECOMBINANT POXVIRUS VACCINE
; NUMBER OF SEQUENCES: 143
; CORRESPONDENCE ADDRESS:
; ADDRESSER: Curtiss, Morris & Safford, P.C.
; STREET: 530 Fifth Avenue, 25th Floor
; CITY: New York
; STATE: New York
; COUNTRY: UNITED STATES OF AMERICA
; ZIP: 10036
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/257,073
; FILING DATE: 09-JUN-1994
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/075,783
; FILING DATE: 11-JUN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/852,305
; FILING DATE: 18-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/672,183
; FILING DATE: 20-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Frommer, William S.
; REGISTRATION NUMBER: 25,506
; REFERENCE/DOCKET NUMBER: 454310-2570
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 840-3333
; TELEFAX: (212) 840-0712
; TELE: 425066 CURTIS
; INFORMATION FOR SEQ ID NO: 9:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 628 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide

FRAGMENT TYPE: internal
US-08-257-073-9

Query Match 14.3%; Score 417.5; DB 1; Length 628;
Best Local Similarity 26.7%; Pred. No. 5.4e-33;
Matches 152; Conservative 86; Mismatches 214; Indels 117; Gaps 26;

QY 41 GNPFAANVEMKTFMERFNLTHHOSGIYVDLQGDVEVDTLYREBAGLCPIWKGKHELOQ 100
DB 107 GNPW-----TEYMAKYDIEVHSGGIRVDLGEDEAVAGTORLPSCGCPVHGKILLEN 160
QY 101 PDRLPYRNPLFEDVTEKEKYGSGNPLPGCFNLNFTPSGQRISSPPE-----LLEKSN 156
DB 161 SN-----TFLTPVATGNOYLKD-----CGFAF-----PTEPLMSPTLDEMHFVKDKY 207
QY 157 IKASTDLCRCAEFAKTYAMDKNATKTYRPFYVDSKKRLCHILYVSMQMEGKYSV 216
DB 208 VGNLDELTLCSHHAQNMII--PNDKNSNYKYPAVYDDKDKCHILYIAAQENNGRCYN- 264
QY 217 KGEPRDLTWYCKPKRKSTVENHHLIYGSAVGEN--PDAFISCPNQAALRGVFGVKKGR 275
DB 265 KDESRRNSMFCRPAKDISFQNY-----TYSKNVVDNMEKVCPRKNLQNAKFGLVDSN 319
QY 276 CLDYELTD-TVIERVESKACQCVKTFENDGVASDQPHYTP----- 315
DB 320 CEDIHVNEFPAIDFE-----CNKLVFELS--ASDQPKYEGHLDYEKIKGFKNKAS 373
QY 316 -LTSQASWMDMP--LHOSDQPHSGGVGRNYGYVDTTGEGKCALSDQVPCLVSDSA 372
DB 374 MKSRIRKSAFLPTGAPKADRYKSHGKGYMGNVTEIQ--KCEIFNVKPTCLINNSY 430
QY 373 VSYTAGSISETPNF-----IIPSNPSTPTPTPEALQ--CTIDK 411
DB 431 IATTLSPHTEVNNPSCSLYKDEIMKEIERESKRIKLNDNDGANKTMDLQEFLLSDK 490
QY 412 FPDSE-GACDVO-----ACKRQKTSVGGQIOSTVDCIA-----DEQNECGSN----- 454
DB 491 --DSLKRCPDEPMVNSNTRCFVCKVERAEVTSNNEVVVAEYKDEYADLPEHKPTMD 548
QY 455 --TALIAGLAVGVLLALLGGGCPYAKRLDRNKQVAAHHEHFOSDRGARKRPSDL 512
DB 549 KKKIILIASAAVAVALATILM--VLYLKR--KGAKEYDKDDEPODYGKNSR--NDEN 600
QY 513 QEAEPSPMEAEENITEQDSETHVMEGDY 541
DB 601 LDPEASFWGEEK--RASHTPVLMKEFY 626

RESULT 2
US-08-929-329-5
Sequence 5, Application US/08929329
Patent No. 6120770
GENERAL INFORMATION:
APPLICANT: Adams, John H
APPLICANT: Dalton, John P
APPLICANT: Kappe, Stefan
TITLE OF INVENTION: Plasmidum Proteins Useful for Preparing
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:
ADDRESSEE: Barnes & Thornburg
STREET: 11 S Meridian
CITY: Indianapolis
STATE: Indiana
COUNTRY: USA
ZIP: 46204
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/929,329

FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Breen, John P
REGISTRATION NUMBER: 38,833
REFERENCE/DOCKET NUMBER: 835910-28685
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 231-7745
TELEFAX: (317) 231-7433
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1507 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Plasmidum yeell1

US-08-929-329-5
Query Match 4.1%; Score 120; DB 3; Length 1507;
Best Local Similarity 18.8%; Pred. No. 0.021;
Matches 87; Conservative 52; Mismatches 151; Indels 172; Gaps 21;

QY 34 TLASSTGNPQAVNEMKTFMERFNLTHH-----OSGIYVDLQGDKEVD--- 78
DB 18 TFSIRADNP-----QDEFMDRFDILNNHVNIKMTNSGSLAQNLKFDIYDEDNISKL 71
QY 79 -----GTLYREBAGLCPIWKGK----- 96
DB 72 NSLENARLCPNNEKGNIR--GSCPDKTFMSMDLDKDEYSEDFLNEISLGLNKKLLI 128
QY 97 ELQOPDRI-----PYRNPLFEDVPTKEY-----KQSGNPLPGGFNL 133
DB 129 DVEIPVNSGLAMYGQGFANCPYDKNHVNDIKNEKEYDMCPKFSNKO----- 178
QY 134 NFVTPSGORISPFMELEKXSNIKA--STDLCRCAEFAKTYAMDKNATKTYRY--- 187
DB 179 ----ISTRIKYP--LISKTYTFSHGLGRLGASNTBPLATNPLENYTOKMRPKL 231
QY 188 -----PFVYDSKKRLCHILYVSMQMEGKYSVK 217
DB 232 VETLEDGSIYHCGICPCFRDFOKCKFRDLVARNHKTKECIIIGTH---EKKTTVCN 287
QY 218 GEPDPLTWYCKPKRKSTVENHHLIYGSAVGENPDAFISK--PQOALRGYFGV--WKKG 274
DB 288 SDNSRRNRCRFSIHK--EKGDMWTYASFTL--RPD--YETKCPRRYPPLNNSSEFGYFNVYTG 343
QY 275 RCLDVTETLDTVIERVESKACQCVKTFENDGVASDQPHYPLVTSQASWMDMPHOSDQ 334
DB 344 NCSEPTKLYD--NSVTSFNECIEKLP--NFVYAEDEP--EKRNMYLMGVAVLNKQK 397
QY 335 HSGGVGRNYGYVDTTGEGKCALSDQVPCLVSDSAVSYT 376
DB 398 NS-----MNDLGVCALLKEKPTCVLKKQNYYSFT 426

RESULT 3
US-08-327-832-5
Sequence 5, Application US/08327832
Patent No. 5840832
GENERAL INFORMATION:
APPLICANT: Ono, Santa J.
APPLICANT: Strominger, Jack L.
TITLE OF INVENTION: Transcription Factor Regulating MHC
TITLE OF INVENTION: Expression, cDNA and Genomic Clones Encoding Same and
TITLE OF INVENTION: Retroviral Expression Constructs Thereof
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, N.W.

CITY: Washington, D.C.
STATE: District of Columbia
COUNTRY: U.S.A.
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/327,832
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Posorske, Laurence H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 1107,46362
TELECOMMUNICATION INFORMATION:
TELEPHONE: 20-2 508-9153
TELEFAX: 202 508-9299
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1104 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-327-832-5

Query Match 3.7%; Score 107.5; DB 2; Length 1104;
Best Local Similarity 19.7%; Pred. No. 0.23;
Matches 103; Conservative 61; Mismatches 159; Indels 199; Gaps 29;

QY 85 PAGLCPIWGKHIELQDPRLPYRNFLVDVTEKEVYKSGNPLPGGFNLNFTVPSGORIS 144
DB 579 PCGOTPL-SQLLEIGSSS-----KRTCDVPVPSCG-KVCGKPLPCG-SLDPIHCEKICH 630
QY 145 PFMELLEKNKSNIKASTDLGRCAEFAPKTVMAD--KNNKATKYRYPFYVD--SKKRL 197
DB 631 EGDGVPVRSVISC-----RC--SPRTKELPCTSLKSEDAF-----FMCDKRCNKKRL 677
QY 198 CHILYVMQMLEGKKYCSVKGEPPDLTWYCFKPKKSTENHLLYGSAYVGENDAFISK 257
DB 678 C-----GHHKNE-----IC-----CVDKEH-----K 694
QY 258 CPNOLRGYRFGVWK-----KGRCLDYTELDTVIEBVESKACQWTFENDGVASDOP 311
DB 695 CPLNGKRLKGLRCEBPCRHGNC-----QTCWQASFDE----- 729
QY 312 HTYPLTSQASWMDWP-----LHOSDOP--HSGG----- 338
DB 730 ---LTHCGASVITYRPGCTRPPECTGTQCARVHECDHPYHSGHSEKCPCTFLTK 785
QY 339 --VGR---NYGYYVDIT-----GEGKCALSDOVPCLVSDAASVYTAAGS 380
DB 786 WCMGKHEFRSNIPCHLVDISGLPCSATLPCGMKHCQRLCHKGECLVDE----- 834
QY 381 LSEETPNFIISNSVTPPTETALQCTADKFPDSFGACDVQACK-RKSTSCVGGQIOST 439
DB 835 -----PCKPCTTPRADCGHPCMAPCHTSS--PCPYTACKAYVELQCEGGR-RKE 881
QY 440 SVDCTADEQNECGSNTALAGLAVGVLLALLGGGCFYAKRLDRNKGVQAAHHNEHFQS 499
DB 882 MVIC-----SEASTYQRIAAISMASKITDMQLGGSVEISKLITK-KEVHQARLECDDEC 935
QY 500 DRGAKKRPSPD--LMQEAEP-----SFWDKAENIEOD 530
DB 936 SALERKKLAEAFHISEDSPFNIRSSGSKFSDSLKEDARD 977

RESULT 4
US-08-828-584-5
Sequence 5, Application US/08828584
Patent No. 5908762

GENERAL INFORMATION:
APPLICANT: Ono, Santa J.
APPLICANT: Strominger, Jack L.
TITLE OF INVENTION: Transcription Factor Regulating MHC
Expression, cDNA and Genomic Clones Encoding Same and
TITLE OF INVENTION: Retroviral Expression Constructs Thereof
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Banner, Birch, McKie & Beckett
STREET: 1001 G Street, N.W.
CITY: Washington, D.C.
STATE: District of Columbia
COUNTRY: U.S.A.
ZIP: 20001
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/828,584
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Posorske, Laurence H.
REGISTRATION NUMBER: 34,698
REFERENCE/DOCKET NUMBER: 1107,46362
TELECOMMUNICATION INFORMATION:
TELEPHONE: 20-2 508-9153
TELEFAX: 202 508-9299
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1104 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-828-584-5

Query Match 3.7%; Score 107.5; DB 2; Length 1104;
Best Local Similarity 19.7%; Pred. No. 0.23;
Matches 103; Conservative 61; Mismatches 159; Indels 199; Gaps 29;

QY 85 PAGLCPIWGKHIELQDPRLPYRNFLVDVTEKEVYKSGNPLPGGFNLNFTVPSGORIS 144
DB 579 PCGOTPL-SQLLEIGSSS-----KRTCDVPVPSCG-KVCGKPLPCG-SLDPIHCEKICH 630
QY 145 PFMELLEKNKSNIKASTDLGRCAEFAPKTVMAD--KNNKATKYRYPFYVD--SKKRL 197
DB 631 EGDGVPVRSVISC-----RC--SPRTKELPCTSLKSEDAF-----FMCDKRCNKKRL 677
QY 198 CHILYVMQMLEGKKYCSVKGEPPDLTWYCFKPKKSTENHLLYGSAYVGENDAFISK 257
DB 678 C-----GHHKNE-----IC-----CVDKEH-----K 694
QY 258 CPNOLRGYRFGVWK-----KGRCLDYTELDTVIEBVESKACQWTFENDGVASDOP 311
DB 695 CPLNGKRLKGLRCEBPCRHGNC-----QTCWQASFDE----- 729
QY 312 HTYPLTSQASWMDWP-----LHOSDOP--HSGG----- 338
DB 730 ---LTHCGASVITYRPGCTRPPECTGTQCARVHECDHPYHSGHSEKCPCTFLTK 785
QY 339 --VGR---NYGYYVDIT-----GEGKCALSDOVPCLVSDAASVYTAAGS 380
DB 786 WCMGKHEFRSNIPCHLVDISGLPCSATLPCGMKHCQRLCHKGECLVDE----- 834
QY 381 LSEETPNFIISNSVTPPTETALQCTADKFPDSFGACDVQACK-RKSTSCVGGQIOST 439
DB 835 -----PCKPCTTPRADCGHPCMAPCHTSS--PCPYTACKAYVELQCEGGR-RKE 881
QY 440 SVDCTADEQNECGSNTALAGLAVGVLLALLGGGCFYAKRLDRNKGVQAAHHNEHFQS 499
DB 882 MVIC-----SEASTYQRIAAISMASKITDMQLGGSVEISKLITK-KEVHQARLECDDEC 935

QY 500 DRGAKKRPD---LMQAEF-----SFMDEAENIED 530
Db 936 SALERKKRLAEFHISDSDPNIRSSGSKFSDLIKEDARXO 977

RESULT 5

US-08-484-438-8
Sequence 8, Application US/08484438
Patent No. 5811098
Patent No. 5811098 5780031
GENERAL INFORMATION:
APPLICANT: Plovman, Gregory D.
APPLICANT: Culouscou, Jean-Michel
APPLICANT: Shoyab, Mohammed
APPLICANT: Siegal, Clay B.
APPLICANT: Hellstr m, Ingegerd
APPLICANT: Hellstr m, Karl E.
TITLE OF INVENTION: HER4 HUMAN RECEPTOR TYROSINE KINASE
NUMBER OF SEQUENCES: 42
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/484,438
FILING DATE: 07-JUN-1995
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/323,442
FILING DATE: 14-OCT-1994
APPLICATION NUMBER: US 08/150,704
FILING DATE: 10-NOV-1993
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/981,165
FILING DATE: 24-NOV-1992
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Mirock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 5624-230
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-8864/9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-484-438-8

Query Match 3.6%; Score 104; DB 2; Length 1255;

Best Local Similarity 22.2%; Pred. No. 0.64; Matches 107; Conservative 45; Mismatches 173; Indels 156; Gaps 27;

QY 81 LVRBPAGLPIWGKHLELOPRLPYRNNPLEDPTEKEYKSGGNLPGG---FNNLPYT 137
Db 256 LHFNNHSGIC-----ELHCPALVTYNTTFESMPN-----PGRITFGASCVT 297
QY 138 PSQRISPPMELLEKSNIKASTDLGRCAEFA---FTVAMDKNKAKTKRYPPFVDS 193

Db 298 AC-----PYNYL-----STDVGSCTLVCEPLHNEVTADBTQRCCKSKPCA--- 339

QY 194 KKRLLCH-----ILYVSMQLMGKKYC-----SVKGPPDLTWYCFKPRK 232

Db 340 --RVCYGLGMEHLREVRNAVTSANIQEPAGCKKIFGSLAFPLESFDGDPANTAPLOEQ 397

QY 233 SVTENHHLIYGSAYVGENPDAF--ISKPN-QALRG-----YRFGV-WKKGRC 276

Db 398 QVFETLEIETGYLYISAMPDLSPLDVSFQULQYIRGRILHNGAVSLTLQGLISMLGRS 457

QY 277 LDVTELTDTYIERVESAAQCWKTFFENDGYASDQ---PPTYPLTSGASNNDDKPLHQSD 332

Db 458 L--RELCSGLALIHNNHLCFVHT---VPMQLFNNPH-----QAL-----LHTAN 498

QY 333 QPHSGVGRVNGFYVYDT-----TGEKCALSDQ-----VPCLVSSAASVYTAAG 379

Db 499 RPEDECYEGELACHQLCARALLSGFTQCVCNSQFLRGCEBCECVLOGLPREYNAR 558

QY 380 SLSEETPNFIIPNSVYTPPTETALQCTAD-----K 412

Db 559 HCLPCHPE-QQPNQSVTCFGE-ADQCVAQAHYKDBPFCVACPSGVKPDLSYMPIWK 616

QY 413 PDSTGACDVQACKRQKTSVCGGQIGTSVDTADEQNECGSNTRALLGLAVGVLLALL 472

Db 617 PDEGAC--QPC---PINCTHSCVDLDDKCGPAEQR--ASPLISVS--AVGILLVVL 667

QY 473 G 473

Db 668 G 668

RESULT 6

US-08-625-101-2 Application US/08625101

Sequence 2, Patent No. 5869445

GENERAL INFORMATION:
APPLICANT: Cheever, Martin A.

TITLE OF INVENTION: COMPOUNDS FOR ELICITING OR ENHANCING IMMUNE
TITLE OF INVENTION: REACTIVITY TO HER-2/neu PROTEIN FOR PREVENTION
TITLE OF INVENTION: OR TREATMENT OF MALIGNANCIES IN WHICH THE HER-2/neu

TITLE OF INVENTION: ONCOGENE IS ASSOCIATED

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue

CITY: Seattle
STATE: Washington

COUNTRY: USA

ZIP: 98104-7092

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/625,101
FILING DATE: 01-APR-1996

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.

REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C7

TELEPHONE: (206) 622-4900

TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-625-101-2

Query Match	3.6%	Score 104;	DB 2;	Length 1255;
Best Local Similarity	22.5%	Pred. No. 0.64;		
Matches 108; Conservative	43;	Mismatches 174;	Indels 156;	Gaps 27;

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QY 81 LYNEPGLCIPMGKHTIELQDPRLPRUNNFLEADVTEKEYQSGNPLPGC---FNLMFVT 137
D 256 LHMNHSGIC-----ELHCPLALVYNTDFTESMEN-----PEGYTFGASCVT 297
QY 138 PSGORISPFPEMLLEKNSNIKASTDLGRCAEPA---FKTVAMDKNNKATYRYRPFYDS 193
D 298 AC-----PYNL-----STDVGSCTLYCPLHNGSVTAEDGTGRCEKSKPCA--- 339
QY 194 KKKLCH-----ILVSMQMEGKCYC-----SYKGEPPDLTWYCFKPRK 232
D 340 --FVCYGLGMEHLREBRAVLTASNIQEPAGCKKIFGSLAFLPESFDPGDASTAETDLQEQ 397
QY 233 SVTENHHLIYGSAYVENPDAF--ISKCN-QALNG-----YRGV-WKKGRC 276
D 398 QVETLEBITGYLIYAMPDLSPLDSVFONLQVIRGRIHLHNGAYSLTLQIGLSIMGLRS 457
QY 277 LDVTELDITVIERVESKACQWKTPENDVASDQ---PHTYPLTISOASNMDMPLHQSD 332
D 458 L--RELGSGLALIHNTHLCFVHT-----VPPDQLFKNPH-----QAL-----LHTAN 498
QY 333 QPHSGGVRNYGVFYVDITGE-----GKCALSDQ-----VPDCLVSDSAASVYAAG 379
D 499 RPDECEYGBELACHQICARGHCKMGPRPGQCVNCSQFLAGQCEVBCRYLQSLPREYNNAR 558
QY 380 SLSEETPNFIIPSNVSPPTPETAQCTAD-----KF 412
D 559 HCLPCHPE--CQFONGSVTCEGPE-ADQCAAHYKDPFCVARCPSGVKPDLSYMPWK 616
QY 413 PDSFGACDVQACKRQRTSCVGGIOGSTSVDTCLADEQNECGSNITALIAGLVGILLALL 472
D 617 PDEEGAC--QPC---DINCTHSCVDLDKGCPCAEOR--ASPLTSIIS--AVWGILLVVL 667
QY 473 G 473
D 668 G 668

```

RESULT 7
 US-08 356-786-2
 : Sequence 2, Application US/08356786
 : Patent No. 5877305
 : GENERAL INFORMATION:
 : APPLICANT: Huston, James S.
 : APPLICANT: Oppermann, Hermann
 : APPLICANT: Houston, L. L.
 : APPLICANT: Ring, David B.
 : TITLE OF INVENTION: Biosynthetic Binding Protein for Cancer
 : TITLE OF INVENTION: Marker
 : NUMBER OF SEQUENCES: 16
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Edmund R. Pitcher, Teesta, Hurwitz, & Thibault
 : STREET: Exchange Place, 53 State Street
 : CITY: Boston
 : STATE: Massachusetts
 : COUNTRY: USA
 : ZIP: 02109
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 :
 : SOFTWARE: PatentIn Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/356,786
 : FILING DATE:
 : CLASSIFICATION: 424
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: 07/831,967
 : FILING DATE: 06-FEB-1992

```

1  .ATTORNEY/AGENT INFORMATION:
2
3  NAME: Pitcher, Edmund R.
4  REGISTRATION NUMBER: 27,829
5  REFERENCE/DOCKET NUMBER: CRP-053
6
7  TELECOMMUNICATION INFORMATION:
8
9  TELEPHONE: (617) 248-7000
10
11 TELEFAX: (617) 248-7100
12
13 INFORMATION FOR SEQ ID NO: 2:
14
15 SEQUENCE CHARACTERISTICS:
16
17 LENGTH: 1255 amino acids
18
19 TYPE: amino acid
20
21 TOPOLOGY: linear
22
23 MOLECULE TYPE: protein
24
25 US-08-356-786-2

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Query Match	3.6%	Score 104;	DB 2;	Length 1255;
Best Local Similarity	22.5%;	Pred. No. 0.64;		
Matches 108; Conservative	43;	Mismatches 174;	Indels 156;	Gaps 27;

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QY      81  LYRPDAGICLPWGNHIELOQEDRLPRYNNNFLEADVTEKEYKQSGNPLRGSG---FLNLNVT 137
Db      256  LHPHNSGIC-----ELHCPALVTYNTDTRESMPN-----PEGKTYFCASCVT 297
QY      138  PSGORISPPFMEELLEKSNSNIKASTDLGRCAEFA---FKYVAMDKNNKATKYRYPFYVDS 193
Db      298  AC-----PYNVL-----STDVGSCTLVCPHLNQEVTAADGTQRCCKSKRCA--- 339
QY      194  KGRICH-----ILYVSNQLMBEKKYC-----SYKGEPPDLTWYCFKFRK 232
Db      340  --RVCYGLGMEHLREVRVAITSANIOEPAQCKKIFGSLFLPDESFGDASNTAPLOPEOL 397
QY      233  SYTENHLLIYSAIYVGENPDAF--ISKCPN-QALRG-----YRGGV-WKRCR 276
Db      398  QVFETLEETIGYLIISAMPDSILPRLSPFQNIQVIRGRILHNGAVSLTQGLGISWLGURS 457
QY      277  LDYTELIDTVLEARYESAQOCWVKTFENDVNASDQ---PHTYPLTSQASMDMWMLHOSD 332
Db      458  L--RELSSGLALIHNNHLCFVHT-----VMDQLFRNPH-----QAL-----LHTAN 498
QY      333  QPHSGGVGRNYGYFVYDVTGE-----GKCALSDQ-----VPDCLVSDSANAASYTAAG 379
Db      499  RPDECEGVGBGLACHQLCARGHCMWRGPPTQCYNCSQFLRGQECVEBCRVLQGLPREYVNAAR 558
QY      380  SLSEETPNFIIPSNPSVTPPTPEALQCTAD-----KF 412
Db      559  HCLPCHPE-QOPQNGSVTCFEGPE-ADQCVACAHYKDPFCVACRCPSGVKKPDLSPYMIKF 616
QY      413  PDSGACDVQACRQKTSVCGVGQIQSTSVSDCTABEQNECGSNTALINAGVILLALL 472
Db      617  PDEBGAC-QPC---PINCTHSCTVDLDDKCGPAEOR-ASPLTSIIS--AAVIGILLVVL 667
QY      473  G 473
Db      668  G 668

```

RESULT 8
 US-08-467-083-68
 Sequence 68. Application US/08467083
 Patent No. 5726023
 GENERAL INFORMATION:
 APPLICANT: Cheever, Martin A.
 APPLICANT: Disis, Mary L.
 TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/NEU PROTEIN
 TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
 TITLE OF INVENTION: HER-2/NEU ONCOGENE IS ASSOCIATED
 NUMBER OF SEQUENCES: 68
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Seed and Berry
 STREET: 6300 Columbia Center, 701 Fifth Avenue
 CITY: Seattle
 STATE: Washington
 COUNTRY: US

Db 398 QVFETLEETITGLYISAMPDLSLPDLSVFQNLQVIRGRIILHNGAYSLTLQGLISWLGSR 457
Qy 277 LDYTELDTLVIERVESKAQCVKTFENDVASDQ---PHTYPLTSQASNDMPHLHOSD 332
Db 458 L--RELGSGLALIHNNHLCFVHT-----VPWDQLFRNPH-----QAL-----LHTAN 498
Qy 333 QPHSGGVGRNYGFYVDT-----TGEGKALSDQ-----VPDCLVSDSAASYTAG 379
Db 499 RPDECVGEGLACHQLCARHCWGPGPTQCVCNCSQFLRGQECVEECRVLQGLPREYVNR 558
Qy 380 SLSEETPFILPSNPSVTPPTETALQCTAD-----KF 412
Db 559 HCLPCHPE-COPQNGSVTCFGE-ADQCVACAHYKDPFCVARGSPGVKPLSYMPIKF 616
Qy 413 PDSFACDVQACKROKTSVCGQIOSTSVDTADQNECGSNTALLIAGLAVGVLLALL 472
Db 617 PDEGAC--QPC---PINCTHSCVDLDDKGCRAEQR--ASPLTSIIS--AVVGIILLVVL 667
Qy 473 G 473
Db 668 G 668

RESULT 12

US-08-466-680B-68
Sequence 68, Application US/08466680B
Patent No. 6075122

GENERAL INFORMATION:

APPLICANT: Cheever, Martin A.
APPLICANT: Disig, Mary L.
TITLE OF INVENTION: IMMUNE REACTIVITY TO HER-2/neu PROTEIN
TITLE OF INVENTION: FOR DIAGNOSIS AND TREATMENT OF MALIGNANCIES IN WHICH THE
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seed and Berry LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: US
ZIP: 98104-7092

COMPUTER READABLE FORM:

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,680B
FILING DATE: 06-JUN-1995

CLASSIFICATION: 424

ATTORNEY/AGENT INFORMATION:
NAME: Sharkey, Richard G.
REGISTRATION NUMBER: 32,629
REFERENCE/DOCKET NUMBER: 920010.448C4
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031

INFORMATION FOR SEQ ID NO: 68:

SEQUENCE CHARACTERISTICS:
LENGTH: 1255 amino acids
TYPE: amino acid
TOPOLOGY: linear
US-08-466-680B-68

Query Match

Best Local Similarity 3.5%; Score 103; DB 3; Length 1255;
Matches 108; Conservative 43; Mismatches 174; Indels 156; Gaps 27;

Qy 81 LVREPAGLCPITWGHIELOQPDRLPYRNNFLEVDPEKEKYQSGNPLPGG---FNLNFTY 137
Db 256 LHNHSGIC-----ELHCPALVTYNTDTFESMPN-----PEGRYTFGASCVT 297
Qy 138 PSQGRISPFMELEKSNIKASTDLCRCAEFA-----FKTVAMDKNKATKRYPFVYDS 193

Db 298 AC-----PYNVL-----STDVGSCTLVCPILHNOEVTAEADGTORCEKSKPCA--- 339
Qy 194 KKRICH-----ILVSMQLMGKKYC-----SVKGPBDLTWCFKPRK 232
Db 340 --RVCYGLGMEHLREVRAYTSANIQEFAGCKKIFGSLAFLESPFDGDPASNTAPLQPEQL 397
Qy 233 SVTENHHLIYSAVAVGENPDAF--ISKCPN-QALRG-----YRFGV-WKKGRG 276
Db 398 QVFETLEETITGLYISAMPDLSLPDLSVFQNLQVIRGRIILHNGAYSLTLQGLISWLGSR 457
Qy 277 LDYTELDTLVIERVESKAQCVKTFENDVASDQ---PHTYPLTSQASNDMPHLHOSD 332
Db 458 L--RELGSGLALIHNNHLCFVHT-----VPWDQLFRNPH-----QAL-----LHTAN 498
Qy 333 QPHSGGVGRNYGFYVDT-----TGEGKALSDQ-----VPDCLVSDSAASYTAG 379
Db 499 RPDECVGEGLACHQLCARHCWGPGPTQCVCNCSQFLRGQECVEECRVLQGLPREYVNR 558
Qy 380 SLSEETPFILPSNPSVTPPTETALQCTAD-----KF 412
Db 559 HCLPCHPE-COPQNGSVTCFGE-ADQCVACAHYKDPFCVARGSPGVKPLSYMPIKF 616
Qy 413 PDSFACDVQACKROKTSVCGQIOSTSVDTADQNECGSNTALLIAGLAVGVLLALL 472
Db 617 PDEGAC--QPC---PINCTHSCVDLDDKGCRAEQR--ASPLTSIIS--AVVGIILLVVL 667
Qy 473 G 473
Db 668 G 668

RESULT 13

US-09-527-487-2
Sequence 2, Application US/09527487
Patent No. 6528060

GENERAL INFORMATION:

APPLICANT: Nicolette, Charles
TITLE OF INVENTION: HER2 ANTIGENIC PEPTIDES
FILE REFERENCE: 126881309200
CURRENT APPLICATION NUMBER: US/09/527,487
CURRENT FILING DATE: 2000-03-16
NUMBER OF SEQ ID NOS: 9
SOFTWARE: Patentin Ver. 2.1

SEQ ID NO 2
LENGTH: 1255
TYPE: PRT

ORGANISM: Homo sapiens
US-09-527-487-2

Query Match

Best Local Similarity 3.5%; Score 103; DB 4; Length 1255;
Matches 107; Conservative 44; Mismatches 174; Indels 156; Gaps 27;

Qy 81 LVREPAGLCPITWGHIELOQPDRLPYRNNFLEVDPEKEKYQSGNPLPGG---FNLNFTY 137
Db 256 LHNHSGIC-----ELHCPALVTYNTDTFESMPN-----PEGRYTFGASCVT 297
Qy 138 PSQGRISPFMELEKSNIKASTDLCRCAEFA-----FKTVAMDKNKATKRYPFVYDS 193
Db 298 AC-----PYNVL-----STDVGSCTLVCPILHNOEVTAEADGTORCEKSKPCA--- 339
Qy 194 KKRICH-----ILVSMQLMGKKYC-----SVKGPBDLTWCFKPRK 232
Db 340 --RVCYGLGMEHLREVRAYTSANIQEFAGCKKIFGSLAFLESPFDGDPASNTAPLQPEQL 397
Qy 233 SVTENHHLIYSAVAVGENPDAF--ISKCPN-QALRG-----YRFGV-WKKGRG 276
Db 398 QVFETLEETITGLYISAMPDLSLPDLSVFQNLQVIRGRIILHNGAYSLTLQGLISWLGSR 457
Qy 277 LDYTELDTLVIERVESKAQCVKTFENDVASDQ---PHTYPLTSQASNDMPHLHOSD 332
Db 458 L--RELGSGLALIHNNHLCFVHT-----VPWDQLFRNPH-----QAL-----LHTAN 498

QY 333 OPHSGGVNNGFYVDITGE-----GICALSDQ-----VPDCLVSDSAVSYTAAG 379
DB 499 REDECEVGLACHQICARGHCWGPPTQCVCNCSQPLRGQECVBEGRVLQGLPREVYVAR 558
QY 380 SLSEEPNPIIISNSBVTPTPTETALQCTRAD-----KF 412
DB 559 HCLPCHPE-CQPNQNSVTCFGE-ADQCVACAHYKDPFCVAPCPGKVPDLSTYMEIWK 616
QY 413 PDSFGACDVQACRQKTSVCGGQIOSTSVDTADEQNEGCSNTALAGLAVGVLTLAL 472
DB 617 PBEERAC-QPC---PINCTHSCVDLDDKCCPABQR--ASPUTISVS--AVGILLVVL 667
QY 473 G 473
DB 668 G 668
RESULT 14
US-08-929-329-6
; Sequence 6, Application US/08929329
; Patent No. 6120770
; GENERAL INFORMATION:
; APPLICANT: Adams, John H
; APPLICANT: Dalton, John P
; APPLICANT: Kappe, Stefan
; TITLE OF INVENTION: Plasmidium Proteins Useful for Preparing
; TITLE OF INVENTION: Vaccine Compositions
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Barnes & Thornburg
; STREET: 11 S Meridian
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/929,329
; FILING DATE:
; CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
; NAME: Breen, John P
; REGISTRATION NUMBER: 38,833
; REFERENCE/DOCKET NUMBER: 835910-28685
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 231-7745
; TELEFAX: (317) 231-7433
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 934 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
; ORGANISM: Plasmidium berghei
; US-08-929-329-6
Query Match 3.5%; Score 102.5; DB 3; Length 934;
Best Local Similarity 20.5%; Pred. No. 0.56;
Matches 89; Conservative 49; Mismatches 150; Indels 147; Gaps 23;
QY 34 TISASTSGNPQANV-EMKTFMERFNLTHHSGIYVLDGQKEVDGTYREPAGLCPW 92
DB 47 TNSGLGKQDFKFDIYDEDNINSKFNJESAO-----LCSNHENDG-IYR---GSCPDY 96

QY 93 GKH-----TELQOPDRL-----PYRNNFL 111
DB 97 GKTFFMNDKQEVNEDFLNEISLGLNKKLLIDLEIPYNSGLAMANYQGLFANCPYDKNA 156
QY 112 EDVPLEKEY-----KOS-----GNPLPGFNLFVTTSGQRI 143
DB 157 NDIKKEKEDYDMCFDKFYNKQNISTRIKQLLISKYTFGSHGLGRGASN----- 207
QY 144 SPPELLEKQSNIA-----STDGRCEFAFKYVAMDKKATKY 185
DB 208 TEYPLHINPLENYTKQMRYPKLVETLEDOSIYSHCIGPCPD-----RFDNKCPR- 259
QY 186 RYPFYDSKRLCHILYVSMQLEGGKYCVGEPDPLTWYCFKPKRSXTENHHIYSGA 245
DB 260 DLVAFNKHKTKECIIIGH-----EKKTKKNCSDHSRRNNGCFSSIKK-EKKDKTYSS 314
QY 246 YVGENPDAPISK-PNQLRGYRFGV--WKKGRCLDYTELTD-TVIERVESKAQCVWYKF 301
DB 315 FL--RPD-YETKCPRYPLNNSFEFGYFNVTGKCESPTKYDNTVI---SFOCIETKLF 367
QY 302 ENDGVASDQPHYPLITQASNDWVPLHQSDQPHSGGVGRNYGFYVDITGSGKALSQ 361
DB 368 -SFNYANENPD-QKRSNYLWGWWLENKQNKLS-----MNDLGVCLLKE 411
QY 362 VPDCLVSDSAVSYT 376
DB 412 RPTCVLKKQNYST 426
RESULT 15
US-09-086-483A-6
; Sequence 6, Application US/09086483A
; Patent No. 6214580
; GENERAL INFORMATION:
; APPLICANT: NI, et al.
; TITLE OF INVENTION: HUMAN TUMOR NECROSIS FACTOR RECEPTOR TR10
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: HUMAN GENOME SCIENCES, INC.
; STREET: 9410 KEY WEST AVENUE
; CITY: ROCKVILLE
; STATE: MD
; COUNTRY: US
; ZIP: 20850
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/086,483A
; FILING DATE: May-29-98
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/050,936
; FILING DATE: May-30-97
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 60/069,112
; FILING DATE: Dec-9-97
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: BROOKES, ANDERS A.
; REGISTRATION NUMBER: 36,373
; REFERENCE/DOCKET NUMBER: PF379
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (301) 309-8504
; TELEFAX: (301) 309-8439
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 467 amino acids
; TYPE: amino acid

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; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-09-086-483A-6

```

Query Match	3.5%;	Score 101.5;	DB 3;	Length 467;
Best Local Similarity	24.2%;	Pred. No. 0.23;		
Matches 59;	Conservative 27;	Mismatches 83;	Indels 75;	Gaps 14

```

QY      313  TYELPTQASNDNDW---PL-----HOSDQPHSGGAVGRNVGFYYVDITGEGKCALSDQ 361
Db      110  TIKLHDQSIQTQOWEHSPLGELCPGSHRSERP--GACNR-----CTEGVGITYNASN 160
QY      362  VPQGLVSDSAANVSYTAAGSLSETPFIITPSNPSTVPTPTETALQCTADKRPDSFGACDV 421
Db      161  LFACL-----PCTACKSDEEB-----RSPCTT--TRNTACQCKPGRTRNNSA--- 201
QY      422  QACKRQKTSVCVGGQIOSTSVDCCTADEQNEC-----GSN-----TALAGLAVGVVL 467
Db      202  EMCRKCGSTGCPRMVVK--DCTPMWDICCHAKESGNGHNITWILVYLVLPPLLVAVLI 259
QY      468  LIALLGSG-----CYFAKRLDRNKGVQ-AAHHE-----HEFQSDRGAKKR 507
Db      260  VCCCIIGSGCGGDKPCMDRVCFWRLGILRRPGAEADNAHIELIISNDLSISTFVSEQOMESQ 319
QY      508  PSDL  511
Db      320  PADL  323

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RESULT 16
US-09-580-212-6
; Sequence 6, Application US/09580212

Query Match	3.5%	Score 101.5	DB 4	Length 467
Best Local Similarity	24.2%	Pred. No. 0.23		
Matches	59	Conservative	27	Mismatches 83; Indels 75; Gaps 14

QY	313	TYPLTQSASWMDW--PL-----	HSDDPHSGVGGRNYGFYYVDITGGKALSDQ	361
DB	110	TIKLHDOSIGTOQWHSPIGELCPGSHSRSEPP--GACNR-----	CTEGGYTNASNIN	160
QY	362	VDDCHVSDSAANVYTAAGLSSETPMFIIIPNSPVTPPPTALQCTADKPFPSQACDV	421	
DB	161	LPACL-----PCTACKSDEEE-----RSPCTT--TRNTACQCKPBTFFANDSA---	201	
QY	422	QACKRQKTSVCGGQIGSTSVDTADQNEC-----GSN-----	TALIGLAVGVLY	467
DB	202	EMCRKCKSTCGPRGMVKV--DCTPMWEDIECYHKESGNGINIIWILVTLLVPLLLAAVLI	259	
QY	468	LLALLGGG-----CYFAKRLDRKNGV--AAHNE-----	HEFQSDRGRKKR	507
DB	260	VCCCTIGSGGGGPKCMKDRVCFMFKLGLLRPGAGNDNHNHIIISNADSLSTFVSEQQMESQ	319	

QY	508	PSDL	511
Db	320	PADL	323

RESULT 17
US-09-013-895A-2
; Sequence 2, Application US/09013895A

```

Query Match Similarity      3.5%; Score 101.5; DB 4; Length 468;
Benchmark Similarity      24.2%; Pred. No. 0.23;
Matches      59; Conservative      27; Mismatches      83; Indels      75; Gaps      14

Db      313 TYPLTQASWMDW---EL-----HSDQPHSGGVGRNYGYVDTTSGKCALSDQ 361
      110 TIKLHDQSIGTQOWEHSPLGELCPGSHSRER--GACNR-----CTEGGYTNASNIN 160
Qy      362 VPDCLVSSAAVSYTAAGSLSETNFIIIPSPSTPTPTETALQCTADKPFDSFGACGV 421
      161 LFACI-----PCTACKSDEEE-----RSPCTT--TRNTACCKGCTGFNDNSA--- 201
Db      442 QACKRQTSVCVGGOISTSTVDTADEONEC-----GSN-----TALIIAGLAVGVL 467
      202 EMCRKCRSTGCGPRGMVKV--DCTPMSDIECHAKESGNGHNIMVILVTLVPLLVAVLI 259
Qy      468 LIALIGG-----CYFAKFLDRNKVQ--AAHE-----HEFQSDRGARKKR 507
      260 VCCCGISGCGGDPKCMDRVCFWRLGILTRGPGAEADNAHBEILSNADSLSTFVSEQWESQ 519
Db      508 PSDL 511
      |||

```

Db 320 PADL 323

RESULT 18

US-09-565-918-2

Sequence 2, Application US/09565918
Patent No. 6433147
GENERAL INFORMATION:
APPLICANT: Rosen, Craig A.
APPLICANT: Ni, Jian
APPLICANT: Pan, James G.
APPLICANT: Gentz, Reiner L.
APPLICANT: Dixit, Vishva M.
TITLE OF INVENTION: Death Domain Containing Receptor 4
FILE REFERENCE: 1488.1300005
CURRENT APPLICATION NUMBER: US/09/565,918
PRIOR FILING DATE: 2000-05-05
PRIOR APPLICATION NUMBER: US 60/132,922
PRIOR FILING DATE: 1999-05-06
PRIOR APPLICATION NUMBER: US 09/013,895
PRIOR FILING DATE: 1998-01-27
PRIOR APPLICATION NUMBER: US 60/037,829
PRIOR FILING DATE: 1997-02-05
PRIOR APPLICATION NUMBER: US 60/035,722
PRIOR FILING DATE: 1997-01-28
NUMBER OF SEQ ID NOS: 13
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 2
LENGTH: 468
TYPE: PRT
ORGANISM: Homo sapiens
US-09-565-918-2

Query Match 3.5%; Score 101.5; DB 4; Length 468;
Best Local Similarity 24.2%; Pred. No. 0.23; Indels 75; Gaps 14;
Matches 59; Conservative 27; Mismatches 83;

313 TYPLTSQASWDMW---PL-----HSDQPHSGVGRNYGYVDVTGEGKCALSDQ 361
110 TIKLHDQSIGTQWHEHSPGELCPGSHRSERP--GACNR-----CTEGVGTNANN 160
QY 362 VPDCIVSDSAVSYTAAGSLSEETPNFIIPSPSVTPPTPTALACTADKPPDSFGACDV 421
Db 161 LFACI-----PCTACKSDEE-----RSPCTT--TRNTAQCCKGTFRNDNSA--- 201
QY 422 QACKRQKTSVCGGQIGSTSVDTADBEQNEC-----GSN-----TALAGLAVGV 467
Db 202 EMCKRCSTGCGPRGMVKV--DCTPMSDIECVHKGSGNGHNIWVILVTVPLLVAVLI 259
QY 468 LLALLGGG-----CYFAKRLDRNKGVQ-AAHHE-----HEFOSDRGARKKR 507
Db 260 VCCIGSGCGGDPKCMDRVCFWRLGLRGPABDNANHEILSNADSLSTFVSEQOMESQE 319
QY 508 PSDL 511
Db 320 PADL 323

RESULT 19

US-09-448-868-2

Sequence 2, Application US/09448868
Patent No. 6461823
GENERAL INFORMATION:
APPLICANT: Ni, Jian
APPLICANT: Rosen, Craig A.
APPLICANT: Pan, James G.
APPLICANT: Gentz, Reiner L.
APPLICANT: Dixit, Vishva M.
TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4; Death
TITLE OF INVENTION: Receptor 4), Member of the TNF-Receptor
TITLE OF INVENTION: Superfamily and Binding to Trail (Ap02-L)
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:

ADDRESSEE: HUMAN GENOME SCIENCES, INC.

STREET: 9410 KEY WEST AVENUE

CITY: ROCKVILLE

STATE: MD

COUNTRY: US

ZIP: 20850

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/448,868

FILING DATE: HERewith

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 09/013,895

FILING DATE: 27-JAN-1998

CLASSIFICATION:

ATTORNEY/AGENT INFORMATION:

NAME: STEFFE, ERIC K.

REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 1488.1300004

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 371-2540

TELEFAX: (202) 371-2600

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 468 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-448-868-2

Query Match 3.5%; Score 101.5; DB 4; Length 468;
Best Local Similarity 24.2%; Pred. No. 0.23; Indels 75; Gaps 14;
Matches 59; Conservative 27; Mismatches 83;

313 TYPLTSQASWDMW---PL-----HSDQPHSGVGRNYGYVDVTGEGKCALSDQ 361
110 TIKLHDQSIGTQWHEHSPGELCPGSHRSERP--GACNR-----CTEGVGTNANN 160
QY 362 VPDCIVSDSAVSYTAAGSLSEETPNFIIPSPSVTPPTPTALACTADKPPDSFGACDV 421
Db 161 LFACI-----PCTACKSDEE-----RSPCTT--TRNTAQCCKGTFRNDNSA--- 201
QY 422 QACKRQKTSVCGGQIGSTSVDTADBEQNEC-----GSN-----TALAGLAVGV 467
Db 202 EMCKRCSTGCGPRGMVKV--DCTPMSDIECVHKGSGNGHNIWVILVTVPLLVAVLI 259
QY 468 LLALLGGG-----CYFAKRLDRNKGVQ-AAHHE-----HEFOSDRGARKKR 507
Db 260 VCCIGSGCGGDPKCMDRVCFWRLGLRGPABDNANHEILSNADSLSTFVSEQOMESQE 319
QY 508 PSDL 511
Db 320 PADL 323

RESULT 20

US-10-039-785-1

Sequence 1, Application US/10039785
Patent No. 6538938
GENERAL INFORMATION:
APPLICANT: Salcedo et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
TITLE OF INVENTION: Receptors
FILE REFERENCE: PFS50
CURRENT APPLICATION NUMBER: US/10/039,785
PRIOR FILING DATE: 2002-05-07
CURRENT APPLICATION NUMBER: 60/369,860
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 60/341,237

PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 60/331,310
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/331,044
PRIOR FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: 60/327,364
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/323,807
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/309,176
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 60/294,981
PRIOR FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/293,473
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 468
TYPE: PRT
ORGANISM: Homo sapiens
US-10-039-785-1

Query Match 3.5%; Score 101.5; DB 4; Length 468;
Best Local Similarity 24.2%; Pred. No. 0.23;
Matches 59; Conservative 27; Mismatches 83; Indels 75; Gaps 14;

QY 313 TYPPTSQASWMDM---PL-----HSDQPHSGVGNGVFFYYVDTTGSEKALSDQ 361
DB 110 TTKLHDQSIGTQOWEHSPIGELCPGSHSRSP--GACNR-----CTEGVYTNASNN 160
QY 362 VPDCIVSDSAVSYTAAGSLSEETPNFIIPNSVTPPETALQCTADKFPDSFGACDV 421
DB 161 LRAFL-----PCTACKSDEER-----RSBCTT--TRNTACQCKPGTFRINDSA--- 201
QY 422 QACKROKTSVCGQIOISTVDCPTADEQNEC-----GSN-----TALLAGLAVGVYL 467
DB 202 EMCRKCKSTGCPRMVAVK--DCTPMADIECVHKESGNHNIWLVVTLVPLLVAVLVI 259
QY 468 LVALLGCG-----CYFAKRLDRNKQVQ-AAHNE-----HEFQSRGARKKR 507
DB 260 VCCCISSGCGGDKPCMDRVCFMRLGLRGGAEDNAHETLSNADSLSTFVSEQWESOE 319
QY 508 PSDL 511
DB 320 PADL 323

RESULT 21
US-09-216-393B-327
Sequence 327, Application US/09216393B
Patent No. 6514694
GENERAL INFORMATION:
APPLICANT: Milhausen, Michael James
TITLE OF INVENTION: TOXOPLASMA GONDII PROTEINS, NUCLEIC ACID MOLECULES, AND USES THEREOF
FILE REFERENCE: TX-1-C2
CURRENT APPLICATION NUMBER: US/09/216,393B
PRIOR FILING DATE: 1998-12-18
PRIOR APPLICATION NUMBER: 08/994,825
PRIOR FILING DATE: 1997-12-19
NUMBER OF SEQ ID NOS: 366
SOFTWARE: PatentIn version 3.1
SEQ ID NO 327
LENGTH: 571
TYPE: PRT
ORGANISM: Toxoplasma gondii
US-09-216-393B-327

Query Match 3.3%; Score 97.5; DB 4; Length 571;
Best Local Similarity 24.0%; Pred. No. 0.8;
Matches 42; Conservative 24; Mismatches 58; Indels 51; Gaps 6;

QY 353 EGKCALSDQVDCIVSDSAVSYTAAGSLSEETPNFIIPNSVTPPETALQCTADK 412

DB 445 EGEHVPEEIEPE-----GEHVPEEIEPEGEHV--PEEET----- 476
QY 413 PDSFGACVQACKROKTSVCGQIOISTVDCPTADEQNECGSNTALLAGLAVGVYLALL 472
DB 477 PEGEHAPPEETPAPEET-----EKEEEGVVAIAGGVGVLLINGG 520
QY 473 GGGCYFARLDRNKQVQAAHHEFQSDRG---ARKRPSDLMQAEPSFVDEAE 524
DB 521 AGAANYVANO---GGEVAEEDVWFESSEEDGTQAGENRESSETVIEIDDAADND 571

RESULT 22
US-08-252-493C-9
Sequence 9, Application US/08252493C
Patent No. 5891645
GENERAL INFORMATION:
APPLICANT: Rollins, Scott
APPLICANT: Rother, Russell P.
APPLICANT: Evans, Mark J.
APPLICANT: Matis, Louis A.
TITLE OF INVENTION: PORCINE E-SELECTIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSER: Seth A. Fidel
STREET: 25 Science Park, Box 15
CITY: New Haven
STATE: Connecticut
COUNTRY: USA
ZIP: 06511
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 750 Kb storage
COMPUTER: PC compatible
OPERATING SYSTEM: DOS 6.2
SOFTWARE: WordPerfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/252,493C
FILING DATE: June 1, 1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fidel, Seth A.
REGISTRATION NUMBER: 38,449
REFERENCE/DOCKET NUMBER: ALX-138
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 776-1790
TELEFAX: (203) 772-3655
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 484 amino acids
TYPE: amino acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: cDNA to mRNA
DESCRIPTION: predicted amino acid sequence of Porcine E-selectin
US-08-252-493C-9

Query Match 3.3%; Score 97; DB 2; Length 484;
Best Local Similarity 22.3%; Pred. No. 0.68;
Matches 73; Conservative 32; Mismatches 131; Indels 92; Gaps 16;

QY 249 ENPDAPISKCPN-----QALRGYRF-----GVW---KKGRCIDYIELNDT 285
DB 185 ENPVGAVVTCFQSLPMTTCAFECKEGFELIGPEHLQCTSSGSMGKPTCAVT--CDT 242
QY 286 V-----IEVESAQCWVTKTFENDGVASQPHYPLTISQASWMDMPLHOS 331
DB 243 VEHFQNGDVSCNHSIGEPAYKSTCHFTCAEGFQGG--PAQICTAGQMTQOAPVCKA 300
QY 332 -----DQPHSGVGRNRYFYVDTTGE-----GKCALSDQVDCIVSDSAVSYTAAGSL 381

Db 301 VKCPAVSQPKGLVKFTH-----SPTGEFTYKSCAFSC-EGEELNRSQAQLCTSGQOW 354
Qy 382 SEETPNFIIPSNBPTPTPETALQCTADKFPDSFGACDVQACKRKQKTSVCGGQIQSTSV 441
Db 355 TQEVPSQGVQVQSSLEVR-EINMSCGEPV---FGAVCTPACPE-----GWMNGSV 403
Qy 442 DCTADEONECG-----SNTALIAGLAVGVLLALLGGCCTPAKRLDR 484
Db 404 ALT-----CGATGHWGMLPTCEAPAESKIPLAMGLAAGVSFMTSASFLMWLTKRLK 457
Qy 485 NKGVQAAHHEHFEFOSDRGARKRPSDL 512
Db 458 RAKKFPSSSECLQPNGS-YQWPSDL 484

RESULT 23
US-09-276-197-9
Sequence 9, Application US/09276197
Patent No. 6040428
GENERAL INFORMATION:
APPLICANT: Rollins, Scott
APPLICANT: Rother, Russell P.
APPLICANT: Evans, Mark J.
APPLICANT: Matls, Louis A.
TITLE OF INVENTION: PORCINE E-SELECTIN
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Seth A. Fidel
STREET: 25 Science Park, Box 15
CITY: New Haven
STATE: Connecticut
COUNTRY: USA
ZIP: 06511

COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 inch, 750 Kb storage
COMPUTER: PC compatible
OPERATING SYSTEM: DOS 6.2
SOFTWARE: Wordperfect 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/276,197
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/252,493
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Fidel, Seth A.
REGISTRATION NUMBER: 38,449
REFERENCE/DOCKET NUMBER: ALX-138
TELECOMMUNICATION INFORMATION:
TELEPHONE: (203) 776-1790
TELEFAX: (203) 772-3655
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 484 amino acids
TYPE: amino acid
STRANDEDNESS: Single
TOPOLOGY: Linear
MOLECULE TYPE: cDNA to mRNA
DESCRIPTION: predicted amino acid sequence of
DESCRIPTION: Porcine E-selectin
US-09-276-197-9

Query Match 3.3%; Score 97; DB 3; Length 484;
Best Local Similarity 22.3%; Pred. No. 0.68;
Matches 73; Conservative 32; Mismatches 131; Indels 92; Gaps 16;

Qy 249 ENPDATISKCPN-----QALRGYR-----GWM---KKGRCLDYTELDT 285
Db 185 ENPANGVATCPQSLPMWNTTCAFECKEGELIGPEHLQCTSSGSGDKKPTKAVT---CDT 242
Qy 286 V-----IERVESKACQWKTFFENDVASDPHTYPLTSGASWMDWMLHQS 331

Db 243 VGHFQNDVSCNHSISIEFAFYKSTCHPTCAEGFGLQ--PAQLECTAQOGWTQAPVCKA 300
Qy 332 -----DQPSGGVGRNRYGVYVDTTGE-----GKCALSDQVDCLVSDSAVSTAAAGSL 381
Db 301 VKCPAVSQPKGLVKFTH-----SPTGEFTYKSCAFSC-EGEELNRSQAQLCTSGQOW 354
Qy 382 SEETPNFIIPSNBPTPTPETALQCTADKFPDSFGACDVQACKRKQKTSVCGGQIQSTSV 441
Db 355 TQEVPSQGVQVQSSLEVR-EINMSCGEPV---FGAVCTPACPE-----GWMNGSV 403
Qy 442 DCTADEONECG-----SNTALIAGLAVGVLLALLGGCCTPAKRLDR 484
Db 404 ALT-----CGATGHWGMLPTCEAPAESKIPLAMGLAAGVSFMTSASFLMWLTKRLK 457
Qy 485 NKGVQAAHHEHFEFOSDRGARKRPSDL 512
Db 458 RAKKFPSSSECLQPNGS-YQWPSDL 484

RESULT 24
US-09-310-463-4
Sequence 4, Application US/09310463A
Patent No. 6384203
GENERAL INFORMATION:
APPLICANT: Cosman, David J.
APPLICANT: Anderson, Dirk M.
APPLICANT: Borges, Luis
TITLE OF INVENTION: Family of Immunoregulators Designated Leukocyte Immunoglobulin-
FILE REFERENCE: 2624-A
CURRENT APPLICATION NUMBER: US/09/310,463A
CURRENT FILING DATE: 1999-05-12
EARLIER APPLICATION NUMBER: 08/842,248
EARLIER FILING DATE: 1997-04-24
NUMBER OF SEQ ID NOS: 39
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 4
LENGTH: 652
TYPE: PRT
ORGANISM: human
US-09-310-463-4

Query Match 3.3%; Score 96; DB 4; Length 652;
Best Local Similarity 20.4%; Pred. No. 1.4;
Matches 50; Conservative 32; Mismatches 95; Indels 68; Gaps 6;

Qy 293 KAQCWKTFFENDVASDPHTYPLTSGASWMDWMLHQSQDPHSGVGRNRYGVYVDTTG 352
Db 347 QSQGMQGT-----LLTKEGADDPRLRSTYQSK----- 377
Qy 353 EGKCALSDQVDCLVSDSAVSTAAAGSLSE-----TPNFIIPSNBPTPTPET 404
Db 378 -----YQAEPPMGVPTSAHAGTYRCYQSSKPYLLTHPDPLELVVSGSGGSSPTTG 432
Qy 405 LQCTADKFPDSFGACDVQACKRKQKTSVCGGQIQSTVDTADEONECGSNTALIAGLAVG 464
Db 433 -----PTTSAGBEDQPLPTGSDPSSGGRHGVITGLVA 469
Qy 465 GVLLALLGGCCTPAKRLDRNKGVQAAHHEHFEFOSDRGARKRPSD--LMQEAEPSPWDE 522
Db 470 VILLILLILLFLRLRRQCKHWTSTQKADFGHAGVGPETDRGLQWRSSPAA-DA 528
Qy 523 AEENI 527
Db 529 QEENL 533

RESULT 25
US-08-842-248A-4
Sequence 4, Application US/08842248A
Patent No. 6448035
GENERAL INFORMATION:

APPLICANT: Cosman, David J.
TITLE OF INVENTION: Family of Immunoregulators Designated
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: Janis C. Henry, Immunex Corporation
STREET: 51 University Street
CITY: Seattle
STATE: WA
COUNTRY: US
ZIP: 98101
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM/PC Compatible
OPERATING SYSTEM: Microsoft Word 7.0
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/842,248A
FILING DATE: April 24, 1997
CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Henry, Janis C.
REGISTRATION NUMBER: 34,347
REFERENCE/DOCKET NUMBER: 2624
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 587-0430
TELEFAX: (206) 233-0644
TELEX: 756822
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 652 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-842-248A-4

Query Match 3.3%; Score 96; DB 4; Length 652;
Best Local Similarity 20.4%; Pred. No. 1.4;
Matches 50; Conservative 32; Mismatches 95; Indels 60; Gaps 6;

QY 293 KAQCWVTFENDGVASDOPHTYPLTSQASWMDWMPHQSODPHSGVGNNYGYVDTTG 352
DB 347 GQGMWQTF-----LITKEGAADBPWRLRSTYQSK----- 377

QY 353 ESKCALSDQVDPCLVSDSAVSTYTAGSISE-----TNPFIIPSNPVTTPRPETA 404
DB 378 -----YQAFRPMGPVYSAHAGTYRCYSQSSKRYLLTHPSDPLELVSGSPSGPSPPTTG 432

QY 405 LQCTADKFPDSFGACDVOQACKQKTSQVSGQIQSTSDCTADEONEGSGNTALLIAGLAVG 464
DB 433 -----PISTSAQPREDPQLTPGSDPQSLGHHLGVLGILVA 469

QY 465 GVLLALLGGGCFYAKRLDRNKGQVAHNEHFQSDRGARKKRPD-LMQEAPSPFWE 522
DB 470 VILLILLILLILLILLILLHRRQKMTSTQKADQHPAGAVGPEPTDGLQWSSPA-DA 528

QY 523 ABEET 527
DB 529 QBEETL 533

RESULT 26
US-08-929-329-8
Sequence 8, Application US/08929329
GENERAL INFORMATION:
APPLICANT: Adams, John H
APPLICANT: Dalton, John P
APPLICANT: Kappe, Stefan
TITLE OF INVENTION: Plasmidum Proteins Useful for Preparing
NUMBER OF SEQUENCES: 23
CORRESPONDENCE ADDRESS:

ADDRESSEE: Barnes & Thornburg
STREET: 11 S Meridian
CITY: Indianapolis
STATE: Indiana
COUNTRY: USA
ZIP: 46204
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/929,329
FILING DATE:
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: Breen, John P
REGISTRATION NUMBER: 38,833
REFERENCE/DOCKET NUMBER: 835910-28685
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 231-7745
TELEFAX: (317) 231-7433
INFORMATION FOR SEQ ID NO: 8:
SEQUENCE CHARACTERISTICS:
LENGTH: 454 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: internal
ORIGINAL SOURCE:
ORGANISM: Plasmidum falciparum
US-08-929-329-8

Query Match 3.3%; Score 95.5; DB 3; Length 454;
Best Local Similarity 21.1%; Pred. No. 0.87;
Matches 94; Conservative 46; Mismatches 144; Indels 161; Gaps 25;

QY 56 RPNLTHHOSGIVYDL---GQDKEVDGTLREPA-GLEPIGKHTELQDPRLPYRNNFL 111
DB 21 KNIISNTIAGTSOSLFHNYDKTCRNHYVYGRAGSCPNYKALIVQ-----NLL 71

QY 112 EDVPEKEKYKQSGNLPGLFNLNFTP--SGQRISPF--PMELKSNINIKASTDLGRCA 167
DB 72 GE-----EYDKN-----FNLNFINETIRITGLINKYFKQDVVISYENSGIAMHNNMLASC 119

QY 168 E-----FAKTVAMDKNKATK--YRYPFV--YDSKKRLCHILVYSQMLMEG--- 210
DB 120 PHEHEEKLFSVKT--DYNYMKCKSKIFSNRFTWKEDPKTRL--FMVYGLYGGRLG 174

QY 211 -----KXY-----CSYKGEPPDLTWYCFPR----- 230

DB 175 ANIKRDKKEKKEKENITLPMKNPBLIKNLPDCSIS-----YCLAPCLSENSFNKCF 227

QY 231 RKSVTENHLLIYGAVGENPDAFISKCPNQLRGYRFGWKKGRCGLDYTELDITVIERV 290
DB 228 RNLPAVYNHLTNECVILGTHEOERTNSCRRTKEK-----KKPNCQILKRTD----- 275

QY 291 ESKAQCWVTFENDGVASDOPHTYPLTSQASWMDWMPHQS-----DQPHSGGV--- 339
DB 276 -SKDWTYVSSFLRPYETKCPRYLPSKV-----FGTFDQKTKGCKSLMDKAYEVGINKF 330

QY 340 -----GRN--YGFYVDTT-----GEGKCALSDQVDDCLVSDA 371
DB 331 SVCLEYFLVSPKDLVNSGRNNYWGIMADHSHVNNENIEIANGKCYHLVVKPCLVIXEN 390

QY 372 AVSYTAAGSLSEETNPFIIPSNPV 396
DB 391 HPSFTA--LTANTYDF-----NQSV 408

RESULT 27

US-08-121-713D-62
Sequence 62, Application US/08121713D
Patent No. 5639856
GENERAL INFORMATION:
APPLICANT: Goodman, Corey S.
APPLICANT: Kolodkin, Alex L.
APPLICANT: Matthes, David
APPLICANT: Bentley, David R.
APPLICANT: O'Connor, Timothy
TITLE OF INVENTION: The Semaphorin Gene Family
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 Bush Street, Suite 3200
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/121,713D
FILING DATE: 13-SEP-1993
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B94-002-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 724 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-121-713D-62

Query Match 3.2%; Score 94.5; DB 1; Length 724;
Best Local Similarity 20.3%; Pred. No. 2.4;
Matches 62; Conservative 40; Mismatches 96; Indels 107; Gaps 14;

QY 51 KTFMERFLTH-----HHQSGIYVDLGQDKEVDGTLVREPAGL 88
DB 156 KDVIYANLTHLPRESEYVIGVGLGIACPYDPLDNSTAIYENG-----NPGGL 204
QY 89 CPIW-GKIIELQOPRLPYRNNFLEDVPTKEKYKSGNPLPGCFNLNFTVPSGQISFPF 147
DB 205 PGLVSGTMAETKATDVIFRTDLVNTSAKRLKYK-----FKRTLLKYD 246
QY 148 MELLEKSNITASTDLGRCAEFKTVAMDKN--KATKYRYPFYDSKKELCH----- 199
DB 247 SKMLDK-PNFVGSFPIGEGYVFFPRETAVEYINGKA-----VYSRIARVCKKDVCGK 298
QY 200 --ILVSNQMEGKKYCVKGEPPDLTWYCFKPRKSV-----TENHHLIYG 243
DB 299 NLAHNMTATYKALRNCISGEFP---FYNEIQSVYQLPSDKSRFPATFTTSTNGLIG 354
QY 244 SA-----YGENPDPAISKCPNOLAGYRFGW-----KGRCL-DYTELTDTVI 287
DB 355 SAVCSFHINEIQAFNGKFKGQSSN---SAMLPLVLSNRVPEPRGTCVNDTSLNLPDTVL 411
QY 288 ERVES 292
DB 412 NFIRS 416

RESULT 28

US-08-835-268-62
Sequence 62, Application US/08835268
Patent No. 5807826
GENERAL INFORMATION:
APPLICANT: Goodman, Corey S.
APPLICANT: Kolodkin, Alex L.
APPLICANT: Matthes, David
APPLICANT: Bentley, David R.
APPLICANT: O'Connor, Timothy
TITLE OF INVENTION: The Semaphorin Gene Family
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 Bush Street, Suite 3200
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/835,268
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/121,713
FILING DATE: 13-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B94-002-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
TELEFAX: (415) 343-4342
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 724 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-835-268-62

Query Match 3.2%; Score 94.5; DB 1; Length 724;
Best Local Similarity 20.3%; Pred. No. 2.4;
Matches 62; Conservative 40; Mismatches 96; Indels 107; Gaps 14;

QY 51 KTFMERFLTH-----HHQSGIYVDLGQDKEVDGTLVREPAGL 88
DB 156 KDVIYANLTHLPRESEYVIGVGLGIACPYDPLDNSTAIYENG-----NPGGL 204
QY 89 CPIW-GKIIELQOPRLPYRNNFLEDVPTKEKYKSGNPLPGCFNLNFTVPSGQISFPF 147
DB 205 PGLVSGTMAETKATDVIFRTDLVNTSAKRLKYK-----FKRTLLKYD 246
QY 148 MELLEKSNITASTDLGRCAEFKTVAMDKN--KATKYRYPFYDSKKELCH----- 199
DB 247 SKMLDK-PNFVGSFPIGEGYVFFPRETAVEYINGKA-----VYSRIARVCKKDVCGK 298
QY 200 --ILVSNQMEGKKYCVKGEPPDLTWYCFKPRKSV-----TENHHLIYG 243
DB 299 NLAHNMTATYKALRNCISGEFP---FYNEIQSVYQLPSDKSRFPATFTTSTNGLIG 354
QY 244 SA-----YGENPDPAISKCPNOLAGYRFGW-----KGRCL-DYTELTDTVI 287
DB 355 SAVCSFHINEIQAFNGKFKGQSSN---SAMLPLVLSNRVPEPRGTCVNDTSLNLPDTVL 411
QY 288 ERVES 292

Db 412 NFIRS 416

RESULT 29
US-09-060-692-62

Sequence 62, Application US/09060692

Patent No. 5935865

GENERAL INFORMATION:

APPLICANT: Goodman, Corey S.

APPLICANT: Kolodkin, Alex L.

APPLICANT: Matthes, David

APPLICANT: Bentley, David R.

APPLICANT: O'Connor, Timothy

TITLE OF INVENTION: The Semaphorin Gene Family

NUMBER OF SEQUENCES: 100

CORRESPONDENCE ADDRESS:

ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 268 Bush Street, Suite 3200

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/060,692

FILING DATE:

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/121,713

FILING DATE: 13-SEP-1993

ATTORNEY/AGENT INFORMATION:

NAME: Oseman, Richard A.

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: B94-002-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415)343-4341

TELEFAX: (415)343-4342

TELEX:

INFORMATION FOR SEQ ID NO: 62:

SEQUENCE CHARACTERISTICS:

LENGTH: 724 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-09-060-692-62

Query Match 3.2%; Score 94.5; DB 2; Length 724;

Best Local Similarity 20.3%; Pred. No. 2.4;

Matches 62; Conservative 40; Mismatches 96; Indels 107; Gaps 14;

```
QY 51 KTFMERFNLTH-----HHOSGIYVDLGDQKVEDGTLNREPAGL 88
   ||:|||||
Db 156 KQYVIYANLTHLRSEYVIGVGLGIAKCPYDPLDNTAIYENG-----NPGGL 204
   ||:|||||
QY 89 CFIW-GKHIELQOPRLPYRNFLDVPTEKEYKOSGNPLPGGFNLNFTVPSGORISPP 147
   ||:|||||
Db 205 PGLYSTNNEFTKADIVIFRTDLYNTSAKRLKYK-----FKRTLKVD 246
   ||:|||||
QY 148 MELLEKNSTIKASTDLGRCAEPFAKTVAMDKN--KATKYRPFYDSSKRLCH----- 199
   ||:|||||
Db 247 SKWLDK-PNVGSGFDIGEVYVFFRETAVEYINCGKA-----VYSRIARVCKDVGSK 298
   ||:|||||
QY 200 --ILVSNQLMGKKYCSVKGEPDPLTWICFKPRKSV-----TENHHLIYG 243
   ||:|||||
Db 299 NLLAHNMAWATYLLKARLNCISISGEFP-----FYFNEIOSVYQLPSDKSRFPATFTTSTNGLIG 354
   ||:|||||
QY 244 SA-----YVGENPDPAFISKCPNQLARGYRFGV-----KKGRCL-DYTELDTYVI 287
   ||:|||||
Db 355 SANCSEHINIEIOAFAFGKFKREGSSN---SAMLPLVLSNRVPEBRPGICVNDTSLNLPDTVL 411
   ||:|||||
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QY 288 ERVES 292
Db 412 NFIRS 416RESULT 30
US-08-833-391-62

Sequence 62, Application US/08833391

Patent No. 6013781

GENERAL INFORMATION:

APPLICANT: Goodman, Corey S.

APPLICANT: Kolodkin, Alex L.

APPLICANT: Matthes, David

APPLICANT: Bentley, David R.

APPLICANT: O'Connor, Timothy

TITLE OF INVENTION: The Semaphorin Gene Family

NUMBER OF SEQUENCES: 100

CORRESPONDENCE ADDRESS:

ADDRESS: SCIENCE & TECHNOLOGY LAW GROUP

STREET: 268 Bush Street, Suite 3200

CITY: San Francisco

STATE: CA

COUNTRY: USA

ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/833,391

FILING DATE:

CLASSIFICATION: 530

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/121,713

FILING DATE: 13-SEP-1993

ATTORNEY/AGENT INFORMATION:

NAME: Oseman, Richard A.

REGISTRATION NUMBER: 36,627

REFERENCE/DOCKET NUMBER: B94-002-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (415)343-4341

TELEFAX: (415)343-4342

TELEX:

INFORMATION FOR SEQ ID NO: 62:

SEQUENCE CHARACTERISTICS:

LENGTH: 724 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-833-391-62

Query Match 3.2%; Score 94.5; DB 3; Length 724;

Best Local Similarity 20.3%; Pred. No. 2.4;

Matches 62; Conservative 40; Mismatches 96; Indels 107; Gaps 14;

```
QY 51 KTFMERFNLTH-----HHOSGIYVDLGDQKVEDGTLNREPAGL 88
   ||:|||||
Db 156 KQYVIYANLTHLRSEYVIGVGLGIAKCPYDPLDNTAIYENG-----NPGGL 204
   ||:|||||
QY 89 CFIW-GKHIELQOPRLPYRNFLDVPTEKEYKOSGNPLPGGFNLNFTVPSGORISPP 147
   ||:|||||
Db 205 PGLYSTNNEFTKADIVIFRTDLYNTSAKRLKYK-----FKRTLKVD 246
   ||:|||||
QY 148 MELLEKNSTIKASTDLGRCAEPFAKTVAMDKN--KATKYRPFYDSSKRLCH----- 199
   ||:|||||
Db 247 SKWLDK-PNVGSGFDIGEVYVFFRETAVEYINCGKA-----VYSRIARVCKDVGSK 298
   ||:|||||
QY 200 --ILVSNQLMGKKYCSVKGEPDPLTWICFKPRKSV-----TENHHLIYG 243
   ||:|||||
Db 299 NLLAHNMAWATYLLKARLNCISISGEFP-----FYFNEIOSVYQLPSDKSRFPATFTTSTNGLIG 354
   ||:|||||
```

Oy 244 SA----YVGNPDAFISKCPNOLRGYRFGW-----KKGRCL-DYTELTDTVI 287
Db 355 SAVCSFHINEIOAFAFGKFKQSSSN---SAMLPLYNSRVBEPRGTCVNDTSLNLPDVL 411
Oy 288 ERVES 292
Db 412 NFIRS 416

RESULT 31

US-09-060-610-62
Sequence 62, Application US/09060610
Patent No. 6344544
GENERAL INFORMATION:
APPLICANT: Goodman, Corey S.
APPLICANT: Kolodkin, Alex L.
APPLICANT: Matches, David R.
APPLICANT: Bentley, David R.
APPLICANT: O'Connor, Timothy
TITLE OF INVENTION: The Semaphorin Gene Family
NUMBER OF SEQUENCES: 100
CORRESPONDENCE ADDRESS:
ADDRESSEE: SCIENCE & TECHNOLOGY LAW GROUP
STREET: 268 Bush Street, Suite 3200
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/060,610
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/835,268
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: B94-002-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
TELEFAX: (415)343-4342
TELEX:
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 724 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-060-610-62

Query Match 3.2%; Score 94.5; DB 4; Length 724;
Best Local Similarity 20.3%; Pred. No.2.4;
Matches 62; Conservative 40; Mismatches 96; Indels 107; Gaps 14;

Oy 51 KTFMERFNLTH-----HHOSGIYVDLGQDKVEDGTLYREPAGL 88
Db 156 KDVIYIANLTHLPSEVYIGVGLGIACPDPLDNSTAIYVNG-----NPGGL 204
Oy 89 CPPIV-GKHIELQOPDRLEFYRNPLFEDVTEKEYKQSGNPLPGGFNLNFTPSGORISFP 147
Db 205 PGLVSGTNAEFTKADTVIFRTDLVNTSAKRLKYK-----FKRTLKYD 246
Oy 148 MELLEKSNINAKSTDLGRCAEFAKTVAMDKN--KATKRYPPVYDSKRLCH----- 199
Db 247 SKWLDR-PNFVGSFDIGIEYVFFPRETAVEYINGKA-----VYSRIARVCKKDVGK 298
Oy 200 --ILVSMQMEGKKYGSVKGEPPDLTWYCFKPKRSV-----TENHHLIYG 243

Db 299 NLAHNATYIKARLNCISGEFP-----FYFNEIQSVYQLPSDKSRFPATFTSTNGILG 354
Oy 244 SA----YVGNPDAFISKCPNOLRGYRFGW-----KKGRCL-DYTELTDTVI 287
Db 355 SAVCSFHINEIOAFAFGKFKQSSSN---SAMLPLYNSRVBEPRGTCVNDTSLNLPDVL 411
Oy 288 ERVES 292
Db 412 NFIRS 416

RESULT 32

PCT-US94-10151A-62
Sequence 62, Application PC/TUS9410151A
GENERAL INFORMATION:
APPLICANT: The Regents of the University of California
TITLE OF INVENTION: The Semaphorin Gene Family
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR HOHBACH TEST ALABRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: CA
COUNTRY: USA
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/10151A
FILING DATE: 13-SEP-1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Osman, Richard A.
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: PP-58750-PC/RAO
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299 FHT UR
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 724 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US94-10151A-62

Query Match 3.2%; Score 94.5; DB 5; Length 724;
Best Local Similarity 20.3%; Pred. No.2.4;
Matches 62; Conservative 40; Mismatches 96; Indels 107; Gaps 14;

Oy 51 KTFMERFNLTH-----HHOSGIYVDLGQDKVEDGTLYREPAGL 88
Db 156 KDVIYIANLTHLPSEVYIGVGLGIACPDPLDNSTAIYVNG-----NPGGL 204
Oy 89 CPPIV-GKHIELQOPDRLEFYRNPLFEDVTEKEYKQSGNPLPGGFNLNFTPSGORISFP 147
Db 205 PGLVSGTNAEFTKADTVIFRTDLVNTSAKRLKYK-----FKRTLKYD 246
Oy 148 MELLEKSNINAKSTDLGRCAEFAKTVAMDKN--KATKRYPPVYDSKRLCH----- 199
Db 247 SKWLDR-PNFVGSFDIGIEYVFFPRETAVEYINGKA-----VYSRIARVCKKDVGK 298
Oy 200 --ILVSMQMEGKKYGSVKGEPPDLTWYCFKPKRSV-----TENHHLIYG 243
Db 299 NLAHNATYIKARLNCISGEFP-----FYFNEIQSVYQLPSDKSRFPATFTSTNGILG 354
Oy 244 SA----YVGNPDAFISKCPNOLRGYRFGW-----KKGRCL-DYTELTDTVI 287

Db 355 SAVCSFHINEIOAFNKGKFEQSSSN---SAWLPLYNSRVPERRPOTCVNDSNLPDVL 411

QY 288 ERVES 292

Db 412 NFIRS 416

RESULT 33

US-09-107-532A-5645

Sequence 5645, Application US/09107532A

Patent No. 6583275

GENERAL INFORMATION:

APPLICANT: LYNN A Doucette-Stamm and David Bush

TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO

NUMBER OF SEQUENCES: 7310

CORRESPONDENCE ADDRESS:

ADDRESS: GENOME THERAPEUTICS CORPORATION

STREET: 100 Beaver Street

CITY: Maltham

STATE: Massachusetts

COUNTRY: USA

ZIP: 02354

COMPUTER READABLE FORM:

MEDIUM TYPE: CD-ROM ISO9660

COMPUTER: PC

OPERATING SYSTEM: <Unknown>

SOFTWARE: ASCII

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/107,532A

FILING DATE: 30-Jun-1998

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 60/085,598

FILING DATE: 14 May 1998

APPLICATION NUMBER: 60/051571

FILING DATE: July 2, 1997

ATTORNEY/AGENT INFORMATION:

NAME: Ariandello, Pamela Deneke

REGISTRATION NUMBER: 40,489

REFERENCE/DOCKET NUMBER: GTC-012

TELECOMMUNICATION INFORMATION:

TELEPHONE: (781)893-5007

TELEFAX: (781)893-8277

INFORMATION FOR SEQ ID NO: 5645:

SEQUENCE CHARACTERISTICS:

LENGTH: 702 amino acids

MOLECULE TYPE: linear

TOPOLOGY: linear

MOLECULE TYPE: protein

HYPOTHETICAL: YES

ORGANISM: Enterococcus faecium

FEATURE:

NAME/KEY: misc feature

LOCATION: (B) LOCATION 1...702

SEQUENCE DESCRIPTION: SEQ ID NO: 5645:

US-09-107-532A-5645

Query Match 3.2%; Score 94; DB 4; Length 702;

Best Local Similarity 21.6%; Pred. No. 2.5;

Matches 80; Conservative 33; Mismatches 117; Indels 140; Gaps 18;

QY 107 RNNFL--EVP-----TEKEYKQSGNPLPGF-----NINFTYPSQR-I 143

Db 55 KNNFIIPKVPAKNTITVNGASKYKVVHDANKGFTDYGVLGKNNKIRYPSFOKEY 114

QY 144 SEPEMLEKSNISXSTDLGRCAEPFATV-----AMDKNKATK 184

Db 115 GEINLVBSVTTNTKKNIDYKGIYNGKKVNIKVLVSNHLYSDTLPNMLDNNYTKTH 174

QY 185 YR-----YPFVYDSKRLCHILVYVSMQLMGSKKYSVKGEBPDLTWYCFKPKSVTEN 237

Db 175 FDDGVTNNNGAMSKSKRT--VLWISDLVFSGIY-----HSTQNN 214

QY 228 HHLIYSAVYGENP-----DAFIS-KCPNQA-----LRGYRFGWKKGRCLDYTELDT 285

Db 215 VQLV--ATYEDGSPVQPSGDTFFISNLPAGGKSTDLKG--EYAHYDKMNTTDMVVRDT 271

QY 286 VIERVESRAQCWVKTFENDGVAADOPHTYPLTQASNDWMLHOSDQPHSGGVRNYGF 345

Db 272 VLSEFKS-----FYNNLNVVGGHPGSSKLTQAD--NDFNNLH----- 307

QY 346 YVDTGKCALSDQVVDCLVSDSAVSYTRAAGSLSEETNFIIPSP----- 394

Db 308 ---DXLDGPKFGQG-----TVSEKISBANPFLVIGSSNVOTWFTLSAT 348

QY 395 --SVTPPTPE 402

Db 349 IFSVDPDPE 358

RESULT 34

PCT-US93-07923-11

Sequence 11, Application PC/TUS9307923

GENERAL INFORMATION:

APPLICANT: Morimoto, Chikao

APPLICANT: Schlossman, Stuart F.

APPLICANT: Tanaka, Yoshiaki

TITLE OF INVENTION: HUMAN CD26 AND METHODS FOR USE

NUMBER OF SEQUENCES: 16

CORRESPONDENCE ADDRESS:

ADDRESS: Fish & Richardson

STREET: 225 Franklin Street

CITY: Boston

STATE: Massachusetts

COUNTRY: U.S.A.

ZIP: 02110-2894

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM PS/2 Model 502 or 55SX

OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)

SOFTWARE: WordPerfect (Version 5.0)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/07923

FILING DATE: 19930819

CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 07/934,162

FILING DATE: 21-AUG-1992

APPLICATION NUMBER: 07/832,211

FILING DATE: 06-FEB-1992

ATTORNEY/AGENT INFORMATION:

NAME: Frazer, Janis K.

REGISTRATION NUMBER: 34,819

REFERENCE/DOCKET NUMBER: 00530/055002

TELECOMMUNICATION INFORMATION:

TELEPHONE: (617) 542-5070

TELEFAX: (617) 542-8906

INFORMATION FOR SEQ ID NO: 11:

SEQUENCE CHARACTERISTICS:

LENGTH: 593

TYPE: amino acid

STRANDEDNESS:

TOPOLOGY: linear

PCT-US93-07923-11

Query Match 3.2%; Score 93.5; DB 5; Length 593;

Best Local Similarity 20.8%; Pred. No. 2.1;

Matches 99; Conservative 62; Mismatches 155; Indels 161; Gaps 29;

QY 1 MGLVGVQLL-VLVADCTIFASGLSSSTR-SRESQTLASISGNFQANVEKTEMEREN 58

Db 9 IGLLAALAVTTITVAVLLNKGTDAVADSKTYTLT-----DYKNTYRIKLKLSKRWI 63

QY 59 LTHHSGIYVDLGDQKEVDGTLTYREPAGLCPIMGKHIELQDPRLPYRNN--FLEDVPT 116

Db 64 SDHEV-----LYKQENNLIVF-----NAEYGNSSVFLFN-ST 94
Qy 117 EKEKYQSGNPLPGFNLFVTPSPGORISPPMELLEKNKNIKASTDLGRCAPAFKTYVM 176
Db 95 FDEFGHSINDYS-----ISPDGQFI-----LLE----- 117
Qy 177 DKNKATKYRYPF-----VYDSKKRLCHLLVYSMOLMEKKYCSVKGEPDILTWCYFKPR 231
Db 118 --YNYVQWRHSHYSTASYDIYDLNKR-----QLITERI-----PNNQWMTWS- 159
Qy 222 KSVTNHNLVYSAYVGENPDAFISCKPQALRGFRFGVKKGRCLDYTELTDTYIER-- 289
Db 160 ---VGHXL-----AYVMYN-DIYVXIEBP--LPSYRI-TWTKEDIIYIGTIDWYEEBV 207
Qy 290 VESKAQCWKTFFENGVASDQPHTYPLTSQASMNW-MPLHSDQPHSGVGRNRYGYV 348
Db 208 FSAVYALN--WSPNGT-----FLVYAOFNDETEVLE-----YSFYSD 243
Qy 349 DTTGEGKALSDQVDPCLVSDSAVSYTAAGSLSEETPFILPSNPSTVPTPETALQCT 408
Db 244 E-----SLQYF-----KTVRPYPRAGAVN-PTYKFFVYVNTDLSLSTVNTATSIQT 288
Qy 409 ADKFPDSF-----GACDVQACRKQKTSYVG-GQIGSTSVYDCTADEQNECGSNALIA 459
Db 289 A---FASMLIGDHYLCDVTWATQERISLQWLRRIQNYSVMDICDYDESGRWNCIVA 342

RESULT 35
US-09-310-463-2
; Sequence 2, Application US/09310463A
; Patent No. 6384203
; GENERAL INFORMATION:
; APPLICANT: Cosman, David J.
; APPLICANT: Anderson, Dirk M.
; APPLICANT: Borges, Luis
; TITLE OF INVENTION: Family of Immunoregulators Designated Leukocyte Immunoglobulin-
; FILE REFERENCE: 2624-A
; CURRENT FILING DATE: 1999-05-12
; EARLIER APPLICATION NUMBER: US/09/310,463A
; EARLIER FILING DATE: 1997-04-24
; NUMBER OF SEQ ID NOS: 39
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 650
; TYPE: PRT
; ORGANISM: human
US-09-310-463-2

Query Match 3.2%; Score 93.5; DB 4; Length 650;

Best Local Similarity 20.8%; Pred. No. 2.5;
Matches 51; Conservative 34; Mismatches 91; Indels 69; Gaps 7;

Qy 293 KAQCWVKTFFENDGVASDQPHTYPLTSQASMNWMLHSDQPHSGVGRNRYGYVVDITG 352
Db 347 OSQGMQTF-----LITKEGADDPMLRLRSTYOSK----- 377
Qy 353 EGKCALSDQVDPCLVSDSAVSYTAAGSLSE-----TPNFILPSNPSTVPTPETA 404
Db 378 -----YQAEFPMGPVTSAHAGTYRCYGSQSKPYLLTHPSDPLDELVLVSGSGGSPSPTTG 432
Qy 405 LQCTADKRPDSFGACDVQACRKQKTSYVGQIGSTSVYDCTADEQNECGSNALIALGLAVG 464
Db 433 -----PTSTSGPDPDPLT-PTGSDPQSGLRHLGVLIV 468
Qy 465 GVLLTALLGGCGYFAKRLDRNKGVOAHNHEFOSDRGARKRPSD--LMQEAESPWDE 522
Db 469 VILLILLILLFLIRHRROGKMTSTORKADFQHPAGAVPEPFDRLQWRSSPA--DA 527
Qy 523 AEENI 527
|||:

Db 528 OEENL 532

RESULT 36
US-08-842-248A-2
; Sequence 2, Application US/08842248A
; Patent No. 6448035
; GENERAL INFORMATION:
; APPLICANT: Cosman, David J.
; TITLE OF INVENTION: Family of Immunoregulators Designated
; NUMBER OF SEQUENCES: 29
; CORRESPONDENCE ADDRESSES:
; ADDRESS: Janis C. Henry, Immunex Corporation
; STREET: 51 University Street
; CITY: Seattle
; STATE: WA
; COUNTRY: US
; ZIP: 98101
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM/PC Compatible
; SOFTWARE: Microsoft Word 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/842,248A
; FILING DATE: April 24, 1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Henry, Janis C.
; REGISTRATION NUMBER: 34,347
; REFERENCE/DOCKET NUMBER: 2624
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 587-0430
; TELEFAX: (206) 233-0644
; TELEX: 756822
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 650 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-842-248A-2

Query Match 3.2%; Score 93.5; DB 4; Length 650;

Best Local Similarity 20.8%; Pred. No. 2.5;
Matches 51; Conservative 34; Mismatches 91; Indels 69; Gaps 7;

Qy 293 KAQCWVKTFFENDGVASDQPHTYPLTSQASMNWMLHSDQPHSGVGRNRYGYVVDITG 352
Db 347 OSQGMQTF-----LITKEGADDPMLRLRSTYOSK----- 377
Qy 353 EGKCALSDQVDPCLVSDSAVSYTAAGSLSE-----TPNFILPSNPSTVPTPETA 404
Db 378 -----YQAEFPMGPVTSAHAGTYRCYGSQSKPYLLTHPSDPLDELVLVSGSGGSPSPTTG 432
Qy 405 LQCTADKRPDSFGACDVQACRKQKTSYVGQIGSTSVYDCTADEQNECGSNALIALGLAVG 464
Db 433 -----PTSTSGPDPDPLT-PTGSDPQSGLRHLGVLIV 468
Qy 465 GVLLTALLGGCGYFAKRLDRNKGVOAHNHEFOSDRGARKRPSD--LMQEAESPWDE 522
Db 469 VILLILLILLFLIRHRROGKMTSTORKADFQHPAGAVPEPFDRLQWRSSPA--DA 527
Qy 523 AEENI 527
|||:

RESULT 37
US-08-985-950-22
; Sequence 22, Application US/08985950
; Patent No. 6140076

GENERAL INFORMATION:
APPLICANT: Adema, Gosse Jan
TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/985,950
FILING DATE: 05-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/041,279
FILING DATE: 21-MARCH-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/033,181
FILING DATE: 16-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/032,252
FILING DATE: 06-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0670K
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-9196
TELEFAX: (650) 496-1204
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 651 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-985-950-22

Query Match 3.2%; Score 93.5; DB 3; Length 651;
Best Local Similarity 20.8%; Pred. No. 2.5;
Matches 51; Conservative 34; Mismatches 91; Indels 69; Gaps 7;

QY 293 KAQCWKTFENDGVASDDPHYPLTSQASWMDMPLHSDOPHSGVGRNRYGVYVDTTG 352
DB 347 OSQGMWQTF-----LITKGAADDPMLRSTYOSQ----- 377

QY 353 EKGKALSDQVDPCLVSDSAVSYTAAGSLSE-----TNPFIIPSNPSVTPPTETA 404
DB 378 -----YQAEFPMGPYTSAAHAGYRCYGSQSKRPYLTHPSDLLELVSGSPSGPSTTG 432

QY 405 LQCTADKPPDSFGACDVQACRKQKTSYVGGQIQSTSVDTCTADEQNECGSNLTALIGLAVG 464
DB 433 -----PTSTSGPEDPQLT-PTGSDPQSGLRHLGLVIGILVA 468

QY 465 GVLLTALLGGCYFAKRLDRNKGVQAAHNEHFOSDRGARKKRPSPD--LMOEAPSPFWE 522
DB 469 VILLTLLTLLFLILHRRQGHWTSTQRKADQHPAGAVGPEPTDRRLQMRSSPA--DA 527

QY 523 AEENI 527
DB 528 QEENL 532

RESULT 38
US-09-546-049-22
Sequence 22, Application US/09546049
Patent No. 6479638

GENERAL INFORMATION:
APPLICANT: Adema, Gosse Jan
TITLE OF INVENTION: Isolated Mammalian Monocyte Cell Genes;
NUMBER OF SEQUENCES: 22
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/546,049
FILING DATE: 10-APR-2000
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/985,950
FILING DATE: 05-DEC-1997
APPLICATION NUMBER: US 60/041,279
FILING DATE: 21-MARCH-1997
APPLICATION NUMBER: US 60/033,181
FILING DATE: 16-DEC-1996
APPLICATION NUMBER: US 60/032,252
FILING DATE: 06-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0670K
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 852-9196
TELEFAX: (650) 496-1204
INFORMATION FOR SEQ ID NO: 22:
SEQUENCE CHARACTERISTICS:
LENGTH: 651 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 22:
US-09-546-049-22

Query Match 3.2%; Score 93.5; DB 4; Length 651;
Best Local Similarity 20.8%; Pred. No. 2.5;
Matches 51; Conservative 34; Mismatches 91; Indels 69; Gaps 7;

QY 293 KAQCWKTFENDGVASDDPHYPLTSQASWMDMPLHSDOPHSGVGRNRYGVYVDTTG 352
DB 347 OSQGMWQTF-----LITKGAADDPMLRSTYOSQ----- 377

QY 353 EKGKALSDQVDPCLVSDSAVSYTAAGSLSE-----TNPFIIPSNPSVTPPTETA 404
DB 378 -----YQAEFPMGPYTSAAHAGYRCYGSQSKRPYLTHPSDLLELVSGSPSGPSTTG 432

QY 405 LQCTADKPPDSFGACDVQACRKQKTSYVGGQIQSTSVDTCTADEQNECGSNLTALIGLAVG 464
DB 433 -----PTSTSGPEDPQLT-PTGSDPQSGLRHLGLVIGILVA 468

QY 465 GVLLTALLGGCYFAKRLDRNKGVQAAHNEHFOSDRGARKKRPSPD--LMOEAPSPFWE 522
DB 469 VILLTLLTLLFLILHRRQGHWTSTQRKADQHPAGAVGPEPTDRRLQMRSSPA--DA 527

QY 523 AEENI 527

Db 528 OEENL 532

RESULT 39

US-08-230-491A-3

Sequence 3, Application US/08230491A

Patent No. 5587299

GENERAL INFORMATION:

APPLICANT: Rettig, Wolfgang J.; Scanlan, Matthew J.;

APPLICANT: Garin-Chesa, Pilar; Old, Lloyd J.

TITLE OF INVENTION: ISOLATED NUCLEIC ACID MOLECULE CODING FOR

TITLE OF INVENTION: FIBROBLAST ACTIVATION PROTEIN, AND USES

TITLE OF INVENTION: THEREOF

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESS: FELFE & LYNCH

STREET: 805 THIRD AVENUE

CITY: NEW YORK

STATE: NEW YORK

COUNTRY: USA

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: DISKETTE 3.5 inch 1.2 MB STORAGE

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: WORDPERFECT - ASC II

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/230,491A

FILING DATE: 20-APRIL-1994

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. 5587299man D.

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: LUD 330

TELEPHONE: (212) 688-9200

TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 766 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-230-491A-3

Query Match 3.2%; Score 93.5; DB 1; Length 766;

Best Local Similarity 20.8%; Pred. No. 3.3; Mismatches 155; Indels 161; Gaps 29;

Matches 99; Conservative 62; Mismatches 155; Indels 161; Gaps 29;

Matches 99; Conservative 62; Mismatches 155; Indels 161; Gaps 29;

Matches 99; Conservative 62; Mismatches 155; Indels 161; Gaps 29;

Matches 99; Conservative 62; Mismatches 155; Indels 161; Gaps 29;

Matches 99; Conservative 62; Mismatches 155; Indels 161; Gaps 29;

Matches 99; Conservative 62; Mismatches 155; Indels 161; Gaps 29;

Matches 99; Conservative 62; Mismatches 155; Indels 161; Gaps 29;

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Matches 99; Conservative 62; Mismatches 155; Indels 161; Gaps 29;

Matches 99; Conservative 62; Mismatches 155; Indels 161; Gaps 29;

Matches 99; Conservative 62; Mismatches 155; Indels 161; Gaps 29;

Matches 99; Conservative 62; Mismatches 155; Indels 161; Gaps 29;

Matches 99; Conservative 62; Mismatches 155; Indels 161; Gaps 29;

Qy 349 DTGEGKALSDQVDCILVSDAASVYTAAGSLSEETPNFIIPNSPVTPTPETALQCT 408
Db 244 E-----SLQYP-----KTVRVVPYKAGAVN-PTVKFVVVNTDLSLSVTNATSIQIT 288
Qy 409 ADKPPDSF-----GACDYQACKRQKTSVCG-GQIQSTSVDCIAPBQNECGSNTALIA 459
Db 289 A---PASMLIGDHYLCVMTATQERISLQWLRIQNVNSVMDICDYDESSGWNCLVA 342

RESULT 40

US-08-619-280A-3

Sequence 3, Application US/08619280A

Patent No. 5767242

GENERAL INFORMATION:

APPLICANT: Zimmermann, Rainer; Park, John E.;

APPLICANT: Rettig, Wolfgang; Old, Lloyd J.

TITLE OF INVENTION: ISOLATED DIMERIC FIBROBLAST ACTIVATION PROTEIN

TITLE OF INVENTION: ALPHA, AND USES THEREOF

NUMBER OF SEQUENCES: 10

CORRESPONDENCE ADDRESS:

ADDRESS: Felfe & Lynch

STREET: 805 Third Avenue

CITY: New York City

STATE: New York

COUNTRY: USA

ZIP: 10022

COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 2.0 MB storage

COMPUTER: IBM PS/2

OPERATING SYSTEM: PC-DOS

SOFTWARE: Wordperfect

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/619,280A

FILING DATE: 18-MARCH-1996

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/230,491

FILING DATE: 20-APRIL-1994

ATTORNEY/AGENT INFORMATION:

NAME: Hanson, No. 5767242man D.

REGISTRATION NUMBER: 30,946

REFERENCE/DOCKET NUMBER: LUD 5330.1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (212) 688-9200

TELEFAX: (212) 838-3884

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 766 amino acids

TYPE: amino acid

TOPOLOGY: linear

US-08-619-280A-3

Query Match 3.2%; Score 93.5; DB 1; Length 766;

Best Local Similarity 20.8%; Pred. No. 3.3; Mismatches 155; Indels 161; Gaps 29;

Matches 99; Conservative 62; Mismatches 155; Indels 161; Gaps 29;

Matches 99; Conservative 62; Mismatches 155; Indels 161; Gaps 29;

Matches 99; Conservative 62; Mismatches 155; Indels 161; Gaps 29;

Matches 99; Conservative 62; Mismatches 155; Indels 161; Gaps 29;

Matches 99; Conservative 62; Mismatches 155; Indels 161; Gaps 29;

Matches 99; Conservative 62; Mismatches 155; Indels 161; Gaps 29;

Matches 99; Conservative 62; Mismatches 155; Indels 161; Gaps 29;

Matches 99; Conservative 62; Mismatches 155; Indels 161; Gaps 29;

Matches 99; Conservative 62; Mismatches 155; Indels 161; Gaps 29;

Matches 99; Conservative 62; Mismatches 155; Indels 161; Gaps 29;

Matches 99; Conservative 62; Mismatches 155; Indels 161; Gaps 29;

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Matches 99; Conservative 62; Mismatches 155; Indels 161; Gaps 29;

Matches 99; Conservative 62; Mismatches 155; Indels 161; Gaps 29;

Matches 99; Conservative 62; Mismatches 155; Indels 161; Gaps 29;

Matches 99; Conservative 62; Mismatches 155; Indels 161; Gaps 29;

Matches 99; Conservative 62; Mismatches 155; Indels 161; Gaps 29;

Matches 99; Conservative 62; Mismatches 155; Indels 161; Gaps 29;

Matches 99; Conservative 62; Mismatches 155; Indels 161; Gaps 29;

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Db      160  ---VGHL-----ATVMNN-DIYVIEPN-LPSYRI-TWTGKEDIYNGITDWMYEEBV 207
Qy      290  VESKAQCWKTPENDGVASDOPHTYPLTSQASMDM-WPLHQSOPHSGVGGRNYGFYV 348
Db      208  FSAYSALW---WSPNGT-----FLAYAQFNDTEVPLIE-----YSFYSD 243
Qy      349  DTTGEGKCALSDQVDPDCLVSDSAVSYTAAGSLSEETPNFIIPSNPSVTPTPTETALQCT 408
Db      244  E-----SLQYP-----KTVRVYPRAGAVN-PTVKFVYNTDSLSSVTNATSIQIT 288
Qy      409  ADKFPDSF-----GACDVQACKRKOKTSCVG-GOIQTSVDTADREQNECGSNTALIA 459
Db      289  A---PASMIGDHYICDVTWATQERISLQMLRRIQNYSMIDICDYDESSGRNCLVA 342
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Search completed: October 2, 2003, 15:53:02
Job time : 35 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 2, 2003, 15:39:04 ; Search time 83 Seconds

(without alignments)
1034.591 Million cell updates/sec

Title: US-10-039-770A-1

Perfect score: 2322
Sequence: 1 MGLGVGVLLVADCTIFA.....EAEENIEODGETHVGEDY 541

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_19Jun03.*
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24: /SIDSI/gcgdata/geneseq/geneseq-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	452	15.5	86	ABP56991	Toxoplasma gondii
2	431	14.8	622	10 AAP91632	Rhoptry membrane a
3	420.5	14.4	563	12 AAR10551	Plasmodium knowles
4	418	14.3	622	13 AAR27532	Plasmodium falcipar
5	418	14.3	622	16 AAR68840	Plasmodium falcipar
6	412	14.1	622	23 AAU93359	Synthetic P. falcip
7	410	14.0	622	23 AAU93360	P. falciparum apic
8	404	13.8	478	24 ABB99416	Amino acid sequenc
9	403	13.8	654	23 ABB70931	Plasmodium AMA-1/M

10	395	13.5	561	10 AAP91588	Rhoptry membrane a
11	391	13.4	1807	22 AAB85697	Recombinant protei
12	391	13.4	2028	22 AAB85698	Plasmodium vivax 6
13	357	12.2	489	12 AAR10935	Plasmodium yoelii
14	120	4.0	1507	21 AAB24128	Novel human diagno
15	118	4.1	2519	22 AAB61636	Novel human diagno
16	113	3.9	996	22 AAB39322	Novel human diagno
17	113	3.9	1023	22 AAG22883	Novel human diagno
18	113	3.9	1023	22 AAM79772	Human protein SEQ
19	113	3.9	1023	22 AAM79773	Human protein SEQ
20	113	3.9	1023	22 AAM41108	Human polypeptide
21	113	3.9	1076	23 AAU74355	Human cytoskeleton
22	113	3.9	1581	22 AAM78788	Human protein SEQ
23	107.5	3.7	1104	17 AAB94957	NP-X1 DNA-binding
24	104	3.6	355	23 AAB97742	Human proteinase
25	104	3.6	1200	21 AAB21208	Human HER-2/neu pr
26	104	3.6	1213	23 AAB25604	Streptococcus poly
27	104	3.6	1255	17 AAM01111	Human HER-2/neu on
28	104	3.6	1255	20 AAM92406	Human HER-2/neu pr
29	104	3.6	1255	21 AAB21198	Amino acid sequenc
30	104	3.6	1255	21 AAB84780	Human HER-2/neu pr
31	104	3.6	1255	22 AAB85458	Human HER-2/neu pr
32	104	3.6	1255	22 AAG88267	Human tyrosine kin
33	104	3.6	1255	23 AAE20479	Human HER-2/neu pr
34	104	3.6	1255	23 AAE20479	Human HER-2/neu pr
35	104	3.6	1255	23 AAM51143	Human HER-2/neu pr
36	104	3.6	1255	23 AAU77114	Sequence of c-erbB
37	104	3.6	1433	14 AAR39568	Human colon cancer
38	103.5	3.5	365	21 AAB53307	Human breast cance
39	103.5	3.5	1223	23 AAG75613	Human tyrosine kin
40	103	3.5	1223	23 AAU98923	Human HER-2/neu pr
41	103	3.5	1255	21 AAY92620	Human HER-2/neu pr
42	103	3.5	1255	22 AAE12130	Human HER-2/neu pr
43	103	3.5	1255	22 AAB60167	Human HER-2/neu pr
44	103	3.5	1255	23 AAE26349	Human HER-2/neu pr
45	103	3.5	1255	23 AAE26366	Human HER2 antigen

ALIGNMENTS

RESULT 1	ABP56991	standard; Peptide: 86 AA.
ID	ABP56991	
XX	ABP56991	
AC	ABP56991	
XX	10-APR-2003	(first entry)
DT	10-APR-2003	
XX	Toxoplasma gondii	AMAI amino acid sequence fragment.
DE	Toxoplasma gondii	AMAI amino acid sequence fragment.
XX	Elmeria maxima; 250 kDa antigen; sporozoite; merozoite; infection;	
KW	Elmeria maxima; 250 kDa antigen; sporozoite; merozoite; infection;	
KM	vacine; antiparasitic; gene therapy.	
XX	Toxoplasma gondii.	
OS	Synthetic.	
XX	W02003004684-A2.	
FN	W02003004684-A2.	
XX	16-JAN-2003.	
PD	16-JAN-2003.	
XX	03-JUL-2002; 2002MO-US21237.	
PF	03-JUL-2002; 2002MO-US21237.	
XX	06-JUL-2001; 2001US-303670P.	
PR	06-JUL-2001; 2001US-303670P.	
XX	(WITC/) WITCOMBE D.	
PA	(WITC/) WITCOMBE D.	
PA	(SMIT/) SMITH N C.	
XX	(WALL/) WALLACH M.	
XX	(WALL/) WALLACH M.	
PI	Witcombe D, Smith NC, Wallach M;	
XX	Witcombe D, Smith NC, Wallach M;	
XX	WPI; 2003-201556/19.	
DR	WPI; 2003-201556/19.	
XX		

PT New nucleic acid comprising a sequence encoding a 250 kDa polypeptide
PT from sporozoites/merozoites of *Eimeria maxima*, useful for preparing a
PT vaccine against *Eimeria* infection
XX
XX
PS Example 5; Fig 33; 198pp; English.
CC The present invention describes a nucleic acid (1) comprising a
CC sequence encoding a 250 kDa polypeptide from sporozoites/merozoites of
CC *Eimeria maxima* or its homologue or complement. Also described: (1) a
CC vector comprising the nucleic acid; (2) a host cell comprising the
CC vector; (3) a plasmid comprising the nucleic acid; (4) a transformed
CC cell comprising the nucleic acid; (5) producing a recombinant 250 kDa
CC polypeptide; (6) a recombinant polypeptide; (7) a vaccine against
CC *E. tenella*, *E. acervulina*, *E. necatrix*, *E. praecox*, *E. maxima*, *E. mitis*
CC or *E. brunetti* or a microorganism expressing an immunologically
CC cross-reactive antigen; (8) immunising a subject against infection by
CC *Eimeria*, or a microorganism expressing an immunologically cross-reactive
CC antigen; (9) conferring upon a newborn subject of an avian species
CC maternal immunity against infection by *Eimeria*; (10) a fertilised egg
CC from an avian species having an air sac, where the air sac is inoculated
CC with the vaccine; and (11) reducing the output of *Eimeria* oocysts in
CC faeces from a newborn subject of an avian species. (1) has antiparasitic
CC activity and can be used in a vaccine and in gene therapy. The nucleic
CC acid is useful for preparing a vaccine against *E. tenella*, *E. acervulina*,
CC *E. necatrix*, *E. praecox*, *E. maxima*, *E. mitis* or *E. brunetti* infection.
CC The present sequence represents an amino acid sequence used in an example
CC from the present invention.
XX
XX
SQ Sequence 86 AA;
Query Match 15.5%; Score 452; DB 24; Length 86;
Best Local Similarity 100.0%; Pred. No. 1.8e-34;
Matches 86; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Oy 456 ALINGLAVGVLLALLGGGCFARLDRNKGVQAHHHEHFOSDRGARKRPSDLMQEA 515
Db 1 ALINGLAVGVLLALLGGGCFARLDRNKGVQAHHHEHFOSDRGARKRPSDLMQEA 60
Oy 516 EPSFWEAEENIEODGETHVVEGDY 541
Db 61 EPSFWEAEENIEODGETHVVEGDY 86
RESULT 2
AAP91632
ID AAP91632 standard; Protein; 622 AA.
XX
XX
AC AAP91632;
DT 25-MAR-2003 (updated)
DT 25-JAN-1990 (first entry)
XX
XX
DE Rhoptry membrane antigen-1.
XX
XX
KM Malaria; rhoptry membrane antigen-1; antibodies.
XX
XX
OS Plasmodium falciparum D10.
XX
XX
PN WO8907645-A.
XX
XX
PD 24-AUG-1989.
XX
XX
PF 10-FEB-1989; 89WO-AU00056.
XX
XX
PR 12-FEB-1988; 88AU-0006743.
XX
XX
PA (SARA-) SARAWANE PTY LTD.
PI Peterson MG, Crewther PE, Smythe JA, Marshall VM, Silva A;
DR WPI; 1989-263714/36.
DR N-PSDB; AAN90703.
XX

PT Rhoptry membrane antigen of *Plasmodium falciparum*
PT - used for producing antibodies and in immunisation,
PT diagnostic and treatment methods for malaria.
XX
XX
PS Claim 1; Fig 3; 46pp; English.
XX
XX
CC RMA-1 can generate an immune response to malaria, and antibodies which
CC can inhibit growth of the parasite. RMA-1 initially has mol. wt. 80 kD.
CC (updated on 25-MAR-2003 to correct PA field.)
XX
XX
SQ Sequence 622 AA;
Query Match 14.8%; Score 431; DB 10; Length 622;
Best Local Similarity 26.2%; Pred. No. 3.8e-31;
Matches 149; Conservative 86; Mismatches 212; Indels 122; Gaps 24;
Oy 41 GNPQANVEKTMERENLTHHQSGLYVDLGQDKVEYDGLYBPAGLCPIWKGHILQ 100
Db 107 GNPW-----TEWAKYDIEVHGSGIRVDLGEAEVAGTQYRLPSCGCPVFGGIIEN 160
Oy 101 PDRLPYNNFLDYPTKEKYGKSGNPLPGGFNLPVTPSGQRI SPFME---LLEKNSN 156
Db 161 SN-----TTLTPVATGNQYLKD---GGPAP---PTEPLMSPTLDEMRHFKNKY 207
Oy 157 IKASTDGRCAEFAPKTVAMDKNKATKRYPPVYDSKRLCHILYVSMQLMGKKYCSV 216
Db 208 VKNDELTLCSRHAGNMI--PDNDKNSNYKYPAYDDKDKKCHILYIAQENNGPRYCN- 264
Oy 217 KGEPPDLTWYCFKPKSVTENHILYSAVGER-PAFISKPNQALRGYRGVWKGR 275
Db 265 KDESKRSMFCFREPANDISFONY-----TYSKVVVNMKVCPRKVLQNAKFGLVWGN 319
Oy 276 CLDYTELTD-TVIRVVSQAQCVKTFPNDGVASDQHTYP--LTSQASWMDMP----- 327
Db 320 CEDLPVHVSADLFE---CNKLVEELS--ASDQKQEQHHTDYBKIKGFKNNAS 373
Oy 328 -----LHQSQPHSGGVGRNYGYVDTTGCKCALSDQVPCLVSDSAVSYTA 377
Db 374 MKSAFLPTGAFAKDRKSHKGYMGNYNTEQ---KCEIFNVKPTCLINSSYIATTA 430
Oy 378 AGSISEETPNFIITSN-----PSTPTPETAL 405
Db 431 LSHPIEVEHNP--PCSLYKNEIMKEIERESKRILKNDNDGNNKIAPRIFISDDKSL 488
Oy 406 OCTADKFPDSFGADVQACKRKQKTSQVGGQISTSVDTA-----DEONECGSN----- 454
Db 489 KCPCDPEIVSNSTCNFVCK-----CVRRAEVTSNNEVYKKEYKDYADIPHKPTVD 543
Oy 455 --TALINGLAVGVLLALLGGGCFARLDRNKGVQAHHHEHFOSDRGARKRPSDLM 512
Db 544 KMKIIIISSAAVAVLATILM---VYLKVR-----KGNMEKYDKMDEPHYGKSNR-NDEN 595
Oy 513 QEAPPSFWEAEENIEODGETHVVEGDY 541
Db 596 LDPEASFWEGER--RASHTTPVLMEKRY 621
RESULT 3
AAR10551
ID AAR10551 standard; Protein; 563 AA.
XX
XX
AC AAR10551;
DT 25-MAR-2003 (updated)
DT 17-DEC-2001 (updated)
DT 15-APR-1991 (first entry)
XX
XX
DE Plasmodium knowlesi 66kD merozoite antigen protein.
XX
XX
KM Plasmodium merozoite antigens; malaria vaccine.
XX
XX
OS Plasmodium knowlesi.
XX

PX	NN	USN7483516-N.
XX	PD	15-JAN-1991.
XX	PF	22-FEB-1990; 90US-0483516.
XX	PR	22-FEB-1990; 90US-0483516.
PA	(USSH) NAT INST OF HEALTH.	
PA	(USDC) US SEC OF COMMERCE.	
PI	Waterer AP, McCutchan TF;	
DR	MPI: 1991-044381/06.	
N-	N-PDB; AAQ10418.	
PT	Plasmodium mezoite antigen proteins and DNA sequences - useful	
PT	in vaccine prodn., anti-malarial drug design, and in diagnostics	
PS	Disclosure; fig 1; 3pp; English.	
CC	This protein is encoded by a recombinant DNA molecule comprising	
CC	the complete p.knowlesi merozoite antigen gene and e.g. a pUC19	
CC	or vaccinia virus vector sequence and regulatory elements.. This	
CC	allows efficient expression of the antigen on transformation of	
CC	host cells. It is useful in an anti-malarial vaccine for con-	
CC	ferring immunity against the merozoite form of the parasite and	
CC	preventing infection of uninfected red blood cells.	
CC	See also AAOJ10869.	
CC	(Note: Revised entry submitted to correct the patent number format of	
CC	US Government-owned NTIS applications to prevent clashes with ongoing US	
CC	granted patent numbers. For further information please visit the Derwent	
CC	web site at www.derwent.com/dmpi/updates/ntis_us.html.)	
CC	(Updated on 25-MAR-2003 to correct PA field.)	
XX	Sequence 563 AA:	
Dn	Query Match 14.4%; Score 420.5; DB 12; Length 563;	
Dn	Best Local Similarity 24.6%, Pred.No.3.1e-30;	
Dn	Matches 148; Conservative 95; Mismatches 251; Indels 107; Gaps 24	
QY	6 VQVLLVLVADDTIFASGL---SSSTRRESQTLSASTSGNPQAAMW---KTEMERN 58	
Bd	' 4 IYYILFLSAOCLVMHGKEBERNKTRTLRSANNALBKGPILERIRSMPPAKMMEKD 63	
QY	59 LTHHHQSGLIYDLGDDKEYDGTLYRPAGLCFTIGKHIELQQPRLPYRNLFLEDPVT-E 117	
Bd	64 LEHANNSGIIRDLEGDAEFGNSKYRIIPAGKCVPFEGKIIVENS-----VSFLTGVATGA 118	
QY	118 KEYQGSGRPLPGGFNLNFVTBPGSGLISPFP----ELEKNSNIKASTDLGCAPAFRT 173	
Bd	119 ORLKEGGAFPNT-----ADDHISPTTINLKERYKENNDMLKLINDIALCKTHASF 169	
QY	174 VAMDQNNAKTARYEPFYVDYSKKRLCHIIYVMSQLMEKGKYCSVKGEPPDLTWYCERPKS 233	
Bd	170 VIAEDQN--TSYRHAVAYDEDKRKCTCYMYILSLAQEMNGRRYGSPDSQND-AHFCKPDXN 226	
QY	234 VTENHLHTLGSAHYVEGNPDAPFSKCPNOALKRGYRWGMKKGRCLDYTELTDLVIERVESK 293	
Bd	227 -EKFDNYLTLSKVNSND---MENKCRKRNLGNAGKGLAWDGNCBEI-----PVNVLEAR 277	
QY	294 A--OCMVTFENDGYAASDOPHTY--PLTSQASMNMWPPLHQSDOPHSQ----- 337	
Bd	278 SLRECNRLVFEE--ASASDQPROYEEBELIDYEIOGFEFRONNRDMTKSAFLPGAENSDF 335	
QY	338 -GVGENRYFYVDITTGEGKCALSDOVPCLVASAASYTAAG---SLSEETPNFIIBSN 393	
Bd	336 KSKGGVGMMAMPDVS-VNNKYVIFTFKPTCLINDKRFATTALSHPOEVDNPEFCGISYDE 394	
QY	394 -----PSVIPPETALOCTADKPFPSPGACDVQACKROKT 429	
Bd	395 IEREIKOSRMNMTLYSVDERIVLRIFRISTDKESIKCPCPEBHINSICTNEVC----- 449	

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Oy 430 SCV--GGGIQST-----VDCIADQNECGSN--TALLAGLAVGVLLALLGGGCTPK 480
Db 450 NCVEKRAEIKENNEVYIIKEEFKEDYENPDGKHKKMLIIIGVTAVCVVAASLFFERK 509
Oy 481 RLDRKKGVQAAMHEHEFQSDRGARKKRPSDLMQEAEPSPFWDAAEENIEODGETHWVEGD 540
Db 510 KAQDDK-----YDKRDQAEAVGKTANTRKDEMLDPEASFTWGEDK---RASHTTPLVMKRP 561
Oy 541 Y 541
Db 562 Y 562

RESULT 4
AAR27532
ID AAR27532 standard; Protein; 622 AA.
XX
XX AAR27532;
XX
XX 25-MAR-2003 (updated)
XX 08-MAR-1993 (first entry)
XX
XX Plasmodium falciparum AMA1 antigen.
XX
XX Recombinant poxvirus; antimalarial vaccine; malaria; immunise;
XX immunogen.
XX
XX Plasmodium falciparum.
XX
XX OS MO9216616-A1.
XX
XX PD 01-OCT-1992.
XX
XX PF 19-MAR-1992; 92WO-US02207.
XX
XX PR 20-MAR-1991; 91US-0672183.
XX PR 18-MAR-1992; 92US-0852305.
XX
XX PA (VIBRO-) VIROGENETICS CORP.
XX
XX PI De TAISNE C, Paolietti E, Tine JA;
XX
XX DR WPI; 1992-349203/42.
XX DR N-PSDB; AAO29189.
XX
XX PT Recombinant poxvirus - contg. Plasmodium DNA, useful as
XX PT antimalarial vaccine
XX
XX PS Example 4; Fig 5; 74pp; English.
XX
XX
XX This sequence is the Plasmodium falciparum AMA1 antigen.
XX cDNA encoding it was cloned into vaccinia donor plasmids
XX before being inserted into the vaccinia virus to be used in a
XX in vitro prodn. of gene prods. for use as immunogens. As plasmodium
XX genes are conserved among P. falciparum strains, they are widely
XX effective in a vaccine.
XX (Updated on 25-MAR-2003 to correct PN field.)
XX
XX
XX Sequence 622 AA;

Query Match 14.3%; Score 418; DB 13; Length 622;
Best local Similarity 26.5%; Pred. No. 6.3e-10;
Matches 151; Conservative 88; Mismatches 207; Indels 124; Gaps 26

Oy 41 GNPFQANVEMKTFMERFNLTHHHOSGIYVDLGGDKEVDGTLVREBAGLCPIWGHIELQO 100
Db 107 GNPF-----TEWMAKYDIEEWHGSGINVDLGEDAEVAGTGYRLPSGKCPVHGKIIEN 160
Oy 101 PDRLLPRYNPLFEDYPTKEKYQSGNPLPGCFNLNVTTSQGRISFPME---LLEKSN 156
Db 161 SN-----TTFLLPVATGQYLDK-----GGFAF--PTEPLMSPTLDEMRHFYKDNKY 207

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QY 157 IKASTDLGRCAEFKTVAMDKNKATKYRPFYVDSKKRLCHILYVSMQMLEGKCYCV 216
DB 208 VKNDELTLCSRHAGNM1--PNDKSNYKYPAYVDDDKCHILYIAQENNGRYCN- 264
QY 217 KGEPPDLTWYCFKPKRYSTENHLLYGSAYGEN-PDAFISKCPNQAALRGYRFGWKGR 275
DB 265 KDESERNMFCFRPAKDISFQNY-----TYSKVNVDWMEKVCPRKNLQNAKFGIWDGN 319
QY 276 CLDYTELTD-TVIERVESKACQWKTFFENDVASDQPHYTP--LTSQASMDWMP----- 327
DB 320 CEDIPHVEFPALIDFE---CNKLVFELS--ASDQPKQYEQHLTDYEKIKGKFNKQAS 373
QY 328 -----LHSDQPHSGGVGRNYGFYVDTTGBGCALSDQVPCLVSDSAVSYTA 377
DB 374 MIKSAFLPTGAFKADRYKSHGKYNMGNYTETQ--KCEIRNVKPTCLINSSYIATTA 430
QY 378 AGSLSEETPNF-----IIPNSVTPPTPETAQ--CTADKFPDSF 416
DB 431 LSHPIEVENNFCPSLYKDEIMKEIERESKRILKNDNDGKMKIMLQEFLLSDDK--DSL 488
QY 417 -GACDVQ-----ACRQKTSVCGQIOSTSV-----CTADEQNEC 451
DB 489 KRPCDPEWVNSSTCFEYVCKVERAEVTSNNEVVVKEEYDEYADIPBKPTDYKMKII 548
QY 452 GSNTALLAGLAVGVLLALLGGCYFAKRLDRNKGVAHNEHEFOSDRGARKKRPDL 511
DB 519 IASSARAVLAVT--ILMV-----YLYKR-----KGNMEKYDKMDEPDQYGSNSR-NDE 594
QY 512 MQEAPSPFWDEAEENIEODGETHVWEGDY 541
DB 595 MLDPEASFWGEK---RASHTTPVLMEXKY 621

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RESULT 5
AAR68840
ID AAR68840 standard; Protein; 622 AA.
XX
AC AAR68840;
XX
DT 25-MAR-2003 (updated)
DT 24-AUG-1995 (first entry)
XX
DE Plasmodium falciparum AMA-1 gene protein.
XX
KM Plasmodium falciparum AMA-1 gene; recombinant poxvirus;
KW multicomponent multistage malarial vaccines; immunogens;
XX malaria diagnosis.
XX
OS Plasmodium falciparum (3D7).
XX
PN WO9428930-A1.
XX
PD 22-DEC-1994.
XX
PF 10-JUN-1994; 94WO-US06652.
XX
PR 11-JUN-1993; 93US-0075783.
PR 09-JUN-1994; 94US-0257073.
XX
PA (VIRO-) VIROGENETICS CORP.
XX
PI De Taiene C, Paolucci E, Tine JA;
XX
DR WPI, 1995-036113/05.
DR N-PSDB; AAQ80910.
XX
PT Recombinant poxvirus confg. Plasmodium DNA in non-essential
XX Plasmodium immunogens
XX Clatm 3; Fig 5; 163pp; English.
XX
CC AAQ80910 encodes AAR68840 the P. falciparum AMA-1 gene product. New

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recombinant poxviruses containing either the SERA, ABRA, Pf8p70, CC AMA-1, Pf825, Pf816, CSP, Pf8SP2, LSA-1, LSA-1 repeats, MSA-1, CC MSA-1 (N-terminal p33 or C-terminal gp42) genes, or a combination CC of these in non-essential regions of their genomes are claimed. CC These poxviruses (pref. with a virulence reducing genomic CC deletion or disruption) can be used as vaccines against malaria CC and for the prodn. of Plasmodium immunogens. These viruses CC provide multicomponent, multistage vaccines due to their expression CC of sporozoite, liver stage, blood stage and sexual stage proteins. CC (Updated on 25-MAR-2003 to correct PN field.)

Sequence 622 AA;

Query Match 14.3%; Score 418; DB 16; Length 622;

Best Local Similarity 26.5%; Pred. No. 6,3e-30; Matches 151; Conservative 88; Mismatches 207; Indels 124; Gaps 26;

```

QY 41 GNPQANVEMKTFMERFNLTHHQSGLYVDIGQKEVDGTYREPAICLPWGHIELOQ 100
DB 107 GNPW-----TEYMAKYDIEVHSGIRVDIGEDAEVAGTQYRLPSGCKPVFGKILLEN 160
QY 101 PDRLPYRNPFIEDVPTKEKYQSGNPLRGFNLMFVTPSGGRISPFWE-----LLEKSN 156
DB 161 SN-----TTFLLPVATGNQYLKD-----GGFAP--PTEPLMSPTLDEMRHFFYKDNKY 207
QY 157 IKASTDLGRCAEFKTVAMDKNKATKYRPFYVDSKKRLCHILYVSMQMLEGKCYCV 216
DB 208 VKNDELTLCSRHAGNM1--PNDKSNYKYPAYVDDDKCHILYIAQENNGRYCN- 264
QY 217 KGEPPDLTWYCFKPKRYSTENHLLYGSAYGEN-PDAFISKCPNQAALRGYRFGWKGR 275
DB 265 KDESERNMFCFRPAKDISFQNY-----TYSKVNVDWMEKVCPRKNLQNAKFGIWDGN 319
QY 276 CLDYTELTD-TVIERVESKACQWKTFFENDVASDQPHYTP--LTSQASMDWMP----- 327
DB 320 CEDIPHVEFPALIDFE---CNKLVFELS--ASDQPKQYEQHLTDYEKIKGKFNKQAS 373
QY 328 -----LHSDQPHSGGVGRNYGFYVDTTGBGCALSDQVPCLVSDSAVSYTA 377
DB 374 MIKSAFLPTGAFKADRYKSHGKYNMGNYTETQ--KCEIFNVKPTCLINSSYIATTA 430
QY 378 AGSLSEETPNF-----IIPNSVTPPTPETAQ--CTADKFPDSF 416
DB 431 LSHPIEVENNFCPSLYKDEIMKEIERESKRILKNDNDGKMKIMLQEFLLSDDK--DSL 488
QY 417 -GACDVQ-----ACRQKTSVCGQIOSTSV-----CTADEQNEC 451
DB 489 KRPCDPEWVNSSTCFEYVCKVERAEVTSNNEVVVKEEYDEYADIPBKPTDYKMKII 548
QY 452 GSNTALLAGLAVGVLLALLGGCYFAKRLDRNKGVAHNEHEFOSDRGARKKRPDL 511
DB 519 IASSARAVLAVT--ILMV-----YLYKR-----KGNMEKYDKMDEPDQYGSNSR-NDE 594
QY 512 MQEAPSPFWDEAEENIEODGETHVWEGDY 541
DB 595 MLDPEASFWGEK---RASHTTPVLMEXKY 621

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RESULT 6

AAU9359

AAU9359 standard; Protein; 622 AA.

AAU9359;

26-SEP-2002 (first entry)

Synthetic P. falciparum AMA-1 ectodomain (FVO Pf83syn) protein.

Apical membrane antigen-1; AMA-1; protozoacide;

Plasmodium, ectodomain; malaria; parasite; vaccine; immune response;

epitope; FVO Pf83syn; mutant; mutcin.

Plasmodium falciparum.

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OS Synthetic.
XX Key Location/Qualifiers
FH Peptide 1..24
FT /label= Signal_peptide
FT Protein 25..622
FT /label= Mature_FVO_Pf83syn
FT Misc-difference 162
FT /note= "Wild-type Asn substituted by Lys"
FT Misc-difference 288
FT /note= "Wild-type Thr substituted by Val"
FT Misc-difference 373
FT /note= "Wild-type Ser substituted by Asp"
FT Misc-difference 422
FT /note= "Wild-type Asn substituted by Asp"
FT Misc-difference 423
FT /note= "Wild-type Ser substituted by Lys"
XX WO200252014-A2.
XX 04-JUL-2002.
XX 21-DEC-2001; 2001WO-NL00934.
XX 22-DEC-2000; 2000EP-0204697.
XX (BIOM-) STICHTING BIOMEDICAL PRIMATE RES CENT.
XX Kocken CHM, Thomas AW, Blackman MJ, Withers-Martinez C, Holder AA,
XX WPI; 2002-575381/61.
XX N-PSDB; ABK89028.
XX
XX Producing mRNA encoding Plasmodium AMA-1 ectodomain in yeast cell,
XX useful for preparing vaccines for treating or preventing malaria,
XX comprises providing the yeast cell with a nucleic acid encoding the
XX ectodomain
XX
XX Example 1; Fig 1; 42pp; English.
XX
XX The invention discloses the production of mRNA encoding Plasmodium
XX apical membrane antigen-1 (AMA-1) ectodomain, its functional part,
XX derivative and/or analogue in a yeast cell, which has been modified to
XX use the yeast's codon usage. Plasmodium falciparum (Pf) is the most
XX important human malaria parasite. At present there is no effective
XX vaccine against human malaria, but studies have indicated that the AMA-1
XX family of molecules are a target for protective immune responses. The
XX proteins have a predicted ectodomain and cytoplasmic domain and evidence
XX has identified that protection invoked by AMA-1 is directed at
XX conformational epitopes located in the ectodomain. The Plasmodium AMA-1
XX ectodomain, its functional part, derivative and/or analogue and the
XX proteolipid molecule are useful for diagnosing and preparing vaccines
XX or medicaments for preventing malaria caused by Plasmodium falciparum. Pf
XX AMA-1 has an unusually high A+T content and N-glycosylation sites which
XX make expression and deglycosylation in yeast difficult. The method
XX provides an efficient production of Plasmodium falciparum, strain FVO,
XX AMA-1 ectodomain in high amounts due to its effective expression in the
XX yeast Pichia pastoris. This is achieved by mutating the gene sequence
XX (FVO Pf83syn) to utilise the yeast's codon usage and remove the
XX N-glycosylation sites, which are not conserved in Plasmodium. The FVO
XX Pf83syn can be used to create vaccines against Plasmodium induced
XX malaria. The sequence presented is the synthetic P. falciparum AMA-1
XX ectodomain (FVO Pf83syn) protein.
XX
XX Sequence 622 AA:
XX
XX Query Match 14.1%; Score 412; DB 23; Length 622;
XX Best Local Similarity 26.0%; Pred. No. 2,3e-29;
XX Matches 149; Conservative 79; Mismatches 215; Indels 130; Gaps 25;
XX
XX 41 GNPFAANVEMKTFMRFLNTHHSGIYVDGQKVEVDGTLRPAAGLCPTWGKRIELQQ 100
XX ||| : : : : : : : : : : : : : : : : : : : : : : : : : : :
XX 107 GNPM-----TEYMAKYDIEVHGSGIRVDLGEADAEVAGTQYRLPSGKCPVFGKIIEN 160

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QY 101 PDRLPYRNFLFEDVPT-EKEYKOSGNPLPGGFNLNFTVPSGORISPFPM-----ELLEKNS 155
DB 161 S-----KTFPLKPAVATNGQDLKDGFAFP-----PTNPILSPMTLNGMRPFYKNE 206
QY 156 NIKASTDIGRCARFAFPAKTVAMDKNNKATKRYRPVYDSKKRLCHILYVSNOLMGSKYCS 215
DB 207 YVKNLDELTLCSRAAGN--NMPDNDKNSNYKPAVDYNDKCKHILYLAQENNGPRYCN 264
QY 216 VKGEPDLTWYCFPRK--SVTENHLLYGSAYVEN--PDATISCPNALGREGVKK 273
DB 265 -KQSKRNSMFCFRPADKLENY-----VLSKNVVDNMBEVCPRKLNNAKFGLVWD 317
QY 274 GRCLDYELTDVTLVERVESKAQCWKTFFENDVASDQPHYTP--LTSQASNMWMP----- 327
DB 318 GNCEDIPIRVNPF-----SANDLFECKVLTFELS--ASDPKQVEQHLTDVEKIKEGKYNKA 372
QY 328 -----LHSDQPHSGVGVRNYGFYVDTTGEGKCLSDQVPDCLVSDAASVYT 376
DB 373 DMKSAFLPTGAFADRYKSHGKGYNMGVNYRETQ---KCEIFVWKPTCLINDKSYIAT 429
QY 377 AAGSLSETPRPIIPSN-----PSTVPTPTETA 404
DB 430 ALSHPTEVENHP--PCSLYKDEIKKEIERESKRIKLNNDNDEGNKKIIAPRIFISDDKDS 487
QY 405 LQCTADKFPDSFGACDVQACRQKTSQVGGQIQSTST-----VDCTAD--EQNECG 452
DB 488 LKCPDPEBMSQSCRFVCK-----CYERAETSNNEVVYKREYDEYDIEBHRTY 542
QY 453 SNTALI-----AGLVAGVLLALLGGCYFAKRLDRNKGVQAAHHEFGSDRGARKRP 508
DB 543 DNMKIIIASNAVAVLAITLMV-----YLYKR-----KG-NARKYDKMDQPHYKSTSR 591
QY 509 SDLMQEAEPFMDAEENIBDDGETHYMVEDY 541
DB 592 NDEMLDPEASFWGEEK--RASHTTPVLMEXPY 621
XX
XX RESULT 7
XX AAU99360 standard; Protein; 622 AA.
XX
XX AAU99360;
XX
XX 26-SEP-2002 (first entry)
XX
XX P. falciparum apical membrane antigen-1 (AMA-1) ectodomain protein.
XX
XX Apical membrane antigen-1; AMA-1; protozoacide; Plasmodium; ectodomain;
XX malaria; parasite; vaccine; immune response; epitope; FVO Pf83syn.
XX
XX Plasmodium falciparum.
XX
XX Key Location/Qualifiers
FH Peptide 1..24
FT /label= Signal_peptide
FT Protein 25..622
FT /label= Mature_AMA-1
XX
XX WO200252014-A2.
XX
XX 04-JUL-2002.
XX
XX 21-DEC-2001; 2001WO-NL00934.
XX
XX 22-DEC-2000; 2000EP-0204697.
XX
XX (BIOM-) STICHTING BIOMEDICAL PRIMATE RES CENT.
XX
XX Kocken CHM, Thomas AW, Blackman MJ, Withers-Martinez C, Holder AA,
XX WPI; 2002-575381/61.
XX

```

PT Producing mRNA encoding Plasmodium AMA-1 ectodomain in yeast cell,
PT useful for preparing vaccines for treating or preventing malaria,
PT comprising providing the yeast cell with a nucleic acid encoding the
PT ectodomain

Example 1; Page -; 42pp; English.

XX The invention discloses the production of mRNA encoding Plasmodium
CC apical membrane antigen-1 (AMA-1) ectodomain, its functional part,
CC derivative and/or analogue in a yeast cell, which has been modified to
CC use the yeast's codon usage. Plasmodium falciparum (Pf) is the most
CC important human malaria parasite. At present there is no effective
CC vaccine against human malaria, but studies have indicated that the AMA-1
CC family of molecules are a target for protective immune responses. The
CC proteins have a predicted ectodomain and cytoplasmic domain and evidence
CC has identified that protection invoked by AMA-1 is directed at
CC conformational epitopes located in the ectodomain. The Plasmodium AMA-1
CC ectodomain, its functional part, derivative and/or analogue and the
CC proteinaceous molecule are useful for diagnosing and preparing vaccines
CC or medicaments for preventing malaria caused by Plasmodium falciparum. Pf
CC AMA-1 has an unusually high A+T content and N-glycosylation sites which
CC make expression and deglycosylation in yeast difficult. The method
CC provides an efficient production of Plasmodium falciparum, strain FVO,
CC AMA-1 ectodomain in high amounts due to its effective expression in the
CC yeast *Pisichia pastoris*. This is achieved by mutating the gene sequence
CC (FVO Pf83syn) to utilise the yeast's codon usage and remove the
CC N-glycosylation sites, which are not conserved in Plasmodium. The FVO
CC Pf83syn can be used to create vaccines against Plasmodium induced
CC malaria. The sequence presented is the P. falciparum AMA-1 ectodomain
CC which was used to create the synthetic P. falciparum AMA-1 ectodomain
CC (FVO Pf83syn) protein (AAU9359).
CC Note: This sequence is not shown in the specification, but was created
CC by the indexer from information given in example 1.

XX Sequence 622 AA:

Query Match 14.0%; Score 410; DB 23; Length 622;
Best Local Similarity 26.0%; Pred. No. 3.6e-29;
Matches 149; Conservative 80; Mismatches 214; Indels 130; Gaps 25;

QY 41 GNPFOANVEMKTFMERFNLTHHSGIYVDLGQKVEDGTLYREPAAGLCPIWKGHIELQ 100
DB 107 GNPW-----TEYMAKYDIEEVHSGIRVDLGDAEVAAGTQYRLPSGKCPVFGKGIIBN 160
QY 101 PRLPRNNFLIEDVPT-EKEYKQSNPLDGGFVNLNVTSGGRISPFPM-----ELLEKRS 155
DB 161 SN-----TFLKPVATGNDLKDGGFAPF-----PTNPLISPTLNGMRDFYKNE 206
QY 156 NIKASTDLGRCAEFAKTVAMDKNNATKYRYPFYVDSKKRLCHILYVMQLMGKKYCS 215
DB 207 YKANDELTLCSRHAN--MNPNDKNSNYKTPAVDYDKCHILYIAQENNGRYCN 264
QY 216 VKGEPPDLTWYCFKPKR-SVTENHHLIYSAYVGEN-PDAFISKCPNALRGYRGVWK 273
DB 265 -KDQSRNMFGRPAKDKLFENY-----TYLSKVNVNMBEVCPRKMLENAKFEGLAWD 317
QY 274 GRCGLDTLDTVYIEVESKACQWVTFENDVVASQPHYTP--LTSQASNDMWPF----- 327
DB 318 GNCEBIDPHVNEF--SANDLFECKNLVFEIS--ASDQPYOEHLTDYKIKIEGFKNKRA 372
QY 328 -----LHSDQPHSGGVRNRYGFYVDTTEGKCALSDVQDCIVSDSAVSYT 376
DB 373 SMIKSAFLPTGAFAKADRYKSHGKGYMGVYNRETQ--KCEIFNVFPTCLINNSVIAT 429
QY 377 AAGSLSEETPNFTIPSN-----PSVTPPETA 404
DB 430 ALSHPLEVEHNF--PCLYKDEIKKEIERESKRKIKLNDDEGNKKIIPRIFISDDXS 487
QY 405 LOCTADKFPDSFGACVQACKOKTSCYGGQISTG-----VDCIAD--EENEGC 452
DB 488 LKCPCCPEMVQSOSTCFVYCK-----CVERRAEVTSNNVEVYKEEYKDEYADIPKPKPT 542
QY 453 SNTALI-----AGLAVGVLLALLGGGCVFAKRLDNKKGQVAAHHEHFQSDRGAKKRP 508

DB 543 DNMKTIISAAVAVLATILAV-----YLKR-----KG-NAEKYDKMDQPHYCKSTSR 591
QY 509 SDLMQEAAPSFWDEPAEENIEDQDETHWVVEDY 541
DB 592 NDEMIDPEASFWGEER--RASHTTPLYMEKPY 621

RESULT 8

ABB99416 ID ABB99416 standard; Protein; 478 AA.

ABB99416; AC

29-JAN-2003 (first entry) XX

Amino acid sequence of AMA-1 ectodomain protein. DE

Apical membrane antigen-1; AMA-1; ectodomain protein; AMA1/E; KW

membrane protein; apical rhoptry; merozoite; vaccine; malaria. XX

Plasmodium falciparum. OS

Key Location/Qualifiers XX

Peptide 1..18 /note= "His tag" XX

Misc-difference 294 /note= "Thr encoded by AGC" XX

Peptide 468..478 /note= "His tag" XX

WO20027195-A2. XX

03-OCT-2002. XX

25-MAR-2002; 2002WO-US09406. XX

26-MAR-2001; 2001US-278616P. XX

(REED-) REED ARMY INST RES WALTER. XX

Lamar DE, Dutta S, Ware LA, Nair LPV; XX

WPI: 2003-029928/02. XX

N-PSDB; ABV72528. XX

New Plasmodium falciparum apical membrane antigen-1 (AMA-1) ectodomain XX

protein, useful as a diagnostic reagent, for producing antibodies, as a XX

vaccine, or for inducing a protective immune response to malaria XX

infection - XX

Claim 10; Page 88; 88pp; English. XX

The present sequence represents a Plasmodium falciparum apical membrane XX

antigen-1 (AMA-1) ectodomain protein, consisting of amino acids 83-531 XX

of AMA-1, and designated AMA1/E. AMA-1 is an integral membrane protein, XX

localised in the apical rhoptries of the merozoites present within the XX

late stage schizont. The AMA1/E polynucleotide comprises an Escherichia XX

coli codon bias. The AMA1/E polynucleotide is useful as a diagnostic XX

reagent, for producing antibodies, and as a vaccine. It is useful for XX

diagnosing malaria antibodies, monitoring malaria infection or prognosing XX

the response to treatment of patients suffering from malaria infection, XX

or for inducing a protective immune response to malaria infection. XX

Sequence 478 AA:

Query Match 13.8%; Score 404; DB 24; Length 478;
Best Local Similarity 27.0%; Pred. No. 8.7e-29;
Matches 123; Conservative 71; Mismatches 163; Indels 98; Gaps 18;

QY 41 GNPFOANVEMKTFMERFNLTHHSGIYVDLGQKVEDGTLYREPAAGLCPIWKGHIELQ 100
DB 43 GNPW-----TEYMAKYDIEEVHSGIRVDLGDAEVAAGTQYRLPSGKCPVFGKGIIBN 96

DR WPI; 1989-263714/36.
 DR N-PSDB; AAP91632.
 XX RhoPrty membrane antigen of Plasmodium falciparum
 PT - used for producing antibodies and in immunisation,
 PT diagnostic and treatment methods for malaria.
 XX
 PS Disclosure; Fig 3; 46pp; English.
 CC Predicted mol. wt. is 63901 D. This shows great similarity to
 CC P. falciparum RMA-1 protein (sequence in specification-claimed).
 CC (updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 561 AA;
 Query Match 13.5%; Score 395; DB 10; Length 561;
 Best Local Similarity 25.7%; Pred. No. 7,8e-28;
 Matches 147; Conservative 86; Mismatches 202; Indels 138; Gaps 24;
 QY 42 NPFQANVEMKTFMERFNLTHHSGIYVDLQDKEVDGTLYPEAGLCPTGKHIELQDP 101
 DB 53 NPWE-----KFMEXYDIEKVGSGIRVDLGEDARVENQDRIIPSGKCPVWGKITONS 106
 QY 102 DRLPYRNNFLDVPPT-EKEYKQSGNPLPGGFNLNFTPSGGRISFPWE-----LLEKXSN 156
 DB 107 -----KVSFLTRVATGNGKVRGGGLAPP-----QTDVNISFTITDNLKMKQDKE 152
 QY 157 IKASTDLRCGAFAFKVTAMDKNKATKYRPFYVDSKKRLCHILYVSMQMEGKKYCSV 216
 DB 153 ILALNDMLCAKHA--SFYVGTNTVNTVRRHAYVDKSNKTCYILYVAAGNMGFRYCS- 209
 QY 217 KGEPPDLTWYCFKPKKSVTENHHLIYGSAYVGENPDATISKCPNALGIRFGWKKKRC 276
 DB 210 NEEDNENQFCPTPEKK--DEYKNLSYLTKNLRED--WETSCPNKSIQNAKFGWVDGYC 265
 QY 277 LDY--TELTPVIEVESKAQCVWTFENDGVAASDPHTY----- 314
 DB 266 SEYQKKEVHND---KTLLECNQIVFES--ASDQPKQYKHELDYAKIRRGIVDRNGK 318
 QY 315 -----PLTSQASWMDWPLHOSDQPHSGGVGRNYGYVDTTGEKCALSDVQDCLV 367
 DB 319 LIGELMLLIGS-----YRADQVSKSGKGVWAWYDKTK--KCYINKKKPTCL 365
 QY 368 SDSAAVSTYAGSLSEETPNFIISN-----BSVTPTPT 400
 DB 366 NDKDVAATATLSSL-EEGFQESFPDIIYKKKIAEBIKWNNVRNNNGNDTIKPRIFISD 424
 QY 401 PETALQCTADKRPDSFGACDVQACKRKQKTSVGGIOISTVDTADEONEGCSNTA--- 456
 DB 425 DKESINCPCEPTQLTOSTCKFFVC---NCEYERK-QFISENNVEIADDEFSEYAESEPI 478
 QY 457 -----LIAGLAVGVLLALLLGGGCFYAFKRLDRNKGVQAHHNEHFEQSDRGARKRP 508
 DB 479 NKPQMLIIIIIIILAGILASILLI---FYFFK---SNK--PGDDYDKMGQADTYGGAQGR 530
 QY 509 SDLWQEAEPSEFWEAEENIEDQGETHWMEGY 541
 DB 531 KDEMLDPEVSEFWGEDIK---RASHTFPLVLEKPY 560
 RESULT 11
 AAB85697
 ID AAB85697 standard; Protein; 1807 AA.
 XX
 AC AAB85697;
 XX
 DT 29-OCT-2001 (first entry)
 XX
 DE Recombinant protein vIvac1p.
 XX
 KM Multivalent protein; immune response; Plasmodium vivax; parasite;
 XX protozoacide; vaccine; malaria; recombinant; vIvac1.

OS Synthetic.
 OS Plasmodium vivax.
 XX
 PN WO200155181-A2.
 XX
 XX 02-AUG-2001.
 XX
 XX 29-JAN-2001; 2001WO-US02937.
 XX
 XX 31-JAN-2000; 2000US-0179213.
 XX
 XX (USSH) US DEPT HEALTH & HUMAN SERVICES.
 XX
 XX Lal AA, Xiao L, Zhou Z;
 XX
 XX WPI; 2001-514557/56.
 DR N-PSDB; AAH47058.
 PT New recombinant multivalent protein comprising antigenic determinants
 PT derived from more than one stage in a life cycle of Plasmodium vivax,
 PT useful as a vaccine for treating, preventing and reducing malarial
 PT infection -
 XX
 XX Claim 5; Page 39-45; 59pp; English.
 CC The invention relates to recombinant multivalent proteins (I) that
 CC stimulate an immune response to Plasmodium vivax. (I) comprises antigenic
 CC determinants, fragments or conservative substitutions, derived from more
 CC than one stage in a life cycle of a Plasmodium vivax parasite. (I) is
 CC useful as a vaccine for stimulating an immune response, specifically a
 CC protective immune response that confers increased resistance to infection
 CC by Plasmodium parasites, such as P. vivax. (I) is especially useful in
 CC the treatment, prevention and reduction of malarial infection, as
 CC research or diagnostic reagents for the detection of Plasmodium species
 CC in a biological sample, and for conferring immunity against multiple
 CC stages of the malarial parasite. The antibodies produced are useful for
 CC the detection or measurement of antigenic epitopes derived from one or
 CC more stages in a life cycle of a parasite, particularly P. vivax. The
 CC vaccine comprising the recombinant proteins, is cost-effective, health-
 CC promoting intervention for controlling, preventing or treating the
 CC incidence of malaria. The present sequence represents the amino acid
 CC sequence of the recombinant protein vIvac1p, a multivalent and
 CC multistage vaccine against P. vivax.
 XX
 SQ Sequence 1807 AA;
 Query Match 13.4%; Score 391; DB 22; Length 1807;
 Best Local Similarity 26.3%; Pred. No. 1.2e-26;
 Matches 132; Conservative 73; Mismatches 182; Indels 114; Gaps 22;
 QY 5 GVQVLVIVNACTIFASGL-----SSSTRS-----RESQTLASST-SGNPQANVEMK 51
 DB 339 GIYYIIFLSAQLVHIGCGNOKRSLRISANNVLEKGTVERSTRMSFW-----K 392
 QY 52 TFMERFNLTHHSGIYVDLQDKEVDGTLYPEAGLCPTGKHIELQDPRLPYRNNFL 111
 DB 393 AFMEKTYDIERHSSGVRLDGEDAEVENAKRIRAGRPVGVKGIVENSD-----VSFL 447
 QY 112 EDVPT-EKEYKQSGNPLPGGFNLNFTPSGGRISFPWELEKSNITAST---DLGR 166
 DB 448 RPVATGDKLXKDGFAFPN-----ANDHISPMTLANKERYKDNVETMKLNDIALC 498
 QY 167 AEFARKTV-ANDKNNKATKYRPFYVDSKKRLCHILYVSMQMEGKKYCSVKGPPDLTW 225
 DB 499 RTHASFVWAGDQN---SSYRHPAYYDEKKTCHLVLSAODENNGPRYCSDDAQRDVA- 554
 QY 226 YCFKPKRSVLT-ENHHLIYGSAYVGENPDATISKCPNALRGYRFGWKKGRCLDYTELTD 284
 DB 555 FCFKPKDKIESFEN-LVLSLKNVRNDMD---KKCPKRLGNAKRGLWDMGNCBEPYVXE 609
 QY 285 TVIERVESKAQCVWTFENDGVAASDPHTYPLTQASWMDWPLHQ----- 330
 DB 610 V---EAEDLRECNRIIVF--GASASDQPTQY-----EEEMTDYOKIQGFRONNREMIKSAF 660

QY 331 -----SDPHSGVGRNYGYVDITGEGKALSDQVPCLVSDSAVSYTAAGSLSE 383
DB 661 LPVGAFNNDNFKSKRGFMNANF---DSVKKCYIFNTKPTCLINDKNFIATLASHQOE 717
QY 384 ---ETPNFIIPSN-----PSVTPEPTALQCTADKPPDSF 416
DB 718 VDLEPPCSIYKDEIRERIKKSRMNNLYSVDERIVLPRIPIISNDKESIKSCSEPERISN 777
QY 417 GACDVQACKROKTSQVGGQIQ 437
DB 778 STCNFYVC-----NCVEKRV 793

RESULT 12
AAB85698
ID AAB85698 standard; Protein; 2028 AA.

AC AAB85698;

DT 29-OCT-2001 (first entry)

DE Recombinant protein ViVac2p.

KM Multivalent protein; immune response; Plasmodium vivax; parasite;
KW protozoacide; vaccine; malaria; recombinant; ViVac2.

OS Synthetic.

XX Plasmodium vivax.

PN WO200155181-A2.

XX 02-AUG-2001.

PD 29-JAN-2001; 2001WO-US02937.

PR 31-JAN-2000; 2000US-0179213.

PA (USSH) US DEPT HEALTH & HUMAN SERVICES.

PI Lal AA, Xiao L, Zhou Z;

DR WPI; 2001-514557/56.
N-PSDB; AAH47055.

PT New recombinant multivalent protein comprising antigenic determinants
derived from more than one stage in a life cycle of Plasmodium vivax,
useful as a vaccine for treating, preventing and reducing malarial
infection

PS Claim 5; Page 48-55; 59pp; English.

CC The invention relates to recombinant multivalent proteins (I). that
stimulate an immune response to Plasmodium vivax. (I) comprises antigenic
determinants, fragments or conservative substitutions, derived from more
than one stage in a life cycle of a Plasmodium vivax parasite. (II) is
useful as a vaccine for stimulating an immune response, specifically a
protective immune response that confers increased resistance to infection
by Plasmodium parasites, such as P. vivax. (I) is especially useful in
the treatment, prevention and reduction of malarial infection, as
research or diagnostic reagents for the detection of Plasmodium species
in a biological sample, and for conferring immunity against multiple
stages of the malarial parasite. The antibodies produced are useful for
the detection or measurement of antigenic epitopes derived from one or
more stages in a life cycle of a parasite, particularly P. vivax. The
vaccine comprising the recombinant proteins, is cost-effective, health-
promoting intervention for controlling, preventing or treating the
incidence of malaria. The present sequence represents the amino acid
sequence of the recombinant protein ViVac2p, a multivalent and
multistage vaccine against P. vivax.

XX Sequence 2028 AA;

Query Match 13.4%; Score 391; DB 22; Length 2028;
Best Local Similarity 26.3%; Pred. No. 1.4e-26;
Matches 132; Conservative 73; Mismatches 182; Indels 114; Gaps 22;

QY 5 GVOVLVLVADCTIFASGL-----SSSTRS-----RESOTLAST-SGNPFOANVEMK 51
DB 560 GIYYIIFLSAQLHIGKCGNOKPSRLTRSANVLLKGTQVTERSTMSNPW-----K 613
QY 52 TEMERFNLTHHSGIYVDITGEGKALSDQVPCLVSDSAVSYTAAGSLSE 111
DB 614 AFMEKTYDERTHSSGVRLDSEDAEENAKYRIPGRCPVFGKGIIVNSD-----VSFL 668
QY 112 EDVPT-EKEVKQSGNPLPGGFNLNFTVPSGORISPPMELLEKNINIKAST-----DLGRC 166
DB 669 RPVATGQDKLDGGFAFEN-----ANDHISPMTLANKERYKONVETMKINDIALC 719
QY 167 AEFPAKTY-AMDKNNKATKYRPPYDSSKRLCHILYVSMQMBGKTCYKGEPPDLTW 225
DB 720 RTHASFVYMGADQN---SSYRHPAVYDEKERTCHMLYLSAQBNNMGPVYCSFDAQNRDAV- 775
QY 226 YCFKPKRSVT-ENHHLIYGSAYVGENPDPAFISKCPNOLRGVRRGWKKGRCLDYTELTD 284
DB 776 FCFKPDKNESFEN--LVYLSKNVRNDW---KKCPKRLGNAKTGLWVDCBEEIPVKE 830
QY 285 TVIERVESKAQCWVKTPEFNDGASDQPTVPLTSQASNNDWPLHQ----- 330
DB 831 V---EADLRRCNNIVF--GASASDQPTQY----EBEETDVQKIQGGRQNNREMIKSAF 881
QY 331 -----SDPHSGVGRNYGYVDITGEGKALSDQVPCLVSDSAVSYTAAGSLSE 383
DB 882 LPVGAFNNDNFKSKRGFMNANF---DSVKKCYIFNTKPTCLINDKNFIATLASHQOE 938
QY 384 ---ETPNFIIPSN-----PSVTPEPTALQCTADKPPDSF 416
DB 939 VDLEPPCSIYKDEIRERIKKSRMNNLYSVDERIVLPRIPIISNDKESIKSCSEPERISN 998
QY 417 GACDVQACKROKTSQVGGQIQ 437
DB 999 STCNFYVC-----NCVEKRV 1014

RESULT 13
AAR10935
ID AAR10935 standard; Protein; 489 AA.

AC AAR10935;

XX 25-MAR-2003 (updated)

DT 17-DEC-2001 (updated)

DT 15-APR-1991 (first entry)

DE Plasmodium vivax 66kD merozoite antigen protein partial sequence.

XX Plasmodium merozoite antigens; malaria vaccine.

XX Plasmodium vivax.

PN USN7483516-N.

XX 15-JAN-1991.

PD 22-FEB-1990; 90US-0483516.

PR 22-FEB-1990; 90US-0483516.

PA (USSH) NAT INST OF HEALTH.

XX (USDC) US SEC OF COMMERCE.

PI Waters AP, McCutchan TF;

XX WPI; 1991-044381/06.
N-PSDB; AAQ10869.

Plasmodium merozoite antigen proteins and DNA sequences - useful
 in vaccine prodn., anti-malarial drug design, and in diagnostics
 Disclosure; fig 1; 31pp; English.

This protein is encoded by a recombinant DNA molecule comprising
 the complete P. vivax merozoite antigen gene and e.g. a pUC19
 or vaccinia virus vector sequence and regulatory elements. This
 allows efficient expression of the antigen on transformation of
 host cells. It is useful in an anti-malarial vaccine for con-
 ferding immunity against the merozoite form of the parasite and
 preventing infection of uninfected red blood cells.

See also AA010418.
 (Note: Revisited entry submitted to correct the patent number format of
 US Government-owned NTIS applications to prevent clashes with ongoing US
 granted patent numbers. For further information please visit the Derwent
 web site at www.derwent.com/dwpi/updates/ntis_us.html.)
 (Updated on 25-MAR-2003 to correct PA field.)

Sequence 489 AA;

Query Match 12.2%; Score 357; DB 12; Length 489;
 Best Local Similarity 25.6%; Pred. No. 2,4e-24;
 Matches 138; Conservative 75; Mismatches 208; Indels 118; Gaps 24;

```

QY 70 DLGQKEVDGTYRBPAGLCPTWGHIEIQPDRLPYRNNEDVPT-EKEKQSGNPLP 128
DB 1 DLGDEAEVENAKYRIIPAGCKPVFGKIVENSDB---VSFLRPATGQKLKDGPAFP 55
QY 129 GGFNINFTVPSGQRISFPFM---ELLEKSNIKASTDLGRAPFAFKTV-AMDKNKAT 183
DB 56 N-----ANGHSPTMLANKERYKNVEMKMLNDALCRTNPAASVMAQDN---S 103
QY 184 KYRPFVYDSKRLCHILVYVSMQWEGKRYGVKSEPPDLTYCEPKRKSVTENHLLYV 243
DB 104 SYRHPAVVDEKERTCHMLYLSAQEMWGPYCSPPAQNRDAV-FCFKPDNGESFD-NLYVL 161
QY 244 SANYVENPDAFISKCPNQLRGYRGVWKKGRCLOYTELTDIVIERVES--KAQCMVKT 301
DB 162 SKNVNRNDMD---KCEPRKNLGNAGKFLWDGNCEEL---DYVKEVEAGDLRECNRIY 213
QY 302 ENDGVAASDOPHTYPLTSQASNDWMPLHQ-----SDQPSGCVG 340
DB 214 --GAASDOPROY---EEEMTDYQIKQGFRRONREMIKSAFLPGVANSNDPFSKRG 267
QY 341 RNYGFYVDTTSGKCALSDQVPCLVSDSAVSYTAAGSLSE---ETPNFIIPSN--- 393
DB 268 FVMANF---DSYKNKCYIFNTKPTCLINDKNFIATLALSHPOBVDLEFPCSIYKDEIERE 324
QY 394 -----PSVTPTPTALQCTADKFPDSFGACDVQACKRQKTSV- 432
DB 325 IKKQSRNMNLVYSDGERIVLPRIISNDKESIKPCPEPISNSTNFTYVC---NCEV 379
QY 433 -----GGQISTSVDTADSENECGSN---TALTAGLVAGVLLALLGGGCVYPAKL 482
DB 380 KKAETKENNVVLKEFRNYENGESKKNKMLIIIGI-TGVVCVVA-LASMAVYRKA 437
QY 483 DNNKGVQAHHHEHFGSDRGARKKRPDIHQEAEPSEFMDAEENIEQDCEITHVMEGY 541
DB 438 NNIDK-----YDKMDQAEYGGKPTNTRKDEMPLDPEASFWEDEK---RASHTTPLVMEKPY 488

```

RESULT 14

AA024128 ID AAB24128 standard; Protein; 1507 AA.

AC AAB24128;

DT 29-JAN-2001 (first entry)

DE Plasmodium yoelii YM MAEBL protein sequence SEQ ID NO:5.

KW Plasmodium; malaria; parasite; adhesion molecule; MAEBL; vaccine;

KW erythrocyte binding protein; protozoacide; infection.

XX Plasmodium yoelii.

OS US6120770-A.

XX 19-SEP-2000.

XX 12-SEP-1997; 97US-0929329.

XX 12-SEP-1997; 97US-0929329.

XX (UNOT) UNIV NOTRE DAME DU LAC.

XX Adams JH, Dalton JP, Kappe S;

XX WPI; 2000-593710/56.

XX N-PSDB; AAA99265.

XX New erythrocyte binding protein (MAEBL) useful as a vaccine against

XX malaria, for enhancing cell's resistance to infection or for

XX alleviating symptoms associated with the disease

XX Example 4; Column 25-34; 31pp; English.

The present invention describes an isolated polypeptide (I) comprising
 a Plasmodium parasite (malaria parasite) erythrocyte binding protein
 (MAEBL). Also described is an immunogenic composition comprising an
 isolated polypeptide and a carrier, where the polypeptide comprises an
 amino acid sequence, which includes a MAEBL protein cysteine domain.
 CC MAEBL polypeptides and compositions containing them are useful as
 CC vaccines against malaria, to enhance a cell's resistance to infection
 CC by Plasmodium parasites or to alleviate the symptoms associated with
 CC the disease. The present sequence represents a MAEBL protein, which is
 CC used in the exemplification of the present invention.

Sequence 1507 AA;

Query Match 4.1%; Score 120; DB 21; Length 1507;
 Best Local Similarity 18.8%; Pred. No. 0.26;
 Matches 87; Conservative 52; Mismatches 151; Indels 172; Gaps 21;

```

QY 34 TLASASTSGNPQANVEMKTFMERFNLTHH-----QSGIYVLDQDKEVD--- 78
DB 18 TPISTAIINP-----QEDFMDRPDLNNHVNIMKWTNGLAQGLKFDIVEDWISSKL 71
QY 79 -----GLTYRBPAGLCPTWGHIEIQPDRLPYRNNEDVPT-EKEKQSGNPLP 96
DB 72 NSLENARLCPNNEKGNIVR---GSCPDYKTFMSMDLQDEYSEDFLNEISGLNKLKLI 128
QY 97 ELQGPDRL-----PYRNNFLEDVPTKEK-----KQSGNPLPGFNL 133
DB 129 DVEIFVNNISGLAMQGLFANCPYDRKNHNDIKNEYEDVMDCPDKFYSNKD----- 178
QY 134 NFVTPSGQRISFPFELLEKNKSNIKR---STDGRCAEFAFKTVAMDKNKATKYRY--- 187
DB 179 -----ISTRIRIKYF--LISKTYFSGHGLGRLGNTETPLHIYPIEYRFRQKRRPYL 231
QY 188 -----PRVYDSKRLCHILVYVSMQWEGKRYGVKSEPPDLTYCEPKRKSVTENHLLYV 217
DB 232 VETLEDGSIYSHGICPCFDRDPDNKCFRDLPAVAFHMKKECTIIIGTH---EKKTYTCN 287
QY 218 GEPDPLTYVCFKPRKSVTENHLLIYSAVYVGENPDAFISK-PCNALRGYRFGV--WKKG 274
DB 288 SUNSNRNGRCFSSIKK-EKGKDWTYASSFL-RPD-YETKCPRPPLANNSEGGYRNYNTG 343
QY 275 RCLDYTELTDVYIEHVESKAQCWVTFPNDGVAASDOPHTYPLTSQASNDWMPPLHQSDP 334
DB 344 NCESPTKLVD--NSVISFNECTIEKL-F-NFNVANDEPE--EKRNMYLWGVWVLGKKNKL 397
QY 335 HSGGVGRNYGFYVDTTSGKCALSDQVPCLVSDSAVSYT 376
DB 398 NS-----MNDLGVCALLKERTKPTCVLKQNYYSFT 426

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```
RESULT 15
ABG16636
ID ABG16636 standard; Protein; 2519 AA.
XX
AC ABG16636;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #16627.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
XX
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Dmanac RT, Liu C, Tang YT;
XX
DR WPI; 2001-639362/73.
XX
DR N-PSDB; AAS80823.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity.
XX
PS Claim 20; SEQ ID No 46995; 103bp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
XX polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX and gene mapping, and in recombinant production of (II). The
XX polynucleotides are also used in diagnostics as expressed sequence tags
XX for identifying expressed genes. (I) is useful in gene therapy techniques
XX to restore normal activity of (II) or to treat disease states involving
XX (II). (II) is useful for generating antibodies against it, detecting or
XX quantitating a polypeptide in tissue, as molecular weight markers and as
XX a food supplement. (II) and its binding partners are useful in medical
XX imaging of sites expressing (II). (I) and (II) are useful for treating
XX disorders involving aberrant protein expression or biological activity.
XX The polypeptide and polynucleotide sequences have applications in
XX diagnostics, forensics, gene mapping, identification of mutations
XX responsible for genetic disorders or other traits to assess biodiversity
XX and to produce other types of data and products dependent on DNA and
XX amino acid sequences. ABG00010-ABG30377 represent novel human
XX diagnostic amino acid sequences of the invention.
XX Note: The sequence data for this patent did not appear in the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2519 AA;
Query Match 4.0%; Score 118; DB 22; Length 2519;
Best Local Similarity 19.4%; Pred. No. 0.9;
Matches 129; Conservative 66; Mismatches 222; Indels 248; Gaps 28;
OY 15 DCTIFASGLSSSTRESQTLASATSGNPFQANVEMKTFMERFNLTHHOGGIYVDLQD 74
DB 1809 DMSLVASLTSEKVSLEGEKSLSPKSDISF-----LTPRESSPLTSPTPSD 1853
OY 75 -----KEVDGTLTY-----REPAG-----LCPIWGHIELOQPDRLPYRNNEFLD 113
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DB 1854 STSAVKEKATACHSSSSPPIDAAAGBPYGFRAVLPTMQHHLALNR-----D 1901
OY 114 VPTKEKYKQSGNPLPGGFNINLFTVPPSGQRISP-----FPMELLEKNS----- 155
DB 1902 LSTPGLKEDSGGKTGPGFYAQKPEETNSPDEEDYDYESYEKTRTSDVGYEYKIE 1961
OY 156 -NIRASTDLGRCAFAFEKTV-----AMDKNKATK----- 184
DB 1962 RTTSPDSGYSYETIGTKITTPEDGDYSYIEIKTRTPREGGYSYDISKTTSPPEVS 2021
OY 185 -YRYPFV-----YDSKRRLCHIL-----YVSNQLMGKKY-CSVK 217
DB 2022 GSYEKTERSRRLDDISNGYDSEDCGHTLGDPSYSYETTEKITSPRESGYSYETSTK 2081
OY 218 -GEPDULTWYCFKRKSVTEHHHLYSAYGGENPDPAFISKCPQALRGVFGWKKRC 276
DB 2082 TTRTPDSTYCYETAETKTRTPQ--ASTYSYETSD----- 2114
OY 277 LDYTELDTVIERVESKAQCWVKTFFENDGVASDQPHTYPLT--SOASWN-----DMW----- 326
DB 2115 LCYTAEEKSPSEARQDVLDLVSCF-----YKHPTELSPSTINPPLMFASAE 2165
OY 327 PLHQSDQP--HSGGVGNNGFYVDTTGEKCALSDQVPDCLVSDA----- 371
DB 2166 PTBSEKPLTQSGGAPPPG-----GKQGRCQDEFPPTSVESGAPSDSDVPPETE 2218
OY 372 -AVSYTAAGSLSETPNFIIIPSNPSVT-----PPTPETALOCTADKPPDSGACDVQAC- 424
DB 2219 ECPSTITADANIDSEBETIPTDKTVYKHPDPAPVQDPSPPSRHPD--VSNVDPAL 2277
OY 425 -----KROKTSVCGQIOSTSVCTADQNEGSGSTALJAGLVGVLILA 470
DB 2278 IEQNLGKALKKDLKEXKITKPKGTKSSSVYKSD-----GSKKPLAASKPPAGL----- 2328
OY 471 LLAGGCYFARKLDNRKGVQAAHHEFEQSDRGARKKPSDLMQAEPSFME--AEENIE 528
DB 2329 -----KESDVKVSRVASPKKESVEKAAPTTTBEVKAARGEE 2366
OY 529 QDGET 533
DB 2367 KDKET 2371
RESULT 16
ID AAM39322 standard; Protein; 996 AA.
XX
AC AAM39322;
XX
DT 22-OCT-2001 (first entry)
XX
DE Human polypeptide SEQ ID NO 2467.
XX
KW Human; nocutropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokine; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
OS Homo sapiens.
XX
PN WO200153312-A1.
XX
PD 26-JUL-2001.
XX
PF 26-DEC-2000; 2000WO-US34263.
XX
PR 21-JAN-2000; 2000US-0488725.
XX
PR 25-APR-2000; 2000US-052317.
XX
PR 09-JUL-2000; 2000US-0598042.
XX
PR 19-JUL-2000; 2000US-0620312.
```

PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.

XX (HYSE-) HYSEQ INC.

XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao Q, Zhou P, Goodrich R, Drmanac RT;

XX WPI; 2001-442253/47.
DR N-PSDB; AA158478.

PT Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -

XX Example 4; SEQ ID NO 2467; 10078bp; English.

XX The invention relates to human nucleic acids (AA157798-AA161369) and
CC the encoded polypeptides (AA158642-AA162213) with nootropic, and
CC immunosuppressant and cyostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localized neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemia and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.

XX Sequence 996 AA;

XX Query Match 3.9%; Score 113; DB 22; Length 996;

XX Best Local Similarity 20.9%; Pred. No. 0.63; Mismatches 170; Indels 104; Gaps 18;

XX Matches 87; Conservative 55; Mismatches 170; Indels 104; Gaps 18;

QY 100 QPRLPYNNF---LEDVPTKEYKQSG-----NPLPGFNLFVT-----PSQRIISP 145

DB 139 EKXSTPPNNLVNPNQVLETERVRKAPAPVLSPTGVNENVTASAGKDLSTSPKSP 198

QY 146 PMELLEKNSNITKASTDLGRCAEPFAKTVAMDKNKATRYRPFYVDSKKRLCHILYISM 205

DB 199 IPSPVLGRRKPNASQSL-LWCKE-----VTKNYRGVK-----ITNFTT 235

QY 206 QLMGKKYCSYVGE-PPDLTWYCFKPKRSVTENHHLIY-GSAVVG-----ENPDAFISK 258

DB 236 SRRNGSLFCALIHHPBDLIDYKSLNPDIKENKKAAYGPFASIGISRLLEPSDWLLAI 295

QY 259 PNO-----ALRGYRFGVWKKGRCLDYTELTDYIERVESKAQCWTFENDVAGS-D 309

DB 296 PKLVTMTLYQIRAHFSG-----QELNVNQEENSSSTYKVGNYETDNTSSVD 345

QY 310 QHTYPLTISQASWMDWPLHQSDQPHSGVG-RNYGYVYVDTTGSCALSDQVDPCLV 367

DB 346 QEKFY-----AEISDLKREPELQQPIGAVDFLSQDSVFVNDSGESESSEHQTPDDHL 400

QY 368 SSSAANSY-----TAAGSLSEETPNFIIPSNPSTVPTPTPALQC----- 407

DB 401 SPSLASPYRRTKSDTEPQKSGQSGRTSGSDPGICSNITDSTQAOVLLIGKRLKAETL 460

QY 408 -----TADKFPDSFG--ACDVQACGRQKTSCEVGGIO-----STVDTADEON 449

DB 461 ELSDLYVSKKKDMSPPFICEETDEQKLTLDIGSLNLEKKEKLENSLSLCRSDPES 516

ID ABG22883 standard; Protein; 1023 AA.

XX AC ABG22883;

XX 18-FEB-2002 (first entry)

XX Novel human diagnostic protein #22874.

XX Human: chromosome mapping; gene mapping; gene therapy; forensic;

XX food supplement; medical imaging; diagnostic; genetic disorder.

XX Homo sapiens.

XX WO200175067-A2.

XX 11-OCT-2001.

XX 30-MAR-2001; 2001WO-US08631.

XX 31-MAR-2000; 2000US-0540217.

XX 23-AUG-2000; 2000US-0649167.

XX (HYSE-) HYSEQ INC.

XX Drmanac RT, Liu C, Tang YT;

XX WPI; 2001-639362/73.

XX N-PSDB; AA87070.

XX New isolated polynucleotide and encoded polypeptides, useful in

XX PT diagnosis, forensics, gene mapping, identification of mutations

XX PT responsible for genetic disorders or other traits and to assess

XX PT biodiversity -

XX Claim 20; SEQ ID NO 53242; 103bp; English.

XX The invention relates to isolated polynucleotide (I) and

XX CC polypeptide (II) sequences. (I) is useful as hybridisation probes,

XX CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome

XX CC and gene mapping, and in recombinant production of (II). The

XX CC polynucleotides are also used in diagnostics as expressed sequence tags

XX CC to restore normal activity of (II) or to treat disease states involving

XX CC (II). (II) is useful for generating antibodies against it, detecting or

XX CC quantitating a polypeptide in tissue, as molecular weight markers and as

XX CC a food supplement. (II) and its binding partners are useful in medical

XX CC imaging of sites expressing (II). (I) and (II) are useful for treating

XX CC disorders involving aberrant protein expression or biological activity.

XX CC The polypeptide and polynucleotide sequences have applications in

XX CC diagnostics, forensics, gene mapping, identification of mutations

XX CC and to produce other types of data and products dependent on DNA and

XX CC amino acid sequences. ABG00010-ABG30377 represent novel human

XX CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.

XX Sequence 1023 AA;

XX Query Match 3.9%; Score 113; DB 22; Length 1023;

XX Best Local Similarity 20.9%; Pred. No. 0.65; Mismatches 170; Indels 104; Gaps 18;

XX Matches 87; Conservative 55; Mismatches 170; Indels 104; Gaps 18;

QY 100 QPRLPYNNF---LEDVPTKEYKQSG-----NPLPGFNLFVT-----PSQRIISP 145

DB 166 EKXSTPPNNLVNPNQVLETERVRKAPAPVLSPTGVNENVTASAGKDLSTSPKSP 225

QY 146 PMELLEKNSNITKASTDLGRCAEPFAKTVAMDKNKATRYRPFYVDSKKRLCHILYISM 205

DB 226 IPSPVLGRRKPNASQSL-LWCKE-----VTKNYRGVK-----ITNFTT 262

QY 206 QLMGKKYCSYVGE-PPDLTWYCFKPKRSVTENHHLIY-GSAVVG-----ENPDAFISK 258

RESULT 17
ABG22883

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Db 263 SWRNLGSCALIHFRPDLIDYKSLNPQDIKENNKAYDGFASIGISRLLEPSDMVLAI 322
Qy 259 PNO-----ALRGYRFGWKGRCLDYTELDTVIERVESKACQWKTFENDVAS-D 309
Db 323 PDKLTWMTYLYQIRAHFSG-----QELNVQIENSSTKYKGNVETDNTSSVD 372
Qy 310 QPHTYPLTSQASWMDWPLHQSODPHSGVG--RNYGYVYDTTGEKCALSDQVPDCLV 367
Db 373 QEKFY-----AELSDLRKEPELQDPIGAVDFLSQDDSVFVNDSGVSESEHQTDPDHL 427
Qy 368 SDSAAVSY-----TAAGSLSEETPNFIIPSNPSVTPPTPTALQC-----407
Db 428 SPSTASPYCRRTKSDTEPQSKQSSGRTSGSDPDGICNTDSTQAQVLLGKKRLKAEYL 487
Qy 408 -----TADKFPDSFG--ACDVQACKRQKTSQVGGQIQ-----STVDCIADBN 449
Db 488 ELSDLVSDKKKMSPPICETDEQKQTLIDIGSLNLEKELENSRSLKCSDPES 543

RESULT 18
AAM79772
ID AAM79772 standard; Protein; 1023 AA.
XX
AC AAM79772;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human protein SEQ ID NO 3418.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN MO200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US04098.
XX
PR 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
PR 20-JUN-2000; 2000US-0598075.
PR 19-JUL-2000; 2000US-0620325.
PR 01-SEP-2000; 2000US-0654936.
PR 15-SEP-2000; 2000US-0663561.
PR 20-OCT-2000; 2000US-0693325.
PR 30-NOV-2000; 2000US-0728422.
XX
PA (HYSE-) HXSEQ INC.
XX
PI Tang YT, Liu C, Dymnac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y;
PI Zhao QH, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
DR WPI; 2001-476283/51.
DR N-PSDB; AAK52905.
XX
PT Nucleic acids encoding polypeptides with cytokine-like activities,
XX useful in diagnosis and gene therapy -
XX
PS Clam 20; Page 328; 6221pp; English.
XX
CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM76323-AAM80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating

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CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
CC (AAM80020) are omitted as the relevant pages from the sequence listing
CC were missing at the time of publication.
XX
SQ Sequence 1023 AA;
XX
Query Match 3.9%; Score 113; DB 22; Length 1023;
Best Local Similarity 20.9%; Pred. No. 0.65;
Matches 87; Conservative 55; Mismatches 170; Indels 104; Gaps 18;
Qy 100 QPRLPYRNNF---LEDPVTEKEYKQSG-----NPLPGFNLFVT-----PSGORSP 145
Db 166 EPKSTPPNNLVNVPQELTEIRRYKAPAPVLSPTGTVIENTVSGKSLSPKSP 225
Qy 146 FPMELLENKSNIKASTDLGRCAEPAFTVAMDKNKATKYRYPVYDSKKRLCHILVSM 205
Db 226 ISPVLGRKRPVNASQSL-LVMCKE-----VTKNYRGVK-----ITNFTT 262
Qy 206 QLMGKTKCSYKGE-PEDLTWYCFKPKRSTVENHLYI-GSAVYG-----ENPAFISKC 258
Db 263 SWRNLGSCALIHFRPDLIDYKSLNPQDIKENNKAYDGFASIGISRLLEPSDMVLAI 322
Qy 259 PNO-----ALRGYRFGWKGRCLDYTELDTVIERVESKACQWKTFENDVAS-D 309
Db 323 PDKLTWMTYLYQIRAHFSG-----QELNVQIENSSTKYKGNVETDNTSSVD 372
Qy 310 QPHTYPLTSQASWMDWPLHQSODPHSGVG--RNYGYVYDTTGEKCALSDQVPDCLV 367
Db 373 QEKFY-----AELSDLRKEPELQDPIGAVDFLSQDDSVFVNDSGVSESEHQTDPDHL 427
Qy 368 SDSAAVSY-----TAAGSLSEETPNFIIPSNPSVTPPTPTALQC-----407
Db 428 SPSTASPYCRRTKSDTEPQSKQSSGRTSGSDPDGICNTDSTQAQVLLGKKRLKAEYL 487
Qy 408 -----TADKFPDSFG--ACDVQACKRQKTSQVGGQIQ-----STVDCIADBN 449
Db 488 ELSDLVSDKKKMSPPICETDEQKQTLIDIGSLNLEKELENSRSLKCSDPES 543

RESULT 19
AAM79773
ID AAM79773 standard; Protein; 1023 AA.
XX
AC AAM79773;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human protein SEQ ID NO 3419.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN MO200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US04098.
XX
PR 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
PR 20-JUN-2000; 2000US-0598075.
PR 19-JUL-2000; 2000US-0620325.
PR 01-SEP-2000; 2000US-0654936.
PR 15-SEP-2000; 2000US-0663561.
PR 20-OCT-2000; 2000US-0693325.

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Db      263 SWRNGLSFCAILHFRPDLIDKXSLNPDIKENNKKAADGFASIGISRLLEPSDMVLAI 322
Oy      259 PNO-----ALRGYFQWKKGRCLDYTELDTVIERVSKACQWKTPENDGVA-S-D 309
Db      323 PDKLTVMYLYQIRAHFSG-----QELNVQIENSSTKYKGVNLTETDSSVD 372
Oy      310 QPHTYPLTSQASWMDWPHLHSDQPHSGVG--RNYGYYVDTTGEKCALSDQVPCLV 367
Db      373 QEKFY-----AELSDLKREPELQPIGAVDFLSQDSDSVFVNDGVSSESEHQTDPDHL 427
Oy      368 SDSAAVSY-----TAAGSLSEETPNFIISNPSVTPPTETALQC----- 407
Db      428 SPSTASPYCRRTKSDTEPQKSGQSGSRSGSDPGICENTDSTQAQVLLGKKRLKAEVL 487
Oy      408 -----TADKFPDSFG--ACDVQACKROKTSQVGGQIQ-----STVDTCTADEON 449
Db      488 ELSDLVSDKXKDMSPFICETDEQKQTLIDIGSNLEKEKLENSRSLBCRSDBPS 543

RESULT 21
AAU74355
ID      AAU74355 standard; Protein; 1076 AA.
AC      AAU74355;
XX      12-MAR-2002 (first entry)
XX      Human cytoskeleton-associated protein (CYSKP) #26.
XX      Human; cytoskeleton-associated protein; CYSKP; autoimmune disorder;
XX      cell proliferative disorder; inflammatory disorder; prion disease;
XX      vesicle trafficking disorder; gastrointestinal disorder; muscle disorder;
XX      neurological disorder; cell motility disorder; reproductive disorder;
XX      spinal cord disease; central nervous system disorder; mental disorder;
XX      gene therapy; cancer.
XX      Homo sapiens.
XX      OS
XX      MO200185942-A2.
XX      15-NOV-2001.
XX      03-MAY-2001; 2001WO-US14355.
XX      05-MAY-2000; 2000US-201960P.
XX      08-MAY-2000; 2000US-202729P.
XX      05-JUN-2000; 2000US-209705P.
XX      07-JUN-2000; 2000US-210149P.
XX      21-JUN-2000; 2000US-213215P.
XX      (INCY-) INCYTE GENOMICS INC.
XX      Yue H, Tang YT, Au-Young J, Lu DAM, Baughn MR, Hillman JL,
XX      P1 Azimzal Y, Lal P, Yao MG, Bandman O, Burford N, Batra S;
XX      Kearney L, Policky JL;
XX      WPI: 2002-0632248/08.
XX      N-PSDB; AAS99915.
XX      New cytoskeleton-associated proteins and polynucleotides, useful for
XX      diagnosing, preventing and treating cell proliferative, autoimmune,
XX      inflammatory, neurological, cell motility, reproductive and muscle
XX      disorders
XX      Claim 1; Page 153-155; 194pp; English.
XX      The invention relates to human cytoskeleton-associated polypeptides
XX      (CYSKP) and their associated polynucleotide sequences. The sequences are
XX      useful in the treatment of disorders associated with overexpression or
XX      underexpression of CYSKP in a patient. The disorders include cell
XX      proliferative disorders (such as cancer, actinic keratosis,
XX      arteriosclerosis, cirrhosis, hepatitis and psoriasis),

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CC      autoimmune/inflammatory disorders (such as, asthma, atherosclerosis,
CC      osteoporosis, Crohn's disease, rheumatoid arthritis, diabetes mellitus
CC      and anaemia), vesicle trafficking disorders (such as
CC      hypercholesterolaemia, diabetes insipidus, Graves' disease and goitre),
CC      gastrointestinal disorders, prion diseases, neurological disorders (such
CC      as epilepsy, stroke, cerebral neoplasms, Alzheimer's disease,
CC      Huntington's disease, Parkinson's disease, amyotrophic lateral sclerosis
CC      and other motor neuron disorders), cell motility disorders, reproductive
CC      disorders (such as endometriosis and polycystic ovary syndrome), muscle
CC      disorders (such as myoarthritis, migraine, hypertension, hypoglycaemia,
CC      myocardial infarction, epilepsy and muscular dystrophy), spinal cord
CC      diseases, central nervous system disorders (such as Down syndrome and
CC      cerebral palsy) and mental disorders (such as anxiety and schizophrenia).
CC      Sequences AAU74330-AAU74363 represent human CYSKP of the invention.
XX      SQ      Sequence 1076 AA;
XX      Query Match 3.9%; Score 113; DB 23; Length 1076;
XX      Best Local Similarity 20.9%; Pred. No. 0.71;
XX      Matches 87; Conservative 55; Mismatches 170; Indels 104; Gaps 18;
Oy      100 QPDLPLRYRNNF---LEDVPEKEKYGSG-----NPLPGGNLNPV-----PSGQRISP 145
Db      219 EPKSTPPNNLNVNDVQLETERRYKRAPAPVLPVPTGVNENTVSAKDLSIPKSP 278
Oy      146 PPMELLEKNINIKASTDLGRCAEPFAFTVAMDKNKATKRYRPVVDYKRLCHILVYSM 205
Db      279 IPSFVLGRKRPVAGSL-LWVCKE-----VTKRYRGVK-----ITNFTT 315
Oy      206 QLMGKKYCSYKGB-PPDLTWYCFKPRKSVTENHLLY-GSAVVG-----ENPDATSKC 258
Db      316 SWRNGLSFCAILHFRPDLIDYKSLNPDIKENNKKAADGFASIGISRLLEPSDMVLAI 375
Oy      259 PNO-----ALRGYFQWKKGRCLDYTELDTVIERVSKACQWKTPENDGVA-S-D 309
Db      376 PDKLTVMYLYQIRAHFSG-----QELNVQIENSSTKYKGVNLTETDSSVD 425
Oy      310 QPHTYPLTSQASWMDWPHLHSDQPHSGVG--RNYGYYVDTTGEKCALSDQVPCLV 367
Db      426 QEKFY-----AELSDLKREPELQPIGAVDFLSQDSDSVFVNDGVSSESEHQTDPDHL 480
Oy      368 SDSAAVSY-----TAAGSLSEETPNFIISNPSVTPPTETALQC----- 407
Db      481 SPSTASPYCRRTKSDTEPQKSGQSGSRSGSDPGICENTDSTQAQVLLGKKRLKAEVL 540
Oy      408 -----TADKFPDSFG--ACDVQACKROKTSQVGGQIQ-----STVDTCTADEON 449
Db      541 ELSDLVSDKXKDMSPFICETDEQKQTLIDIGSNLEKEKLENSRSLBCRSDBPS 596

RESULT 22
AAU78788
ID      AAU78788 standard; Protein; 1581 AA.
AC      AAU78788;
XX      06-NOV-2001 (first entry)
XX      Human protein SEQ ID NO 1450.
XX      Human; cytokine; cell proliferation; cell differentiation; gene therapy;
XX      vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
XX      tissue growth factor; immunomodulatory; cancer; leukaemia;
XX      nervous system disorder; arthritis; inflammation.
XX      Homo sapiens.
XX      OS
XX      MO200157190-A2.
XX      09-AUG-2001.
XX      05-FEB-2001; 2001WO-US04098.

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PR 03-FEB-2000; 2000US-0496914.
PR 27-APR-2000; 2000US-0560875.
PR 20-JUN-2000; 2000US-0598075.
PR 19-JUL-2000; 2000US-0620325.
PR 01-SEP-2000; 2000US-0654936.
PR 15-SEP-2000; 2000US-0663561.
PR 20-OCT-2000; 2000US-0693325.
PR 30-NOV-2000; 2000US-0728422.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YR, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y, Ma Y,
XX Zhao Q, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW,
XX Xue AJ, Yang Y, Wejhrman T, Goodrich R,
XX
XX WPI, 2001-476283/51.
XX N-PSDB; AAKS1921.
XX
XX Nucleic acids encoding polypeptides with cytokine-like activities,
XX useful in diagnosis and gene therapy -
XX
XX Claim 20; Page 3716-3718; 6221pp; English.
XX
XX The invention relates to polynucleotides (AAK51456-AAK53435) and the
XX encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
XX cytokine, cell proliferation or cell differentiation or which may induce
XX production of other cytokines in other cell populations. The
XX polynucleotides and polypeptides are useful in gene therapy, vaccines or
XX peptide therapy. The polypeptides have various cytokine-like activities,
XX e.g. stem cell growth factor activity, haematopoietic regulating
XX activity, tissue growth factor activity, immunomodulatory activity and
XX activity/inhibin activity and may be useful in the diagnosis and/or
XX treatment of cancer, leukaemia, nervous system disorders, arthritis and
XX inflammation.
XX
XX Note: Records for SEQ ID NO 2110 (AAK52581), 2111 (AAK52582) and 3666
XX (AAM80020) are omitted as the relevant pages from the sequence listing
XX were missing at the time of publication.
XX
XX Sequence 1581 AA;
SQ
Query Match 3.9%; Score 113; DB 22; Length 1581;
Best Local Similarity 20.9%; Pred. No. 1.3;
Matches 87; Conservative 55; Mismatches 170; Indels 104; Gaps 18;
QY 100 QPRLPYRNRF--LEDVTEKEYKQSG-----NPLPGGFLNFTY-----PSGGRISP 145
DB 212 BKSTFPNNLVNPVQDELTERRVRKAPAPVLSPTGVLNMENTVSAGKDLSTSEKPS 271
QY 146 FMELLEKRSNKASPTDLGRCAEFKATVAMDKNKATRYRPFVDSKKRLCHILYVGM 205
DB 272 TSPVLYGRPNASQSL-LWCKE-----VTNNYGVK-----ITNFTT 308
QY 206 QLMGKKYKSVKGE--PPDLTWYCFKPKRSVTENHLLY-GSAVVG-----ENPDAFISK 258
DB 309 SMRNGSLFCALHHPRLDLIDYSLNPQIKENKKAAYGFASIGISRLLEPSDWLAI 368
QY 259 PNO-----ALRGYRFGVKKGRCLDTLTDTYIERVESGAQGVKTFENDGAS-D 309
DB 369 PKRLTWYLYOIRAFHSG-----QELNVVQIEENSSKSTYKVNNEYETDNSSVD 418
QY 310 QHTTYLTLSQASNNWMLHQSOPHSGGVG--RNVGFYVDTTGSKCALSDQVDDCV 367
DB 419 QEKFY-----AELSDIKREPELQOPTSGAVDFISQDVSFVNDGSGESBSEHQTPDH 473
QY 368 SDSAAVSY-----TAAGSLSEETPNFIIPNSPVTPPTETALOC----- 407
DB 474 SBTSTAPYCRRTKSTDETPQKSSQSSGRTSGSDPGICSNMDSITQAVLIGKKRLKAE 533
QY 408 -----TADKFPDSFG--ACDVQACKRKQKTSVCGGQIQ-----STSVDC 449
DB 534 ELSDLYVSKKMDSPFICEETDEOKLTQTLIDGSLMEKEKLENSRLSECRSDPS 589

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RESULT 23
AAR94957
ID AAR94957 standard; Protein; 1104 AA.
XX
XX AAR94957;
AC AAR94957;
XX
XX 17-AUG-1996 (first entry)
DT 17-AUG-1996 (first entry)
XX
XX NF-X1 DNA-binding protein.
DE NF-X1 DNA-binding protein.
XX
XX NF-X1; transcription factor; major histocompatibility complex; MHC;
XX allergy; DNA-binding protein; diagnosis.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
FH Domain 430..900
FT /label= Cysteine-rich_domain
FT 417..468
FT /label= Cysteine-rich_repeat
FT 473..521
FT /label= Cysteine-rich_repeat
FT 533..583
FT /label= Cysteine-rich_repeat
FT 599..647
FT /label= Cysteine-rich_repeat
FT 688..737
FT /label= Cysteine-rich_repeat
FT 799..839
FT /label= Cysteine-rich_repeat
FT 840..890
FT /label= Cysteine-rich_repeat
XX
XX MO9612823-A1.
XX
XX 02-MAY-1996.
XX
XX 20-OCT-1995; 95WO-US12749.
XX
XX 21-OCT-1994; 94US-0327832.
XX
XX (HARD ) HARVARD COLLEGE.
XX (UYGO ) UNIV JOHNS HOPKINS.
XX
XX Ono SJ, Strominger JL;
PI WPI, 1996-230621/23.
XX
XX N-PSDB; AAT18813.
XX
XX Transcription factor, NF-X1 and DNA encoding it - used in regulation
XX of MHC class II expression and in treatment of allergic disease
XX
XX Claim 6; Page 55-58; 93pp; English.
XX
XX Human NF-X1 (AAR94957) is a new DNA-binding protein which regulates
XX expression of major histocompatibility complex (MHC) class II
XX molecules. The sequence was deduced from a cDNA clone (AAT18813)
XX isolated from Raji cells. NF-X1 is a cysteine-rich polypeptide
XX which interacts specifically with the conserved X1 box regulatory
XX element (AAT18812) found in the proximal promoters of class II MHC
XX genes. It contains a cysteine-rich domain (see also AAR94955-56)
XX required for both sequence-specific binding and effector function.
XX Overexpression of NF-X1 specifically represses transcription of
XX the HLA-DRA gene. NF-X1 can be obtd. by expression in transformed
XX host cells and is useful in the treatment of allergic disease.
XX
XX Sequence 1104 AA;
SQ
Query Match 3.7%; Score 107.5; DB 17; Length 1104;
Best Local Similarity 19.7%; Pred. No. 2.4; Indels 199; Gaps 29;
Matches 103; Conservative 61; Mismatches 159; Indels 199; Gaps 29;
QY 85 PAGLCPIWGKIHLEQDPRLPYRNFLDVPTEKEYKQSGNPLPGGFLNFTYPSGGRIS 144

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Db      579 PCGGTPL-SQLLELSSSS-----RKTCDMPVSCG--KVCGRPLPCG-SLDFHHCXKCH 630
Oy      145 PFMPELEKSNINIKASTDLGRCAEFATVAMD-----GNKATKRYFVVD---SKRL 197
Db      631 EGGDCGPRVTRTISC-----RC--SFRTKEIPCTSLKSDAT-----FMCCKKCKKRL 677
Oy      198 CHILVSNQMLEGKKYCSVKGEPRDLTWYCFKPKRSVTEHHLLYGSAYGVENPDATISK 257
Db      678 C-----GRHKNE-----IC-----CVDKEH-----K 694
Oy      258 CPNOALRGYRFGWK-----KGRCLDTLTLDTLYTERVESKAQCWKTENDGVASDQ 311
Db      695 CPLNGRGLRCGLRHCEPRCHRGNC-----QTWQASFDE----- 729
Oy      312 HTYPLTSGASWMDMP-----LHQSQP--HSGG----- 338
Db      730 ----LTCGASVYRPVPCGTRPEECTQTCAVHECHPYHSHSEKCRPCTFLTQK 785
Oy      339 --VGR-----NYGFYVDTT-----GEGKALSDVPDCLVSDSAVSYTAAGS 380
Db      786 WCMGHEFRSNIPCHLVDISGLPCSATLPCGMHKCQLCHKGECLVDE----- 834
Oy      381 LSEETPNFIIPSNSTVPTPETALQCTADKFPDSFGACDVQACK-ROKTSVGGQIQST 439
Db      835 -----PCOKPCTTPRADCGHPCWAPCHTS--PCPYTACAKVELQCEGGR-RKE 881
Oy      440 SVDCTADQNECGSNTALIAGLAVGVLLALLGGCCYFAKRLDRNKGVQAHHHEHFRQS 499
Db      882 MVIC-----SEASSTYQRIAIISMASKITDMQLGGSVESIKLITK-KEVHQRLECDDEC 935
Oy      500 DRGARKKRPD--LMQEAEP-----SFWDEAEENIED 530
Db      936 SALEKKKRLAEAFHISEDSDPFNIRSSGSKFSDSLKEARDK 977

RESULT 24
ABB97742
ID      ABB97742 standard; Protein; 355 AA.
XX
XX      ABB97742;
XX
XX      11-JUL-2002 (first entry)
XX
XX      Human procathepsin W epitopes related protein.
XX
XX      Human; procathepsin W; cathepsin W; monoclonal antibody; epitope.
XX
XX      Homo sapiens.
XX
XX      W0200226831-A1.
XX
XX      04-APR-2002.
XX
XX      09-JUL-2001; 2001WO-EP07877.
XX
XX      29-SEP-2000; 2000DE-1048727.
XX
XX      (LABS-) LABSOFT DIAGNOSTICS AG.
XX
XX      Weber E;
XX
XX      WPI; 2002-330095/36.
XX
XX      New hybridoma cell lines that produces antibodies specific for human
XX      cathepsin W, useful e.g. for diagnosis, therapy and drug targeting
XX
XX      Disclosure; Page 17-19; 23pp; German.
XX
XX      The present invention relates to hybridoma cell lines that produce
XX      monoclonal antibodies directed against a defined epitope of human
XX      (pro)cathepsin W, which are produced by fusing myeloma cells with spleen
XX      cells from an animal that has been immunised with recombinant

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CC      procathepsin W. The antibodies produced are useful for analysis,
CC      diagnosis (detection of human (pro)cathepsin W), purification of
CC      (pro)cathepsin W (also for clarifying processing of the precursor and
CC      functional significance of the mature protein), for drug targeting and
CC      for therapeutic use. The present sequence is a human protein shown in the
CC      exemplification of the invention.
CC      Note: No further information about this sequence is given in the
CC      specification.
XX
XX      Sequence 355 AA;
XX
XX      Query Match 3.6%; Score 104; DB 23; Length 355;
XX      Best Local Similarity 21.7%; Pred. No. 0.88;
XX      Matches 83; Conservative 44; Mismatches 141; Indels 114; Gaps 19;

Oy      18 IFASGLSSSTRSRRESQTLASTSGNPRQAVENKTFMERNTLTHHQSGLYVDLQDKEV 77
Db      44 IFAHNLQAOQLDEEDIGTAIEFGVTPS-----DLTEEFGLYG----- 83
Oy      78 DGLTYREPAGLCPIWGHIELQOQDRLLPYNNFLEDVPTKEKYQSG--NPLPGFNLN 134
Db      84 ----YRAAGGVPSMGEIIESEPE-----ESVPFCDMRKVAGALSPIDQKCN 130
Oy      135 ---FVTPSGRISPPFMELLEKNS-----NIKASTDLRCAE-----FAKTVAM 176
Db      131 CWMAMAAAGN-----IETLMRISFMDPVDVSVYHELDCRCGDCGCHGFVWDAFITV-L 183
Oy      177 DKNNKATKRYVPPFYDSKRLCHILVSNQMLEGKKYCSVKGEPRDLTWYCFKPKRSVTE 236
Db      184 NNSGLASEKQIPFGKRYARHCH-----PKTKQK-----AM--IQDFMLQN 224
Oy      237 NHHLI-----YGSAYGVENPDATISKCPNOALRGYFGWKKGRCLDTYELTDTVI--- 287
Db      225 NEHRIAGYLAITYGITITIN-----MKPQLYKKGVIKATPTTCDDQLVDHSLVLV 275
Oy      288 -ERVESKAQCWKTENDGVASDQHTYPL-TSQASWMDWPLHOSDQPHSGGVGNNG 344
Db      276 GFGSVKSEEGIMAEIVASSQS-QPOPHPPTPYWILKNSMGQWMEKGYFRLHRS----- 328
Oy      345 FYVYDTTGEGRKALSDV--PD 364
Db      329 ---NTGITKFPPLTARQKPD 346

RESULT 25
AAB21208
ID      AAB21208 standard; Protein; 1200 AA.
XX
XX      AAB21208;
XX
XX      12-JAN-2001 (first entry)
XX
XX      Human HER-2/neu protein.
XX
XX      Human HER-2/neu protein.
XX
XX      Human; HER-2/neu; oncogene; tyrosine kinase; cytostatic; vaccine;
XX      breast cancer; prostate cancer; ovarian cancer; lung cancer;
XX      colon cancer.
XX
XX      Homo sapiens.
XX
XX      W0200044899-A1.
XX
XX      03-AUG-2000.
XX
XX      28-JAN-2000; 2000WO-US02164.
XX
XX      29-JAN-1999; 99US-0117976.
XX
XX      (CORI-) CORIXA CORP.
XX      (SMIK ) SMITHKLINE BEECHAM.
XX
XX      Cheever MA, Gheysen D;
XX

```

DR MPI: 2000-505976/45.
 DR N-PSDB; AAA89736.
 XX HER-2/neu extracellular domain/phosphorylation domain fusion proteins
 PT useful for vaccinating against breast, ovarian, colon, lung and
 PT prostate cancers -
 XX
 PS Disclosure; Fig 15; 128bp; English.
 XX
 CC The present sequence is the human HER-2/neu protein. It is a member
 CC of the tyrosine kinase family of receptor-like glycoproteins and shows
 CC homology to the epidermal growth factor receptor (EGFR). It probably
 CC plays a part in cell growth and/or differentiation. The HER-2/neu
 CC gene is an oncogene. An HER-2/neu fusion protein comprising a
 CC HER-2/neu extracellular domain fused to a HER-2/neu phosphorylation
 CC domain may be used to treat or prevent cancer by eliciting or
 CC enhancing an immune response to the HER-2/neu protein. It may be used
 CC to treat malignancies such as breast, ovarian, colon, lung and
 CC prostate cancers, and may be used as an antigen to vaccinate against
 CC these neoplasias.
 CC
 XX Sequence 1200 AA;
 SQ
 Query Match 3.6%; Score 104; DB 21; Length 1200;
 Best Local Similarity 22.5%; Pred. No. 5.9;
 Matches 108; Conservative 43; Mismatches 174; Indels 156; Gaps 27;
 QY 81 LYREPAAGLCPINGKHIETLQPDRLPYRNNFLEDVPEKEKYKSGNPLPG--FNINFT 137
 DB 256 LHFHNSGIC-----ELHCPALVTYNTDTFESMPN-----PGRGYTFGASCVT 297
 QY 138 PSGQRISPPMELLESKSNIKASTDLGRCAEFA---FKTVAMDKNNKATKRYRPPVDS 193
 DB 298 AC-----PYNVL-----STDVGSCTLVCPHLNQEVTAEEDGTQCEKSKPCA--- 339
 QY 194 KKRLLCH-----ILVVMQMLEGSKYTC-----SVKGEPPDLTWYCFKPRK 232
 DB 340 --RVCYGLGMEHREVRATYSANIQFACCKIFGSLALPESFPDDPSANTAPLQPEQL 397
 QY 233 SYTENHLLIYGSAYVGENDAF--ISKCPN-QALRG-----YRFGV-WKKGRG 276
 DB 398 QVFETLEITGYLYISAMPDLSPLDLSVFQNLQVIRGRILHNGAYSLTLOGLGISWLGSR 457
 QY 277 LDVTELDIVIERVESKACQWVTFENDGVASDQ---PHTYPLTSQASNMWMLHOSD 332
 DB 458 L--RELGGSLALIHNTHLCEVHT-----VPMQDLFRNPH-----QAL-----LHTAN 498
 QY 333 QPHSGGVGRNYGFYVDTTGE-----GKCALSDQ-----VPDLVDSAAVSYTAAG 379
 DB 499 RPEDDECVGEGLAGHQLCARGHCWGPRTQCVNCSQFLRQGECEBGRVLAQGLPREVYNAR 558
 QY 380 SLSEETPNFTIPSPSVTPPTPTALQCTAD-----KF 412
 DB 559 HCLPCHPE--CQFONGSVTCFGPE--ADQCVAHAHYKDPFCVAPSGVXPDLISYMPIMWF 616
 QY 413 POSFGACDVQACRKQTSQVCGOIGSTSVDTADEQNEGSNALLAGLAVGSVLLALL 472
 DB 617 PDEEGAC--QPC--PINCTHSCVDLDDKGCPEAQR--ASPLTITS--AVGILLVVL 667
 QY 473 G 473
 DB 668 G 668
 RESULT 26
 ABR25604
 ID ABR25604 strand; Protein; 1213 AA.
 AC ABR25604;
 DT 02-JUL-2002 (first entry)
 XX Streptococcus polypeptide SEQ ID NO 384.

XX
 KM Streptococcus GAS; GBS; group B streptococcus; Streptococcus agalactiae;
 KM group A streptococcus; Streptococcus pyogenes; antibacterial;
 KM antinflammatory; infection; vaccine; meningitis; gene therapy.
 XX
 OS Streptococcus pyogenes.
 XX
 PN WO200234771-A2.
 XX
 PD 02-MAY-2002.
 XX
 PF 29-OCT-2001; 2001WO-GB04789.
 XX
 PR 27-OCT-2000; 2000GB-0026333.
 PR 24-NOV-2000; 2000GB-0028727.
 PR 07-MAR-2001; 2001GB-0005640.
 XX
 PA (CHIR-) CHIRON SPA.
 PA (GENO-) INST GENOMIC RES.
 XX
 PI Telford J, Massignani V, Margarit Ros YI, Grandi G, Fraser C,
 PI Tettelin H;
 DR MPI: 2002-352536/38.
 DR N-PSDB; ABN66235.
 XX
 PT New Streptococcus protein for the treatment or prevention of infection
 PT or disease caused by Streptococcus bacteria, such as meningitis, and
 PT for detecting a compound that binds to the protein -
 PS Claim 1; Page 3194; 4525bp; English.
 XX
 CC The invention relates to a protein (ABP25413-ABP30895) from group B
 CC streptococcus/GBS (Streptococcus agalactiae) or group A streptococcus/GAS
 CC (Streptococcus pyogenes), comprising one of 5483 sequences (S1), given in
 CC the specification. The proteins have antibacterial and antinflammatory
 CC activity. (1), nucleic acids encoding (1), ABN66044-ABN71526 and
 CC antibodies that bind (1) are used in the manufacture of medicaments for
 CC the treatment or prevention of infection or disease caused by
 CC Streptococcus bacteria, particularly S. agalactiae and S. pyogenes.
 CC Nucleic acids encoding (1) are used to detect Streptococcus in a
 CC biological sample. (1) is used to determine whether a compound binds to
 CC (1). A composition comprising (1) or a nucleic acid encoding (1), may be
 CC used as a vaccine or diagnostic composition. The disease caused by
 CC Streptococcus that is prevented or treated may be meningitis. Nucleic
 CC acid encoding (1) may be used to recombinantly produce (1) and may be
 CC used in gene therapy. Antibodies to (1) are used for affinity
 CC chromatography, immunoassays, and distinguishing/identifying
 CC Streptococcus proteins.
 CC
 XX Sequence 1213 AA;
 SQ
 Query Match 3.6%; Score 104; DB 23; Length 1213;
 Best Local Similarity 19.3%; Pred. No. 6;
 Matches 91; Conservative 55; Mismatches 165; Indels 160; Gaps 22;
 QY 115 PTEKEYKSGNPLPGGFNLFVTPSGRISPPM-ELLEKN--SNIKA----- 159
 DB 349 PTLKMT-OCGVREMAIEI-----FKPFWREIYAKAYAGNVKAAKMWERGDERI 398
 QY 160 -----STDLRCAEFAFKTVAMDKNKATKRYRPFV-----YDSKK 195
 DB 399 WDLLEVIKEHVPVLLNRAPTLHRLGIAFEPVLID--GKALRL-HPLVCEAVNADFDQDQ 455
 QY 196 RICHILVVMQMLEGSKYCSYKGEPPDLTWYCFKPRKS---VTENHHLIYGSAYV----- 247
 DB 456 MAIHV-PLSEEAQAEARILMLAAE-----HILNPKDKSPVTPSQDWLVGNVYLTMEDA 508
 QY 248 GENPDAPFSKCNQALRGVREGVWKKGRCLDYTELDIVIERVESKACQWVTFENDGVA 307
 DB 509 GREGGGMIFKDKDEAVMAYRNG-----YAHLSRY-----GIA 541
 QY 308 SDQPHTYPLTSQASNMWMLHOSDQPHSGGVGRNYGFYVDTTGEKCALSDQVDPCLV 367

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Db      542 VDSMKNKP-----WKD-----NQRHK-----IWTVVKGKLFNDIMP----- 573
Qy      368 SDSAAVSYYAAGSLSEETPNFIIPSNPSVTPTPTALQCTADKPPDSFGACDVQACKRQ 427
Db      574 -----EDLPYLOEPNNANITBETPPDKYFLIEPGODIQEVIDRLDIVNPEK 618
Qy      428 KTSVCGG-----QIQTSTVDCCTADEONEGCSNTALAGLAVGVLLALLGGCCYPAK 480
Db      619 KN--LGNIIAETPKRFTTETSAFLRLKDLGYVHSTLAGLTVGIADIPVI----- 667
Qy      461 RLDKRGK--VQAAHHEHFQSDRGARKKRPSPLMQBAEBSFVDEAEENIEQ 529
Db      668 ---DNKAETIIDAAHHRVEEINKAFRRGLMTDDRYVAVTTWRKAKEALEK 715

```

RESULT 27

AAW01111
ID AAW01111 standard; Protein; 1255 AA.

AAW01111;

DT 01-JAN-1997 (first entry)

DE HER-2/neu protein.

KM HER-2/neu; c-erbB1; p185; oncogene; tyrosine protein kinase;

KM breast cancer; ovary cancer; colon cancer; lung cancer;

KM prostate cancer; immunisation; tumour; vaccine; vector.

OS Homo sapiens.

Key Location/Qualifiers
FH Domain 676..1255
FT /label= Intracellular_domain
FT /note= "claimed domain, useful for immunisation"

PN W09630514-A1.

PD 03-OCT-1996.

PF 28-MAR-1996; 96WO-US01689.

PR 31-MAR-1995; 95US-0414417.

PA (UNIW) UNIV WASHINGTON.

PI Cheever MA, Disis ML;

XX WPI; 1996-455361/45.

DR N-PSDB; AAT40739.

PT DNA encoding HER-2/neu poly:peptide(s) - used for prevention or

PT treatment of malignancies with which the HER-2/neu oncogene is

PT associated

PS Claim 2; Page 56-61; 71pp; English.

CC Human HER-2/neu protein (AAW01111), also called p185 or c-erbB2, is
CC the product of the HER-2/neu oncogene (see also AAT40739). The
CC protein is over-expressed in various cancers, including breast,
CC ovarian, colon, lung and prostate. The intracellular domain of the
CC protein can be used to immunise an animal against a malignancy with
CC which the oncogene is associated. The polypeptide can be produced
CC in transformed host cells for use in immunisation. Alternatively,
CC animal cells are transfected in vivo or ex vivo with a viral vector
CC that directs expression of the polypeptide.

SO Sequence 1255 AA;

Query Match 3.6%; Score 104; DB 17; Length 1255;
Best Local Similarity 22.5%; Pred. No. 6.3;
Matches 108; Conservative 43; Mismatches 174; Indels 156; Gaps 27;

```

Qy      81 LYREBAGLCPIWKGKIELOQDRLPYRNNFLEDVPTKEKYQSGNPLPGG---FNLFNVT 137
Db      256 LHFHNSGIC-----ELHCAALVTYNTDTFESNPN-----PEGRYTGASCVT 297
Qy      138 PSQGRISFPELLEKSNKSNIASTDLGRCAEFA---FKTYAMDKNKAKATYRYPFYVDS 193
Db      298 AC-----PYNVL-----STDVGSCTLVCPHLHQEVTAEADGTORCEKSRPCA--- 339
Qy      194 KKRLOCH-----ILVSMQLMEGKKYC-----SVKGEPPDLTWYCFKPRK 232
Db      340 --RVCYIGCMHLEBRAVTSANIQEFAGCKKIGSLAFLPESPDGDPASNTAPLOPEOL 397
Qy      233 SVTNNHLIYGSAYVGENPDAF--ISKCPN-QALRG-----YRFGV-WKKGRC 276
Db      398 QVPELLEEITGYLVIAMPSDLPDLSVQNLQVIRGRLNHGAYSLTLOGLIGSLGLRS 457
Qy      277 LDVTELDVTIERVESKAQCVKTFENDGVASDQ---PHTYPLTSQASNDMPPLHOSD 332
Db      458 L--RELGSGLALIHNNTHLCFVHT---VWDQLFRNPH-----QAL-----LHTAN 498
Qy      333 QPHSGVGRNNGFYVDTTGE-----GKCALSDQ-----VPDCLVSDSAASVYTAG 379
Db      499 RPDECVGEGLACHQLCARHCWGPPTQCVCNCSQFLRGQCEVBECPVLQGLPREYVNA 558
Qy      380 SLSEETPNFIIPSNPSVTPTPTALQCTAD-----KF 412
Db      559 HCLFCHPE-CQPGQSGVTCGPE-ADQCVAANHAKDPFCVARKSPGVKPLSYMPIWK 616
Qy      413 PDSFGACDVQACKRQKTSVCGGQIQSTSVDCCTADEONEGCSNTALAGLAVGVLLALL 472
Db      617 PDEGAC--QPC---PINCTHSCVDLDDKCGPAEQR--ASPLTSIIS--AVGILLVVL 667
Qy      473 G 473
Db      668 G 668

```

RESULT 28

AAW92406
ID AAW92406 standard; Protein; 1255 AA.

AAW92406;

DT 21-APR-1999 (first entry)

DE Human HER-2/neu oncogene protein.

KM HER-2/neu; oncogene; immune response; T cell; B cell; immunisation;

KM malignancy; treatment; tumour.

OS Homo sapiens.

Key Location/Qualifiers
FH Region 676..1255
FT /note= "region which elicits immune response"

PN US5869445-A.

PD 09-FEB-1999.

PF 01-APR-1996; 96US-0625101.

PR 01-APR-1996; 96US-0625101.

PR 17-MAR-1993; 93US-0033644.

PR 12-AUG-1993; 93US-0106112.

PR 31-MAR-1995; 95US-0414417.

PA (UNIW) UNIV WASHINGTON.

PI Cheever MA, Disis ML;

XX WPI; 1999-152835/13.

Qy 473 G 473
 Db 668 G 668
 RESULT 30
 ID AAY84780 standard; Protein; 1255 AA.
 AC AAY84780;
 DT 08-AUG-2000 (first entry)
 DE Amino acid sequence of the SPLICE erB-2 receptor protein.
 KW SPLICE erB-2 receptor protein; cell transformation disorder; cancer;
 KW tumor cell proliferation; tissue degeneration; arthropathy;
 KW bone resorption; inflammatory disease; degenerative disorder;
 KW wound healing.
 OS Homo sapiens.
 XX MO200020579-A1.
 XX 13-APR-2000.
 XX 01-OCT-1999; 99MO-CA00912.
 XX 02-OCT-1998; 98US-0165192.
 XX (UTWC-) UNIV MCMASTER.
 XX Muller WJ, Siegel PM;
 PI WPI; 2000-303768/26.
 DR N-PSDB; AAA14812.
 PT Nucleic acid encoding an erB-2 receptor protein designated SPLICE
 erB-2, inhibitors of the protein are useful for treatment of cancer -
 XX
 PS Claim 3; Fig 2; 60pp; English.
 XX
 CC The present sequence represents a SPLICE erB-2 receptor protein. The
 CC protein has an in-frame deletion of 16 amino acids, 2 of which are
 CC conserved cysteine residues, compared to the unspliced protein. The
 CC erB-2 polynucleotide is used to construct probes for detecting
 CC disorders of cell transformation such as cancer. Antibodies to the
 CC protein may be used to detect SPLICE erB-2 in a sample. Agents
 CC (e.g. antisense oligonucleotides) which inhibit the expression of
 CC SPLICE erB-2 are useful for reducing tumor cell proliferation and
 CC treating cancer. Substances which stimulate SPLICE erB-2 are useful
 CC for treating conditions involving damaged cells including conditions
 CC in which degeneration of tissue occurs, such as arthropathy, bone
 CC resorption, inflammatory diseases, degenerative disorders of the
 CC central nervous system and wound healing.
 XX
 SQ Sequence 1255 AA;
 Query Match 3.6%; Score 104; DB 21; Length 1255;
 Best Local Similarity 22.5%; Pred. No. 6.3;
 Matches 108; Conservative 43; Mismatches 174; Indels 156; Gaps 27;
 Qy 81 LYRBPAGLCPIWKGKIHIEQDRLPYRNPFEDVPTKEVYKOSGNPLFG--FNLANPVT 137
 Db 256 LHPHSGIC-----ELHCPALVYVNDTFESMNN-----PEGYRTGASCVT 297
 Qy 138 PSGORISPPMELLEKSNIRKASTDLGRCAEFA-----FKTVAMPDKNNKATYRYPFYVDS 193
 Db 298 AC-----PYNVL-----STDVGSCTLVCPHNOEYVABDGTORCEKCSRCA--- 339
 Qy 194 KKRLLCH-----ILVVSQMLMEGKKYC-----SVKGEPPDLTWYCFKPRK 232

Db 340 --RVCYGLGMEHLREVRVATSNANOEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQL 397
 Qy 233 SVTENHHLIYGSAYVGENPDAF--ISKCPN-QALRG-----YRFGV-WKKGRC 276
 Db 398 QVFETLEITGYLYISAMPDSLPLSVFQNLQVIRGRILHNKAVSLTLOGIGISWLGIRS 457
 Qy 277 LDYTELDTVYLERVESKAQCWKTFENDGVAADQ-----PHTYPLTSQASWMDMPLHQSD 332
 Db 458 L-RELQSGALILHNHNLGCVHT-----VPMQDLFNNPH-----QAL-----LHTAN 498
 Qy 333 QPHSGVGRNRYGFYVUTTGE-----GKCALSDQ-----VDDCLVSDSAVSYRAAG 379
 Db 499 RPEDECVGEGLACHQLARQHCWGPPTQCVNCSQFLRGQECVCECVLQGLPREYVNA 558
 Qy 380 SLSEETNFIIIPSNVSTPPTPTALQCTAD-----KFA 412
 Db 559 HCLPCHPE-COPONGSYTCRFE-ADCCVACAHKDPFCVAPRSPGVKPLSYMPWKF 616
 Qy 413 PDSFGACDVQACKRKQKTSVCGGQIQSTSVDTADEQNECGSNTALLAGLVALLALL 472
 Db 617 PDEEGAC--QPC---PINCCHSCVDLDDKCGPAEQR--ASPLTISIS--AVVGILVAVVL 667
 Qy 473 G 473
 Db 668 G 668
 RESULT 31
 ID AAB85458 standard; Protein; 1255 AA.
 AC AAB85458;
 DT 25-SEP-2001 (first entry)
 DE Human HER-2/neu protein.
 KW Antigen-presenting cell; immunogenic; immune response; HER-2/neu;
 KW oncogene; cancer; cytostatic; vaccine; p185; c-erbB2.
 XX
 OS Homo sapiens.
 XX MO200153463-A2.
 XX 26-JUL-2001.
 XX 19-JAN-2001; 2001MO-USO1850.
 XX 21-JAN-2000; 2000US-0177545.
 XX (CORI-) CORIYA CORP.
 XX Cheever MA, Hand-Zimmermann S;
 PI WPI; 2001-476112/51.
 DR N-PSDB; AAH23392.
 PT New antigen-presenting cells, useful as vaccines for eliciting or
 PT enhancing an immune response to HER-2/neu protein, particularly useful
 PT for treating or preventing cancer, e.g. breast cancer -
 XX
 PS Claim 2; Page 41-46; 49pp; English.
 CC The invention provides an isolated antigen-presenting cell, which
 CC expresses at least an immunogenic portion of a polypeptide that produces
 CC an immune response to HER-2/neu protein. The antigen-presenting cells are
 CC useful as vaccines for eliciting or enhancing an immune response to
 CC HER-2/neu protein, particularly in treating or preventing malignancies in
 CC which the HER-2/neu oncogene is associated. Specifically, these are
 CC useful for treating or preventing cancer, e.g. breast cancer, ovarian,
 CC colon, lung or prostate cancers. The present sequence represents
 CC the human HER-2/neu protein (also known as p185 or c-erbB2).

SQ Sequence 1255 AA;
 Query Match 3.6%; Score 104; DB 22; Length 1255;
 Best Local Similarity 22.5%; Pred. No. 6.3;
 Matches 108; Conservative 43; Mismatches 174; Indels 156; Gaps 27;

```

QY 81 LYRPAAGLCPIWKGKHEIQDPRLPYRNNFLVDVPTKEKYGKSGNPLPGG---FNLNFT 137
DB 256 LHFHNSGIC-----ELHCPALVYNTDTFSMN-----PEGRTFGASCVT 297
QY 138 PSGQRISPPMELKSNIRKASTDLGRCAEFA---FKTVAMDKNKATKYRYPFYVDS 193
DB 298 AC-----PYNVL-----STDVGSCTLVCPILHNGEVTAEDEGTQCEKSKPCA--- 339
QY 194 KKRLLCH-----ILVYSQLMGKRYC-----SVKGEPPDLTWYCFKPRK 232
DB 340 --RVCYGLGMEHLREVRATVTSANIOEFAGCKKIFGSLAFLPESFDGDPASNTAFLQPEQL 397
QY 233 SVTENNHLIYGSAYVGENPDAF--ISKCPN-QALRG-----YRFGV-WKGRG 276
DB 398 QVFETLEETITGLYISAMPDSLDPDLSVFQNLQVIRGRILHNGAYSLTLQGLISMLGRS 457
QY 277 LDYTELDTVIERVESKACQWVTFENDGVASDQ---PHTYPLTSQASWDMWPLHOSD 332
DB 458 L--RELGSGLALIHNTHTLCFVHT-----VPMDOQLFRNPH-----QAL-----LHTAN 498
QY 333 QHSGGVGNRYGYVDTTGE-----GKCALSDQ-----VPDCLVSDSAAVSYTAAG 379
DB 499 REDECVGBGLACHQICARGHCWGPGPTQCVNCSQFLRGQCEVECRVLOGLPREVYVAR 558
QY 380 SLSEETPNFIISNSPVTPPTETALQCTAD-----KFA 412
DB 559 HCLPCHPE-CQFQNSVTCFQPE-ADQCVACAHYKDPFCVARGSGVYKPDLSYMPIMKF 616
QY 413 PDSFGACDVQACKRQKTSVCGQIOSTSVDTADEQNEGCSNTALAGVGVLLALL 472
DB 617 PDEBQAC--QPC---PINCTHSCVLDDBKGCFAEGR--ASPLTIS--AVVGILLVVL 667
QY 473 G 473
DB 668 G 668
  
```

RESULT 32
 AAG88267
 ID AAG88267 standard; Protein; 1255 AA.
 XX
 AC AAG88267;
 XX
 DT 11-SEP-2001 (first entry)
 XX
 DE HER2/neu amino acid sequence.
 XX
 KW Human; HER2/neu; epitope; human leukocyte antigen; HLA; T cell;
 KM immune response; vaccine; tumour; cancer; cytostatic; immunostimulant;
 XX tumour-associated antigen; T lymphocyte; cytotoxic T lymphocyte; CTL.
 OS Homo sapiens.
 XX
 PN WO200141787-A1.
 XX
 PD 14-JUN-2001.
 XX
 PF 11-DEC-2000; 2000WO-US33591.
 XX
 PR 10-DEC-1999; 99US-0458299.
 XX
 PA (EPIM-) EPIMUNE INC.
 PI Fikes J, Sette A, Sidney J, Southwood S, Chesnut R, Celis E;
 DR Keogh E;
 XX
 WPI; 2001-374995/39.

XX
 PT An isolated prepared HER2/neu epitope useful in a vaccine for inducing
 PT cellular immune responses for the prevention and treatment of cancer -
 XX
 PS Disclosure; Page 15; 199pp; English.
 XX
 CC The present invention describes isolated prepared HER2/neu epitopes (I).
 CC Also described are: (1) a clonal cytotoxic T lymphocyte (CTL) that is
 CC culture in vitro and binds to a complex of an epitope (I), bound to a
 CC human leukocyte antigen (HLA) molecule; (2) a peptide (II) comprising (I)
 CC and a second epitope and the peptide is less than 50 contiguous amino
 CC acids that have 100% identity with a native peptide sequence of HER2/neu;
 CC (3) a vaccine composition (III) comprising (II) and a pharmaceutical
 CC excipient; (4) an isolated nucleic acid encoding a peptide comprising
 CC (I); and (5) an isolated nucleic acid encoding (II). (I) has cytostatic
 CC and immunostimulant activities, and can be used in vaccines. (I), (II)
 CC and (III) are useful for inducing cellular immune responses for the
 CC prevention and treatment of cancer. (I) and (II) are useful for
 CC monitoring or evaluating an immune response to a tumour-associated
 CC antigen when incubated with a T lymphocyte sample from a patient and
 CC detecting the presence of bound T lymphocyte to (I) or (II). Epitope
 CC based vaccines mean that immunosuppressive epitopes that may be present
 CC in whole antigens may be avoided. Selected epitopes may be combined to
 CC enhance immunogenicity. The possible pathological side effects caused by
 CC infectious agents or whole protein antigen is eliminated. The vaccine
 CC provides the ability to direct and focus an immune response to multiple
 CC selected antigens from the same pathogen. Epitope-based anti-tumour
 CC vaccines provides the opportunity to combine epitopes derived from
 CC multiple tumour-associated molecules addressing the problem of tumour-
 CC tumour variability and reducing the likelihood of tumour escape due to
 CC antigen loss. AAG88266 to AAG89121 represent amino acid sequences used in
 CC the exemplification of the present invention.

SQ Sequence 1255 AA;
 Query Match 3.6%; Score 104; DB 22; Length 1255;
 Best Local Similarity 22.5%; Pred. No. 6.3;
 Matches 108; Conservative 43; Mismatches 174; Indels 156; Gaps 27;

```

QY 81 LYRPAAGLCPIWKGKHEIQDPRLPYRNNFLVDVPTKEKYGKSGNPLPGG---FNLNFT 137
DB 256 LHFHNSGIC-----ELHCPALVYNTDTFSMN-----PEGRTFGASCVT 297
QY 138 PSGQRISPPMELKSNIRKASTDLGRCAEFA---FKTVAMDKNKATKYRYPFYVDS 193
DB 298 AC-----PYNVL-----STDVGSCTLVCPILHNGEVTAEDEGTQCEKSKPCA--- 339
QY 194 KKRLLCH-----ILVYSQLMGKRYC-----SVKGEPPDLTWYCFKPRK 232
DB 340 --RVCYGLGMEHLREVRATVTSANIOEFAGCKKIFGSLAFLPESFDGDPASNTAFLQPEQL 397
QY 233 SVTENNHLIYGSAYVGENPDAF--ISKCPN-QALRG-----YRFGV-WKGRG 276
DB 398 QVFETLEETITGLYISAMPDSLDPDLSVFQNLQVIRGRILHNGAYSLTLQGLISMLGRS 457
QY 277 LDYTELDTVIERVESKACQWVTFENDGVASDQ---PHTYPLTSQASWDMWPLHOSD 332
DB 458 L--RELGSGLALIHNTHTLCFVHT-----VPMDOQLFRNPH-----QAL-----LHTAN 498
QY 333 QHSGGVGNRYGYVDTTGE-----GKCALSDQ-----VPDCLVSDSAAVSYTAAG 379
DB 499 REDECVGBGLACHQICARGHCWGPGPTQCVNCSQFLRGQCEVECRVLOGLPREVYVAR 558
QY 380 SLSEETPNFIISNSPVTPPTETALQCTAD-----KFA 412
DB 559 HCLPCHPE-CQFQNSVTCFQPE-ADQCVACAHYKDPFCVARGSGVYKPDLSYMPIMKF 616
QY 413 PDSFGACDVQACKRQKTSVCGQIOSTSVDTADEQNEGCSNTALAGVGVLLALL 472
DB 617 PDEBQAC--QPC---PINCTHSCVLDDBKGCFAEGR--ASPLTIS--AVVGILLVVL 667
QY 473 G 473
  
```

ID	Sequence	Score	DB	Length	Matches	Indels	Gaps
AAE24067	AAE24067 standard; Protein; 1255 AA.	3.6%;	DB 23;	Length 1255;	27,		
XX	AAE24067	22.5%;	Pred. No. 6.3;				
AC	AAE24067	43;	Mismatches 174;	Indels 156;	Gaps 27,		
XX	23-SEP-2002 (first entry)						
DT	Human Her-2 protein.						
XX	Human; Her-2; epidermal growth factor receptor 2; infection; cancer;						
XX	hyperproliferative disorder; prophylaxis; inflammation; antisense;						
KW	tumour; gene therapy; phosphothioate backbone.						
OS	Homo sapiens.						
XX	MO200222636-A1.						
PN	21-MAR-2002.						
PD	12-SEP-2001; 2001WO-US28572.						
PF	15-SEP-2000; 2000US-0663834.						
XX	(ISIS-) ISIS PHARM INC.						
PA	Bennett CF, Cowseart LM;						
XX	WPI; 2002-471192/50.						
DR	N-PSDB; AAD36904.						
XX	Novel antisense oligonucleotide which modulates the expression of Human						
PT	Epidermal Growth Factor receptor, Her2, is useful for treating tumors						
PT	inflammation or to prevent infection in humans -						
XX	Example 13; Page 95-107; 116pp; English.						
PS	The invention relates to antisense compounds targeted to a nucleic						
CC	acid molecule encoding Her2 (human Epidermal Growth Factor receptor 2)						
CC	that specifically hybridises with and inhibits the expression of Her2.						
CC	Antisense compounds of the invention are used for treating diseases or						
CC	conditions associated with Her2 such as hyperproliferative disorders						
CC	e.g. lung, breast, gastric, oesophageal, colon, bladder, salivary,						
CC	neural or cardiac cancer. They are also useful prophylactically e.g.						
CC	to prevent or delay infection, inflammation and tumour formation. The						
CC	invention is also used in gene therapy. The present sequence is human						
CC	Her-2 protein.						
XX	Sequence 1255 AA;						
SO	Query Match	3.6%;	Score 104;	DB 23;	Length 1255;		
	Best Local Similarity	22.5%;	Pred. No. 6.3;				
	Matches 108;	Conservative 43;	Mismatches 174;	Indels 156;	Gaps 27,		
QY	81 LYREBAGICPTWKGKHIIELOQPDRLRYRNNFLEDEVTEKEKYGKSNPLRQCG---FNLVNTV 137						
DB	256 LHFNHSGIC-----ELHCPALVYNTDTFESMPN-----DEGRYTFGASCVT 297						
QY	138 PSGORISPPMELLEKNKSNINIKASTDLGRCAEFA---EKTVMADKNNKATKYRYPFVDS 193						
DB	298 AC-----PNNYL-----STDVGSCTLVCPAHNGEVAHEDTQCEKSKRCA--- 339						
QY	194 KKRLLCH-----ILVYSGQLMGKKYC-----SVKGPPDLTWYCFKPRK 232						
DB	340 --RVCYGLGMEHLREVRVATSNIDFAGCKKIFGSLAFLEPSFGDPASNTAPLQPEQL 397						
QY	223 SVTEHHLLIYGSAVYGGNDPAF--ISKCPN-QALG-----YRGV-WKKGRC 276						
DB	398 QVFETLEETITGLVLSAMPDSLPDISVQNTLOVYIGRLILHNGANSLLTQGLGISMLGURS 457						

QY	277	LDYLETLDTVLIERVBSKXQCKWKTENDGVASDQ----	PHYPLTSGASWMDWMPHOSD	332			
Db	458	L--RELSSGGLALIHNNTHLCFVHT-----	VPMDQLFRNH-----	QAL-----LHTAN			
QY	333	QPHSGVGVRNNGFYVYDTTGE-----	GKCALSDQ-----	VPDCLVSDAASVYTAAG			
Db	499	RPEDECVBEGLAGHQCLCARHGHWGPGPQCVNCSQPLRQGECEEBEERVLQGLPREVYNAR	556				
QY	360	SLSETPNFIIPSNSSVTPPTETALQCTAD-----	KF	412			
Db	413	PDSFGACVQACCKRQKTSQVSGQIQSTSVDCTADEQNECGSNMTALAGAVGVLTLAL	472				
QY	617	PDEBAC--QPC---PINCHSCVLDLDDKGCFAQR--	ASPLTSLIS--AVVGLLVVL	667			
QY	473	G	473				
Db	668	G	668				
RESULT 34							
ID	AAE20479	standard; Protein; 1255 AA.					
AC	AAE20479;						
DT	01-JUL-2002	(first entry)					
DE	Human Her-2/neu protein.						
KW	Human; Her-2/Neu protein; immune response; gene therapy; breast cancer; human leukocyte antigen; HLA; vaccine; malignancy; cytostatic.						
OS	Homo sapiens.						
FT	Key	Location/Qualifiers					
FT	Region	1021..1030					
FT	/note= "Naturally processed HLA-B44-restricted epitope"						
XX	WO200214503-A2.						
XX	21-FEB-2002.						
XX	14-AUG-2001; 2001WO-US41733.						
XX	14-AUG-2000; 2000US-225152P.						
XX	28-SEP-2000; 2000US-236428P.						
XX	21-FEB-2001; 2001US-270520P.						
XX	(CORI-) CORIXA CORP.						
XX	Hand-zimmermann S, Cheever MA, Foy TM, Lodes MJ, Kalos MD, Mcneill PD, Vedvick TS;						
XX	WPI; 2002-280758/32.						
XX	N-PSDB; AAD32743.						
XX	Novel isolated Her-2/Neu polypeptide composition useful for therapy, prevention and diagnosis of cancer, preferably breast cancer						
XX	Disclosure; Page 114-117; 129pp; English.						
XX	The invention relates to an isolated Her-2/Neu polypeptide composition effective for eliciting an immune response. The invention is useful for eliciting an immune response in a patient, where the patient is human leukocyte antigen (HLA)-B44 positive or is affected with breast cancer. The composition is useful for the therapy and diagnosis of cancer, preferably breast cancer, in pharmaceutical compositions, e.g., vaccine and other compositions for the diagnosis, prevention and treatment of human malignancies, for stimulating and/or expanding T cells specific for Her-2/Neu polypeptide and for inhibiting the development of cancer in a						

CC human patient, as probe or primer for nucleic acid hybridisation, to
 CC selectively form duplex molecules with complementary stretches of the
 CC entire Her-2/Neu gene or gene fragments of interest, to isolate a full
 CC length gene from a suitable library, and to direct expression of a
 CC polypeptide in appropriate host cells. The composition is useful in
 CC prophylactic or therapeutic applications and for the treatment of cancer,
 CC preferably for the immunotherapy of breast cancer and other Her-2/Neu-
 CC associated malignancies. The invention is useful in gene therapy. The
 CC present sequence is human Her-2/neu protein.

XX Sequence 1255 AA;

Query Match 3.6%; Score 104; DB 23; Length 1255;
 Best Local Similarity 22.5%; Pred. No. 6.3; Mismatches 174; Indels 156; Gaps 27;
 Matches 108; Conservative 43;

QY 81 LVRBPAGLCPIWKGKHEIQDPRLPYRNNFLEDPTEKEYKOSGNPLPGG---FNLNFT 137
 DB 256 LHPNHSGLC-----ELHCPALVTYNTDTPESMPN-----PEGRTFGASCVT 297
 QY 138 PEGQRISPPMELLEKNISIKASTDLGRCABFA---FKTVAMDKNNKATKRYRPVYDS 193
 DB 298 AC-----PYNVL-----STDVGSCTLYCPHNOEVTADGTQRCCKSKPCA--- 339
 QY 194 KKRLLCH-----ILVSMQMEGKKYC-----SVKGEPPDLTWYCFKPKRK 232
 DB 340 --RVCTGLGMEHLREVRVAVTSANIQEPAGCKIFGSLAFPSFGDDPSNTAPLOPEBL 397
 QY 233 SVTENHLLIYGSAYVGENPDAF--ISKCPN-QALRG-----YRFGV-WKKGRC 276
 DB 398 QVFETLEITGLYLIYAWPDSLPLDLSVFNOLQVIRIRILHNGAYSLTGLGISMGLRS 457
 QY 277 LYTTELTLTVIERVESKAOCKWKTFFNDGVASDQ---PHTYPLTSQASMNWMPLHOSD 332
 DB 458 L--RELSSGLALIHNTHLCFVHT-----VPMQDLFRNPH-----QAL-----LHTAN 498
 QY 333 QHSGSGVGNNGYVYDITGE-----GKCALSDQ-----VPDCLVSDSAVSYTAG 379
 DB 499 RREDECEVGGGLACHQICANHGCKGPPPTQVNCQPLRBOECVEECRVLQGLPREVYNAK 558
 QY 380 SLSEETPNFIIIPSNPSVTPTPTETALQCTAD-----KF 412
 DB 559 HCLPCHRE--CQPNQSVTCEGPE-AAQCVAACHYKDPFCVAPCPSPGVKPDLSYMPIMWF 616
 QY 413 PPSFGACDVQACKRQKTSVCGGIGSTSVDTCTADEONEGSGNTALLAGLAVGVLLALL 472
 DB 617 PDEEGAC--QPC---PINCTHSCVDLDDKGCAPABQR--ASPLTSIIS--AVGILLVVL 667
 QY 473 G 473
 DB 668 G 668

RESULT 35

AAMS1143
 ID AAMS1143 standard; Protein; 1255 AA.

XX AC AAMS1143;

XX DT 17-JUN-2002 (first entry)

XX DE Human Her-2/neu oncogene-encoded p185 glycoprotein.

XX KW Her-2/neu; oncogene; cancer; tumour; vaccine; human; p185;

XX KM tyrosine kinase; receptor; c-erbB2; gene therapy.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

XX FT Domain 1..653

FT Domain /note= "extracellular domain"
 FT 676..1255
 FT /note= "intracellular domain"

FT Domain 990..1255
 FT /note= "phosphorylation domain"

XX WO200212341-A2.

XX 14-FEB-2002.

XX 03-AUG-2001; 2001WO-US24283.

XX 03-AUG-2000; 2000US-0632507.

XX (SMIX) SMITHLINE BECHAM BIOLOGICALS.

XX Cheever MA, Gheysen D;

XX WPI; 2002-241743/29.

XX N-PSDB; ABA92250.

PT Her-2/neu fusion protein for treating or preventing cancer by eliciting
 PT or enhancing an immune response to the protein, has Her-2/neu
 PT extracellular domain fused to Her-2/neu intracellular or
 PT phosphorylation domain

PS Claim 68; Fig 7; 141p; English.

CC The present sequence is that of human Her-2/neu (p185 glycoprotein
 CC or c-erbB2), an oncogenic self-protein and target for anti-cancer
 CC vaccines. The Her-2/neu gene is amplified and p185 is overexpressed
 CC in a variety of cancers, including breast, ovarian, colon, lung and
 CC prostate cancer. Her-2/neu is a member of the tyrosine kinase
 CC family of receptor-like glycoproteins. It comprises an extracellular
 CC domain with homology to the epidermal growth factor receptor
 CC (EGFR), a highly hydrophobic transmembrane domain and a C-terminal
 CC intracellular domain that also shows homology to EGFR. Its
 CC overexpression correlates with a poor prognosis in breast and
 CC ovarian cancers. The invention provides Her-2/neu fusion
 CC proteins, nucleic acids encoding them, viral vectors, and vaccines
 CC comprising the fusion proteins or nucleic acid molecules. In
 CC preferred fusion proteins, the extracellular domain of a Her-2/neu
 CC protein is fused to a Her-2/neu intracellular domain or
 CC phosphorylation domain (or its DeltaCD fragment). An immune
 CC response to Her-2/neu protein is elicited or enhanced by
 CC administering the fusion protein in the form of a vaccine, or by
 CC transfecting cells of an animal *ex vivo* with a nucleic acid
 CC encoding the fusion protein, and delivering the transfected cells
 CC to the animal. The fusion proteins, nucleic acids, and isolated
 CC specific T-cells are useful for inhibiting the development of a
 CC cancer, especially breast, ovarian, colon, lung or prostate cancer
 CC in a patient. T cells that specifically react with a Her-2/neu
 CC fusion protein can be used to remove tumour cells from a sample in
 CC order to inhibit the development of cancer in a patient.

XX Sequence 1255 AA;

Query Match 3.6%; Score 104; DB 23; Length 1255;
 Best Local Similarity 22.5%; Pred. No. 6.3; Mismatches 174; Indels 156; Gaps 27;
 Matches 108; Conservative 43;

QY 81 LVRBPAGLCPIWKGKHEIQDPRLPYRNNFLEDPTEKEYKOSGNPLPGG---FNLNFT 137
 DB 256 LHPNHSGLC-----ELHCPALVTYNTDTPESMPN-----PEGRTFGASCVT 297
 QY 138 PEGQRISPPMELLEKNISIKASTDLGRCABFA---FKTVAMDKNNKATKRYRPVYDS 193
 DB 298 AC-----PYNVL-----STDVGSCTLYCPHNOEVTADGTQRCCKSKPCA--- 339
 QY 194 KKRLLCH-----ILVSMQMEGKKYC-----SVKGEPPDLTWYCFKPKRK 232
 DB 340 --RVCTGLGMEHLREVRVAVTSANIQEPAGCKIFGSLAFPSFGDDPSNTAPLOPEBL 397
 QY 233 SVTENHLLIYGSAYVGENPDAF--ISKCPN-QALRG-----YRFGV-WKKGRC 276

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Db      398 QVFETLEBITGYLYISAMPDLSLPSFONLOVIRGRILHNGAVSLTLQGLGISWLGIRS 457
Qy      277 LDYTELDTVIERVESKAQCWKTFENDGVASDQ-----PHTYPLTSQASWMDWMPHLQSD 332
Db      458 L--RELGGGLALIHNTHLCFVHT-----VPMDOFLFRNPH-----QLL-----LHFRAN 498
Qy      333 QPHSGGVGRNGFYVDTTGE-----GKCALSDQ-----VPDCLVSDSAVSYTAAG 379
Db      499 RPEDECVEGLACHQLCARGHGMGPPTQCVNCSQFLRGQECVEECRYLQGLPREYVNA 558
Qy      380 SLSEETPFIIIPSNPSVTPTPTETALQCTAD-----KF 412
Db      559 HCLPCHPE-COPONGSVTCFGE-ADQCVACAHYKDPFCVACRCPGKPLSYMPIKF 616
Qy      413 PDSFGACDVQACKROKTSVCGGQISTSVDTADEBQNEGCSNTALAGLAVGVLLALL 472
Db      617 PDEBGAC--QPC--PINCTHSCVDLDDKGCPEABQR--ASPLTSIIS--AVGILLVVL 667
Qy      473 G 473
Db      668 G 668

```

RESULT 36

AAU77114 ID AAU77114 standard; Protein; 1255 AA.

AAU77114;

05-JUN-2002 (first entry)

Human Her-2/neu polypeptide.

Human; Her-2/neu; cytostratic; haematological malignancy; CML;

acute myelogenous leukaemia; AML; chronic myelogenous leukaemia; CLL;

chronic lymphocytic leukaemia; myeloma; non-Hodgkin's lymphoma; MDS;

Hodgkin's lymphoma; T cell therapy.

Homo sapiens.

MO200213847-A2.

21-FEB-2002.

13-AUG-2001; 2001MO-US25408.

14-AUG-2000; 2000US-0638280.

28-SEP-2000; 2000US-0675904.

(CORI-) CORIXA CORP.

Gaiger A, Cheever MA, Hand-zimmermann S;

WPI; 2002-280741/32.

N-PSDB; ABK10730.

Inhibiting haematological malignancy development by administering

polypeptide comprising immunogenic portion of Her-2/neu, polynucleotide

encoding the polypeptide, or antigen presenting cells expressing the

polypeptide

Dioclosure; Page 71-74; 74pp; English.

The invention relates to a method for inhibiting development of

haematological malignancy in a patient by administering a polypeptide

comprising an immunogenic portion of Her-2/neu or a polynucleotide

encoding the polypeptide. Antigen presenting cells that express the

Sequence 1255 AA;

Query Match 3.6%; Score 104; DB 23; Length 1255;

Best Local Similarity 22.5%; Pred. No. 6.3;

Matches 108; Conservative 43; Mismatches 174; Indels 156; Gaps 27;

```

Qy      81 LYREPAGLCPIWGHIELOQDRLPYRNNELEDPTEKEYQSGNPLFG--FNLEFVT 137
Db      256 LHPNHSIGIC-----ELHCPALVTYNTDTFESMPN-----PEGRYTFGASCVT 297
Qy      138 PSQGISFPEMELLEKSNNITASTDLGRCAEFA----FKTVAMDKNKATKRRPFVDS 193
Db      298 AC-----PYNVL-----STDVGSCTLVCPHLNQEVTAEQGTORCEKSKPCA--- 339
Qy      194 KKRLLCH-----ILVSMQLMEGKKYC-----SVKGEPPDLTWYCFKPRK 232
Db      340 --RVCYGLGMHLEVRVAIVSANIQEPAGCKKIGSLALPESFDGDPASNTAPLQPEQL 397
Qy      233 SVTENHLLIYGSAYVGENPDAF--ISKCPN-QALRG-----YRFGV-WKKGRC 276
Db      398 QVFETLEBITGYLYISAMPDLSLPSFONLOVIRGRILHNGAVSLTLQGLGISWLGIRS 457
Qy      277 LDYTELDTVIERVESKAQCWKTFENDGVASDQ-----PHTYPLTSQASWMDWMPHLQSD 332
Db      458 L--RELGGGLALIHNTHLCFVHT-----VPMDOFLFRNPH-----QLL-----LHFRAN 498
Qy      333 QPHSGGVGRNGFYVDTTGE-----GKCALSDQ-----VPDCLVSDSAVSYTAAG 379
Db      499 RPEDECVEGLACHQLCARGHGMGPPTQCVNCSQFLRGQECVEECRYLQGLPREYVNA 558
Qy      380 SLSEETPFIIIPSNPSVTPTPTETALQCTAD-----KF 412
Db      559 HCLPCHPE-COPONGSVTCFGE-ADQCVACAHYKDPFCVACRCPGKPLSYMPIKF 616
Qy      413 PDSFGACDVQACKROKTSVCGGQISTSVDTADEBQNEGCSNTALAGLAVGVLLALL 472
Db      617 PDEBGAC--QPC--PINCTHSCVDLDDKGCPEABQR--ASPLTSIIS--AVGILLVVL 667
Qy      473 G 473
Db      668 G 668

```

RESULT 37

AAAR39568 ID AAR39568 standard; Protein; 1433 AA.

AAAR39568;

25-MAR-2003 (updated)

07-FEB-1994 (first entry)

Sequence of c-erbB-2 tumour antigen.

Tumour antigen; c-erbB-2; glycoprotein.

Homo sapiens.

MO9316185-A2.

19-AUG-1993.

05-FEB-1993; 93WO-US01055.

06-FEB-1992; 92US-0831967.

(CETU) CETUS ONCOLOGY CORP.

(CREA-) CREATIVE BIOMOLECULES INC.

Houston LL, Huston JS, Oppermann H, Ring DB;

WPI; 1993-272889/34.

N-PSDB; AAQ46083.

```

XX New single chain Fv polypeptide binding to C-erbB-2 tumour
PT antigen - for imaging or treating breast or ovarian cancer etc.
XX
XX Disclosure: pages 48-54; 87pp; English.
XX
XX c-erbB-2 refers to a protein antigen expressed on the surface of
CC tumour cells, such as breast and ovarian tumour cells, which is an
CC approx. 200,000 mol. wt. acidic glycoprotein having an isoelectric
CC pt. of about 5.3 (see AA046083, AA039568). X in AA039568 represents
CC the location of a stop codon in AA046083.
CC (Updated on 25-MAR-2003 to correct PN field.)
XX
XX Sequence 1433 AA;
SQ
Query Match 3.6%; Score 104; DB 14; Length 1433;
Best Local Similarity 21.3%; Pred. No. 7.8;
Matches 103; Conservative 47; Mismatches 173; Indels 160; Gaps 26;

QY 81 LYREFAGLCPIWGKHI ELQPPDLPRNNFLDVPREKKYKSGNPLPGS---FNLNFT 137
DB 256 LHFHNSGIC-----ELHCPALVTYNTDTFESMPN-----PEGKRYTFGASCVT 297
QY 138 PEGQRISPPMELLEKNNSIKASTDLCRCAEFA---FKTVAMDKNNKATKYRPFVYDS 193
DB 298 AC-----FNYVL-----STDVGSCTLVCPILHNGSVTAEQGRCEKSKCA--- 339
QY 194 KRLRLH-----LLVSMQIMESKCYC-----SVKGEPPDLTWYCFKPRK 232
DB 340 --RVCGIGLMEHLREVRAVTSANIOEFACCKRIFGSLAFLPESFDODPSANPLAPEHL 397
QY 233 SVTEHHHLVGSAYVGENDAF--ISKCN-CALRGY-----RFGWKKGRCICDYTEL 283
DB 398 QVFETLEQITGYLYISAMPDSLPLDLSVFONLOVIRRIIHNAGYSLTGLGISMGLRS 457
QY 284 -----DVIRESKAKQCVKTFENDGVAADPHYPLTSGASNMNDWPLHQ 330
DB 456 LAELSGGLALHNHNTLSFVHYTP--WDOLFNN-----PH-----QAL-----LHT 496
QY 331 SPOPHSGGVGRNYGYVDTTGE-----GKCALSDQ-----VPDCLVSDSAVSYTA 377
DB 497 ANRPEDCEVGEGLACHQLCARGHCWGPPTQCVNCSQFLRGQBCVECHVLOGLPREYVA 556
QY 378 ASSLSEPTNFIIIPNSVSTPPPTETALQCTAD----- 410
DB 557 AHCILPCHE-CQPOGSVTCFGE-ADQCVACAHYKDPFCVACPSGVKCDLSMPWT 614
QY 411 KPPDSFGACDVQACKRKQTSQVGGQIQSTSVDTADEQNEGCSNTALLIAGLAVGVLLIA 470
DB 615 KPPDEEGAC--QPC---PINCCHSCVDLDDKGCPRAGQ--ASPLISIIIS--AVVGLIIV 665
QY 471 LIG 473
DB 666 VLG 668

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RESULT 38

AAB53307 standard; Protein; 365 AA.

AAB53307;

09-MAR-2001 (first entry)

Human colon cancer antigen protein sequence SEQ ID NO:847.

Human; colon cancer; colon cancer antigen; diagnosis; detection; immunomodulatory; muscular; gynaecological; gastrointestinal; immunodeficiency; cytotoxic; cardioactive; neuroprotective; vulnary; neurotropic; anti-infective; antibacterial; gene therapy; wound; neural disorder; immune system disorder; muscular disorder; reproductive disorder; gastrointestinal disorder; renal disorder; infectious disease; cardiovascular disorder.

```

XX Homo sapiens.
OS
XX WO20005351-A1.
XX
XX 21-SEP-2000.
XX
XX 08-MAR-2000; 2000WO-US05883.
XX
XX 12-MAR-1999; 99US-0124270.
XX
XX (HUMA-) HUMAN GENOME SCT INC.
XX
XX Rosen CA, Ruben SM;
XX
XX WPI, 2000-587534/55;
XX
XX N-PSDB; AAC98064.
XX
XX Colon cancer associated gene sequences, referred to as colon cancer
PT antigens, useful for the treatment, prevention, and diagnosis of colon
PT disorders such as colon cancer -
XX
XX Claim 11; Page 1395-1396; 2104pp; English.
XX
XX AAC97991 to AAC98763 encode the human colon cancer associated proteins,
XX called human colon cancer antigens, given in AAB53234 to AAB54006. The
XX human colon cancer antigens can have cytoskeletal, cardioactive, muscular;
XX neuroprotective, immunomodulatory, gynaecological, gastrointestinal,
XX and vulnary, neurotropic, anti-infective and antibacterial activities, and
XX can be used in gene therapy. The colon cancer antigen polynucleotides,
XX proteins and antibodies to the proteins are useful for the prevention,
XX treatment and diagnosis of colon disorders, such as colon cancer. The
XX polynucleotides may be used in diagnostics and research, such as for
XX chromosome identification, and as hybridisation probes. The proteins
XX may also be used to prevent diseases such as neural disorders, immune
XX system disorders, muscular disorders, reproductive disorders,
XX gastrointestinal disorders, wounds, renal disorders, infectious
XX diseases, and cardiovascular disorders. AAC98764 to AAC98772 and
XX AAB54007 represent sequences used in the exemplification of the present
XX invention.
XX
XX Sequence 365 AA;
SQ

```

Query Match 3.5%; Score 103.5; DB 21; Length 365;
 Best Local Similarity 19.7%; Pred. No. 1;
 Matches 93; Conservative 48; Mismatches 121; Indels 211; Gaps 22;

```

QY 101 PDRLEPRNNFLDEVFTEKE---YKQGNP-----LFG---GFNLNFTPSGORIS-P 145
DB 6 FGGCEWVLP.SLPDQTDLDRPPGRSRTGRPDAMAMLEPGFLCGALLGFLCISGLAVEVK 65
QY 146 PFMELLEKNNSIKASTDLCRCAEFAFKTVAMDKNNKATKYRPFVYDSKKLCHILYISM 205
DB 66 VTEPL-----STPLGKTAELT-----C----- 83
QY 206 QLMGKKTCSYVGEPPDLTWYCFKPRKSVTEHHHLVGSAYVGENDAFISKCPNALRG 265
DB 84 -----TSTSVGDSFALENSFVQGRKPISSHPLTYT-----NG 118
QY 266 YRFGWKKGRCICDYTELDTVIRESVSKAQCVKTFENDGVAADPHYPLTSGASNDW 325
DB 119 HLVPYSGSKSRVSLQNPPTV-----GVA-----TLKLTLD----- 148
QY 326 WFLHOSDQPHSGGVGRNYGYVDTTGEKCALSDQVDPDCLVSDSAVSYTAAGLSSET 385
DB 149 --VHPSD-----TGYTLQVNNP--DPYTNGLGLNLTIV----- 179
QY 366 PNFILPNSP-----SVTPPTETALQCTADK-----FPDSFGACDVQACKR 426
DB 180 --LVPSNPPLCGSQSQSTVSGSTALRCSSSEGAPKYVNWVRLGFFPPSPESWQ----- 233
QY 427 OKTSCVGGQIQSTSVDTCTAD-----EQNEGCS-----NTALLIAGLAVG--G 465

```

Db 234 ---DEVSGQLITLNLSTSSGTYRCVATNMGASCELTLSTEPSQGRVAGALIGVLG 290
Qy 466 VLLIALLGGGCGYFAKRLDRNKGVQAAHHEHFQSDRGARKRP---SDLMQEA 515
Db 291 VLLLSV-----AAFLVRFQKERKKPKETYGSGDLRADA 325

RESULT 39
AAC75613
ID AAC75613 standard; Protein; 365 AA.
XX
XX AAC75613;
XX
XX 03-SEP-2001 (first entry)
XX
XX Human colon cancer antigen protein SEQ ID NO:6377.
XX
XX Human, colon cancer; colon cancer antigen; diagnosis; detection;
XX colorectal carcinoma; chromosome 11.
XX
XX Homo sapiens.
XX
XX MO200122920-A2.
XX
XX 05-APR-2001.
XX
XX 28-SEP-2000; 2000MO-US26524.
XX
XX 29-SEP-1999; 99US-0157137.
XX 03-NOV-1999; 99US-0163280.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX Ruben SM, Barash SC, Birse CE, Rosen CA;
XX WPI; 2001-235357/24.
XX DR N-PSDB; AAH35018.
XX
XX Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
XX useful for preventing, diagnosing and/or treating colorectal cancers -
XX
XX Claim 11; Page 7849-7851; 9803PP; English.
XX
XX AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
XX cancer-associated nucleic acid molecules (N) and proteins (P), where
XX the proteins are collectively known as colon cancer antigens. The colon
XX cancer antigens have cytostatic activity and can be used in gene
XX therapy and vaccine production. N and P may be used in the prevention,
XX diagnosis and treatment of diseases associated with inappropriate P
XX expression. For example, N and P may be used to treat disorders
XX associated with decreased expression by rectifying mutations or deletions
XX in a patient's genome that affect the activity of P by expressing
XX inactive proteins or to supplement the patient's own production of P.
XX Additionally, N may be used to produce the colon cancer-associated P,
XX by inserting the nucleic acids into a host cell and culturing the cell
XX to express the proteins. N and P can be used in the prevention, diagnosis
XX and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
XX and AAB77789 represent sequences used in the exemplification of the
XX present invention.
XX
XX N.B. Pages 66 to 682 and page 7053 of the sequence listing were
XX missing at time of publication, meaning no sequences are present for
XX SEQ ID NO:1027 to 1052, 7921 and 7922.
XX
XX Sequence 365 AA;

Query Match 3.5%; Score 103.5; DB 22; Length 365;
Best Local Similarity 19.7%; Pred. No. 1;
Matches 93; Conservative 48; Mismatches 121; Indels 211; Gaps 22;

Qy 101 PDRLPYRNPFLEDPTEKE-----YKSGNP-----LPG-----GNLNFVTPSGQRIS-P 145
Db 6 PGGCPWVLPSPDTOTDLDRPPGSRKRGPDAAAEALPGPLCAGLGLGSLAVEVK 65

Qy 146 FPMELLENKSNIKASTDLGRCAEFATVAMDKNKAKTKYRPVYDSKKRLCHILYVSM 205
Db 66 VPTPL-----STPLGKTAELT-----C----- 83
Qy 206 QLMGKKYCYGVKEPDLTWCFKPKRSVTENHLLTIGSAVGENPDALFISKCPNALRG 265
Db 84 -----TYSYTSVGDSPFALEWSFVQPKRPISESHPILYFT-----NG 118
Qy 266 YRFGWKKGRCLDVTDLDTYIERVESKAQCQWVTFENDGVASDPHTYPLTSGASNMWD 325
Db 119 HLYPTGSKSKVSLQNPPTV-----GVA-----TLKLT----- 148
Qy 326 WPLHQSDQPHSGGVGRNVGFYVDTTGEKCALSDQVDPDCLVSDAASVYTAAGLSHET 385
Db 149 --VHPSD-----TGTYLCQVNNP-PDFTYNGLGLNLTV----- 179
Qy 386 PNFIIPSNP-----SVTPPEPIALQCTADK-----PDSFGACVQACKR 426
Db 180 --LVPPSNPLCSQSGQTSVGSSTALRCSSSEGAKPVMVRLGTFPTPSPGSMVQ---- 233
Qy 427 QKTSVGGQIGSTVDCTAD-----BQNEGCS-----NTALINGLAVG---G 465
Db 234 ---DEVSGQLITLNLSTSSGTYRCVATNMGASCELTLSTEPSQGRVAGALIGVLG 290

Qy 466 VLLIALLGGGCGYFAKRLDRNKGVQAAHHEHFQSDRGARKRP---SDLMQEA 515
Db 291 VLLLSV-----AAFLVRFQKERKKPKETYGSGDLRADA 325

RESULT 40
AAU98923
ID AAU98923 standard; Protein; 1223 AA.
XX
XX AAU98923;
XX
XX 24-SEP-2002 (first entry)
XX
XX Human breast cancer antigen, Her2 variant.
XX
XX Human, Her2; cytostatic; antiviral; immunostimulant;
XX cell-mediated immune response; tumour; breast cancer;
XX virus infection; prostate cancer; colorectal cancer; pancreatic cancer;
XX lymphoma; leukaemia; hepatocellular carcinoma; lentivirus; herpesvirus;
XX human immunodeficiency virus; HIV; flavivirus; pestivirus.
XX
XX Homo sapiens.
XX
XX MO200240059-A2.
XX
XX 23-MAY-2002.
XX
XX 01-NOV-2001; 2001MO-US45626.
XX
XX 01-NOV-2000; 2000US-0704232.
XX
XX (AMBI-) AMERICAN FOUND BIOLOGICAL RES INC.
XX (MINC/) MINCHEFF M S.
XX (LOUK/) LOUKINOV D I.
XX (ZOUB/) ZOUBAK S.
XX
XX Mincheff MS, Loukinov DI, Zoubak S;
XX WPI; 2002-527524/56.
XX DR N-PSDB; ABR66207.
XX
XX Inducing a cell-mediated immune response against a target antigen,
XX reducing undesired cells and stimulating presentation of an antigen by
XX a cell, comprises administering a polynucleotide encoding a variant of
XX an antigen -
XX
XX Claim 21; Page 134-138; 146PP; English.
XX
XX The invention relates to a method of inducing a cell-mediated immune

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OM protein - protein search, using sw model

Run on: October 2, 2003, 16:00:20 ; Search time 43 Seconds
(without alignments)
1209.936 Million cell updates/sec

Title: US-10-039-770a-1

Perfect score: 541
Sequence: 1 MGWGVQLLVLPVADCTIFA.....EAEENIDGERTHWVEGDY 541

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283308 seqs, 96168682 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database :
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	1.7	387	2	EB3679
2	9	1.7	401	2	G87364
3	9	1.7	923	2	G90656
4	9	1.7	923	2	G85507
5	8	1.5	130	2	S52116
6	7	1.5	230	2	D70718
7	8	1.5	287	2	A60643
8	8	1.5	383	2	AF3503
9	8	1.5	396	2	AF1903
10	8	1.5	463	2	AH0189
11	8	1.5	466	2	JO2263
12	8	1.5	480	2	F70785
13	8	1.5	1126	2	T01491
14	8	1.5	1268	2	S52781
15	8	1.5	1348	2	S51656
16	8	1.5	3430	1	GNWVWV
17	8	1.5	3433	1	GNWVWV
18	8	1.5	3434	1	GNWVWV
19	8	1.3	23	2	A60996
20	7	1.3	122	2	T51036
21	7	1.3	133	2	G64863
22	7	1.3	133	2	H90837
23	7	1.3	133	2	A85696
24	7	1.3	141	2	JO1561
25	7	1.3	151	2	AG1972
26	7	1.3	160	2	C70513
27	7	1.3	161	2	F82322
28	7	1.3	169	2	H87591
29	7	1.3	175	2	B83411

30	7	1.3	178	2	AG2369	cytochrome b6/f-co
31	7	1.3	182	2	T16472	hypothetical prote
32	7	1.3	185	2	T36745	probable RNA polym
33	7	1.3	188	2	C81224	conserved hypotnet
34	7	1.3	204	2	D83334	conserved hypotnet
35	7	1.3	206	2	A40305	biliary glycoprote
36	7	1.3	207	2	C82979	hypothetical prote
37	7	1.3	206	2	C82979	hypothetical prote
38	7	1.3	215	2	JX0244	pyroglutamate1-pepti
39	7	1.3	215	2	S23432	pyroglutamate1-pepti
40	7	1.3	217	2	AG3100	replicative DNA he
41	7	1.3	217	2	A64133	ATP-binding transp
42	7	1.3	218	2	H65023	hypothetical 22.2K
43	7	1.3	218	2	C85891	hydrogenase 4 Fe-S
44	7	1.3	218	2	G91046	conserved hypotnet
45	7	1.3	220	2	D75611	conserved hypotnet
46	7	1.3	220	2	T21730	hypothetical prote
47	7	1.3	224	2	T35897	probable secreted
48	7	1.3	226	2	G70148	ribosomal protein
49	7	1.3	227	2	E25973	pertussis toxin ch
50	7	1.3	234	2	S29000	G protein-coupled
51	7	1.3	234	2	C98186	hypothetical prote
52	7	1.3	235	2	E82106	basal-body rod mod
53	7	1.3	241	2	S53812	BmgATP beta isofor
54	7	1.3	245	2	T15739	hypothetical prote
55	7	1.3	246	2	AF0429	conserved hypotnet
56	7	1.3	247	2	A96932	phosphoserine phos
57	7	1.3	247	2	AC1332	potassium channel
58	7	1.3	247	2	AC1703	potassium channel
59	7	1.3	248	2	T04758	hypothetical prote
60	7	1.3	251	2	T11784	PBCV-1 33kd peptid
61	7	1.3	255	2	AC1293	ABC transporter (A
62	7	1.3	255	2	A11664	ABC transporter (A
63	7	1.3	257	2	S00682	IGF R receptor al
64	7	1.3	258	2	B83044	hypothetical prote
65	7	1.3	264	2	T35056	probable integral
66	7	1.3	267	2	T02616	hypothetical prote
67	7	1.3	269	2	D69996	amino acid ABC tra
68	7	1.3	271	2	F83188	phosphatidate cyti
69	7	1.3	272	2	TC4832	phosphatidate cyti
70	7	1.3	272	2	AD0080	undecaprenol kinas
71	7	1.3	276	1	BVECGG	g1g6 protein - Bsc
72	7	1.3	276	2	C91162	protein of g1p reg
73	7	1.3	276	2	D86008	transcription anti
74	7	1.3	277	2	C97073	transcription anti
75	7	1.3	278	2	A39037	carcinomaembryonic
76	7	1.3	278	2	UC1507	biliary glycoprote
77	7	1.3	278	2	UC1506	biliary glycoprote
78	7	1.3	289	2	B69207	conserved hypotnet
79	7	1.3	291	2	AG1170	ABC transporter, p
80	7	1.3	291	2	A11527	ABC transporter, p
81	7	1.3	293	2	B83054	hypothetical prote
82	7	1.3	298	2	G64350	coenzyme F420 hydr
83	7	1.3	305	2	UC4525	nucleic acid-bindi
84	7	1.3	307	2	A36955	translocation prot
85	7	1.3	308	2	D83629	probable permease
86	7	1.3	314	2	F86805	cation transporter
87	7	1.3	315	2	F80165	envelope glycoprot
88	7	1.3	322	2	F84948	NMDH2 dehydrogenas
89	7	1.3	324	2	A44241	clavaminat synth
90	7	1.3	324	2	S13497	CAMP-binding prote
91	7	1.3	327	2	B69856	oligopeptide trans
92	7	1.3	327	2	S53811	BmgATP beta isofor
93	7	1.3	333	2	S11464	CMBP1 protein - si
94	7	1.3	335	2	A10295	plative vitamin B1
95	7	1.3	338	2	B75285	probable iron ABC
96	7	1.3	341	2	UC1511	biliary glycoprote
97	7	1.3	341	2	UC1512	biliary glycoprote
98	7	1.3	344	2	E72173	DDR protein - vari
99	7	1.3	355	2	T52177	root hairless prot
100	7	1.3	372	2	B72579	probable drug resi
101	7	1.3	376	2	S45107	hypothetical prote
102	7	1.3	379	2	T22392	hypothetical prote

103	7	1.3	387	2	G72506	hypothetical prote
104	7	1.3	392	2	A82481	probable transcrip
105	7	1.3	399	2	G86872	galactokinase (EC
106	7	1.3	400	2	T45319	hypothetical prote
107	7	1.3	401	2	E70646	probable fadE23 pr
108	7	1.3	403	2	H69362	succinyl-diaminopi
109	7	1.3	405	2	T35370	probable transmemb
110	7	1.3	405	2	A12934	chromate transport
111	7	1.3	405	2	B86934	conserved hypotnet
112	7	1.3	409	2	F98347	probable transport
113	7	1.3	412	2	F95394	probable transmemb
114	7	1.3	417	2	B83357	probable MFS trans
115	7	1.3	417	2	T26295	hypothetical prote
116	7	1.3	424	2	S15146	hypothetical prote
117	7	1.3	424	2	F83556	hypothetical prote
118	7	1.3	426	2	H87507	hypothetical prote
119	7	1.3	436	2	G75363	integral membrane
120	7	1.3	444	2	D69472	nodulation protease
121	7	1.3	447	2	T49350	hypothetical prote
122	7	1.3	449	2	A1075	inner membrane pro
123	7	1.3	449	2	T49125	hypothetical prote
124	7	1.3	450	2	G81652	2-amino-4-hydroxy-
125	7	1.3	458	1	MMMSR1	biliary glycoprote
126	7	1.3	458	2	JC1509	biliary glycoprote
127	7	1.3	459	2	F97937	hypothetical prote
128	7	1.3	459	2	H95069	transmembrane prot
129	7	1.3	461	2	A27672	hypothetical gag p
130	7	1.3	462	1	QOBE04	HHRP4 protein - hu
131	7	1.3	466	2	T07404	probable glucosylt
132	7	1.3	469	2	D81017	chloride channel p
133	7	1.3	473	2	A86208	hypothetical prote
134	7	1.3	474	2	T36685	probable sodium/pr
135	7	1.3	477	2	F87329	hypothetical prote
136	7	1.3	480	2	A82042	xanthine/uracil pe
137	7	1.3	481	2	A26483	bindin precursor -
138	7	1.3	485	2	B40552	bindin fertilizati
139	7	1.3	499	1	DELVN4	NADH2 dehydrogenas
140	7	1.3	503	1	B69532	multidrug resistan
141	7	1.3	509	2	A53741	transcription fact
142	7	1.3	512	2	B83060	iron (III)-transpo
143	7	1.3	518	2	AG3135	NAD-dehydrogenase
144	7	1.3	518	2	E98152	NAD-dependent form
145	7	1.3	518	2	F75460	hypothetical prote
146	7	1.3	521	2	JC1508	biliary glycoprote
147	7	1.3	521	2	S34338	biliary glycoprote
148	7	1.3	526	2	UC4101	aspartate ammonia-
149	7	1.3	530	2	D87255	apolipoprotein N-a
150	7	1.3	541	2	D82302	iron(III) ABC tran
151	7	1.3	550	2	T06379	SAR DNA-binding pr
152	7	1.3	554	2	A11829	hypothetical prote
153	7	1.3	563	2	C86397	protein T7N9.10 [i
154	7	1.3	563	2	S21043	cytochrome b6 homo
155	7	1.3	570	2	T46911	hypothetical prote
156	7	1.3	578	2	A13604	transport ATP-bind
157	7	1.3	585	2	T51361	nitrate transporer
158	7	1.3	586	2	PC6006	acetylating protei
159	7	1.3	586	2	UC2407	homothallic switch
160	7	1.3	592	2	E70488	cytochrome-c oxida
161	7	1.3	600	2	T00759	hypothetical prote
162	7	1.3	600	2	G96720	nitrate transporer
163	7	1.3	600	2	S07638	spore coat protein
164	7	1.3	602	2	S71557	pyruvate decarboxy
165	7	1.3	606	2	A72429	oligopeptidase ABC t
166	7	1.3	608	2	S05790	hypothetical prote
167	7	1.3	610	2	D83656	auxin response fac
168	7	1.3	618	2	T08917	hypothetical prote
169	7	1.3	643	1	FOLJLK	gag polyprotein -
170	7	1.3	647	2	T23814	hypothetical prote
171	7	1.3	658	2	C82512	hypothetical prote
172	7	1.3	665	2	E84940	transketolase (EC
173	7	1.3	670	2	F88297	protein M28.1 [imp
174	7	1.3	690	2	S28222	peroxidase (EC 1.1
175	7	1.3	706	2	S57374	probable DNA helic
176	7	1.3	723	1	JN0531	p-aminobenzoic aci
177	7	1.3	727	1	A38206	procollagen-lysine
178	7	1.3	733	2	D83588	conserved hypotnet
179	7	1.3	738	2	T45936	hypothetical prote
180	7	1.3	741	2	D75500	ATP-dependent ctp
181	7	1.3	745	2	T39952	hypothetical prote
182	7	1.3	755	2	B75346	probable competent
183	7	1.3	773	2	AH2061	hypothetical prote
184	7	1.3	782	2	T48246	ribonuclease II-11
185	7	1.3	794	2	E72202	hypothetical prote
186	7	1.3	800	2	S37387	internalin A precu
187	7	1.3	802	1	TVH084	fibroblast growth
188	7	1.3	830	2	F83288	conserved hypotnet
189	7	1.3	839	2	F75518	hypothetical prote
190	7	1.3	839	2	T12827	hypothetical prote
191	7	1.3	894	1	A41527	protein-lysine k
192	7	1.3	942	2	T19553	hypothetical prote
193	7	1.3	959	2	B60017	outer capsid prote
194	7	1.3	968	2	T39908	probable coiled co
195	7	1.3	971	2	T00268	hypothetical prote
196	7	1.3	994	1	A47474	NAD ADP-ribosyltra
197	7	1.3	1010	2	T41077	hypothetical struc
198	7	1.3	1014	2	T24412	hypothetical prote
199	7	1.3	1081	2	T31094	surface antigen B8
200	7	1.3	1090	2	AG1749	glycosidase homolo
201	7	1.3	1091	2	AF1380	glycosidase homolo
202	7	1.3	1104	1	A36866	microbial collagen
203	7	1.3	1174	2	E64888	probable pyruvate
204	7	1.3	1174	2	H90878	probable oxidoredu
205	7	1.3	1174	2	B85740	probable oxidoredu
206	7	1.3	1174	2	AH0663	probable pyruvate-
207	7	1.3	1177	2	AG0284	probable pyruvate-
208	7	1.3	1187	2	A12044	pyruvate (flavodox
209	7	1.3	1191	2	S70963	pyruvate (flavodox
210	7	1.3	1197	2	T39613	pyruvate (flavodox
211	7	1.3	1199	2	S77082	pyruvate-flavodoxi
212	7	1.3	1202	2	AD2156	hypothetical prote
213	7	1.3	1267	2	T37867	latent transformin
214	7	1.3	1251	2	A57293	hypothetical prote
215	7	1.3	1526	2	T19473	hypothetical prote
216	7	1.3	1659	2	H97926	endo-beta-N-acetyl
217	7	1.3	1659	2	G95057	complement C3 prec
218	7	1.3	1663	1	C3HU	complement C3 prec
219	7	1.3	1663	1	C3MS	complement C3 prec
220	7	1.3	1663	1	C3RT	complement C3 prec
221	7	1.3	1666	1	C3GP	complement C3 prec
222	7	1.3	1857	1	S01787	fatty-acid synthas
223	7	1.3	1910	2	AF0394	probable adhesin h
224	7	1.3	1964	2	T09059	notch4 - mouse
225	7	1.3	2337	2	T40577	probable phosphati
226	7	1.3	2337	2	T1076	tyrocidine synthet
227	6	1.1	227	2	PH1171	T-cell receptor al
228	6	1.1	228	2	S26515	T-cell receptor al
229	6	1.1	229	2	PH0806	T-cell receptor al
230	6	1.1	230	2	A60822	cytochrome P450 PB
231	6	1.1	231	2	S42491	STP5 protein - Str
232	6	1.1	232	2	A56366	intestinal trefoil
233	6	1.1	233	2	A34259	cytochrome P450mt4
234	6	1.1	234	2	T46861	clitrate synthase [
235	6	1.1	235	2	C72270	hypothetical prote
236	6	1.1	236	2	S54144	tmal protein - mou
237	6	1.1	237	2	C69745	hypothetical prote
238	6	1.1	238	2	D81666	hypothetical prote
239	6	1.1	239	2	F82414	hypothetical prote
240	6	1.1	240	2	D87342	hypothetical prote
241	6	1.1	241	2	B86806	hypothetical prote
242	6	1.1	242	2	B61384	Comper's gland muc
243	6	1.1	243	2	E84200	hypothetical prote
244	6	1.1	244	2	T23216	hypothetical prote
245	6	1.1	245	2	F75371	hypothetical prote
246	6	1.1	246	2	A47438	airway epithelial
247	6	1.1	247	2	A56128	lingual antimicrob
248	6	1.1	248	2		

249	6	1.1	65	2	A30478	NADH2 dehydrogenas	322	6	1.1	109	2	G64609	hypothetical prote
250	6	1.1	65	2	F89906	hypothetical prote	323	6	1.1	109	2	C83432	conserved hypotnet
251	6	1.1	67	2	S45538	hypothetical prote	324	6	1.1	111	2	S54635	probable membrane
252	6	1.1	71	2	A12988	fibrinase associate	325	6	1.1	111	2	T36386	probable lsr2-like
253	6	1.1	73	2	F70641	hypothetical prote	326	6	1.1	111	2	A13591	hypothetical prote
254	6	1.1	75	2	G69394	H+-transporting At	327	6	1.1	113	2	A57141	ferredoxin 2 (4Fe-4
255	6	1.1	75	2	D82592	hypothetical prote	328	6	1.1	113	2	D84255	hypothetical prote
256	6	1.1	76	2	S61818	M-like protein enn	329	6	1.1	114	2	D83976	cytochrome caa3 ox
257	6	1.1	76	2	A43537	heat-stable antige	330	6	1.1	115	2	T04407	probable phospholi
258	6	1.1	76	2	I53107	CD4 precursor - r	331	6	1.1	115	2	D75434	hypothetical prote
259	6	1.1	77	1	A69093	hypothetical prote	332	6	1.1	116	1	IPAF	insulin precursor
260	6	1.1	79	2	A10052	probable membrane	333	6	1.1	116	2	H83562	conserved hypotnet
261	6	1.1	80	2	S23963	intestinal trefoil	334	6	1.1	117	2	T26752	hypothetical prote
262	6	1.1	80	2	A48966	B cell surface ant	335	6	1.1	117	2	T17315	hypothetical prote
263	6	1.1	81	2	LMSPA	H+-transporting tw	336	6	1.1	118	2	E83556	hypothetical prote
264	6	1.1	81	1	LMRZA	H+-transporting tw	337	6	1.1	119	2	B49905	hypothetical prote
265	6	1.1	81	1	LMZMC	H+-transporting tw	338	6	1.1	119	2	AD0935	protein secretion
266	6	1.1	81	1	LMNTA	H+-transporting tw	339	6	1.1	119	2	T47169	probable membrane
267	6	1.1	81	1	LMWVA	H+-transporting tw	340	6	1.1	120	2	T44554	hypothetical prote
268	6	1.1	81	1	LMWVA	H+-transporting tw	341	6	1.1	121	2	AD2578	transcription regu
269	6	1.1	81	2	A29599	H+-transporting tw	342	6	1.1	121	2	C97360	hypothetical prote
270	6	1.1	81	2	A41441	intestinal trefoil	343	6	1.1	122	1	WITAI	alpha-amylase/cryp
271	6	1.1	81	2	S30258	phycocyanin linker	344	6	1.1	122	2	E70764	hypothetical prote
272	6	1.1	82	2	S73167	H+-transporting tw	345	6	1.1	122	2	AE0803	hypothetical prote
273	6	1.1	82	2	S26958	H+-transporting tw	346	6	1.1	122	2	S07364	hypothetical prote
274	6	1.1	82	2	S58349	H+-transporting tw	347	6	1.1	123	2	G72458	seminal vesicle se
275	6	1.1	82	2	T07211	H+-transporting tw	348	6	1.1	124	2	A72629	hypothetical prote
276	6	1.1	82	2	T09628	hypothetical prote	349	6	1.1	126	2	S12988	hypothetical prote
277	6	1.1	83	2	S39516	H+-transporting tw	350	6	1.1	126	2	A55688	brain natriuretic
278	6	1.1	83	2	G70765	H+-transporting tw	351	6	1.1	126	2	D95013	natriuretic peptid
279	6	1.1	84	2	E84010	hypothetical prote	352	6	1.1	126	2	E97885	hypothetical prote
280	6	1.1	84	2	S28248	NADH2 dehydrogenas	353	6	1.1	126	2	F81143	hypothetical prote
281	6	1.1	86	2	B96709	hypothetical prote	354	6	1.1	126	2	AD3508	transcription regu
282	6	1.1	86	2	T47355	hypothetical prote	355	6	1.1	127	2	I46269	granulocyte-macrop
283	6	1.1	89	2	C84016	hypothetical prote	356	6	1.1	127	2	E75301	hypothetical prote
284	6	1.1	90	2	UC7395	salmon-type gonado	357	6	1.1	128	2	AB2487	hypothetical prote
285	6	1.1	90	2	A23735	gonadoliberin prec	358	6	1.1	128	2	S31009	hypothetical prote
286	6	1.1	90	2	I51095	gonadoliberin prec	359	6	1.1	128	2	A81153	gene 64 protein -
287	6	1.1	90	2	G96915	bofa B. subtilis o	360	6	1.1	129	2	H72806	type I restriction
288	6	1.1	91	2	H86378	hypothetical prote	361	6	1.1	129	2	AP0560	probable DNA prima
289	6	1.1	91	2	AC3378	hypothetical prote	362	6	1.1	130	2	S31003	probable methylate
290	6	1.1	92	1	BVCNP	Sugar fermentation	363	6	1.1	130	2	S46702	hypothetical prote
291	6	1.1	92	2	C91137	regulatory factor	364	6	1.1	131	2	S77285	hypothetical prote
292	6	1.1	92	2	F85982	Sugar fermentation	365	6	1.1	131	2	B72460	probable vacuolar
293	6	1.1	94	2	S62084	M-like protein ann	366	6	1.1	132	2	F97165	hypothetical prote
294	6	1.1	95	2	A10903	Ner-like regulator	367	6	1.1	133	2	I38653	melanoma antigen M
295	6	1.1	96	2	A42799	hypothetical prote	368	6	1.1	133	2	S46688	hypothetical prote
296	6	1.1	97	1	FETA	ferredoxin [2Fe-2S	369	6	1.1	133	2	AF3232	hypothetical prote
297	6	1.1	97	2	T34765	small hydrophobic	370	6	1.1	133	2	H75386	hypothetical prote
298	6	1.1	98	1	PEFM2	ferredoxin [2Fe-2S	371	6	1.1	133	2	AB2421	glutathione peroxi
299	6	1.1	98	1	PEFM2E	ferredoxin [2Fe-2S	372	6	1.1	134	2	S68899	hypothetical prote
300	6	1.1	98	2	S28199	ferredoxin [2Fe-2S	373	6	1.1	134	2	F97984	hypothetical prote
301	6	1.1	98	2	I54366	dopamine D4 recept	374	6	1.1	135	2	S57892	T cell receptor WI
302	6	1.1	98	2	T03028	glycine-rich prote	375	6	1.1	135	2	A45835	ly6 homolog RK10 p
303	6	1.1	99	2	T03297	lipid transfer pro	376	6	1.1	135	2	F87515	hypothetical prote
304	6	1.1	99	2	A60879	seminal vesicle se	377	6	1.1	136	2	T49378	hypothetical prote
305	6	1.1	99	2	B95115	hypothetical prote	378	6	1.1	137	2	B83234	hypothetical prote
306	6	1.1	101	2	H72211	hypothetical prote	379	6	1.1	138	2	G40605	response regulator
307	6	1.1	102	2	D90203	ATP synthase subun	380	6	1.1	138	2	S24084	envelope protein -
308	6	1.1	102	2	A64845	hypothetical prote	381	6	1.1	138	2	S24073	envelope protein -
309	6	1.1	102	2	H86816	hypothetical prote	382	6	1.1	138	2	S24106	envelope protein -
310	6	1.1	103	2	AF0856	conserved hypotnet	383	6	1.1	138	2	H81258	probable periplasm
311	6	1.1	103	2	S72917	hypothetical prote	384	6	1.1	138	2	C82758	hypothetical prote
312	6	1.1	105	2	C30535	hypothetical prote	385	6	1.1	139	2	A38612	insulin-like growt
313	6	1.1	106	2	F10088	Ig kappa chain v r	386	6	1.1	139	2	H64064	colR protein - Hae
314	6	1.1	106	2	AE1842	multidrug exporter	387	6	1.1	139	2	S43580	c28A5.5 protein -
315	6	1.1	107	2	D82537	ferredoxin XF2601	388	6	1.1	140	2	H71903	hypothetical prote
316	6	1.1	107	2	B83766	hypothetical prote	389	6	1.1	140	2	AH1980	hypothetical prote
317	6	1.1	107	2	F96029	hypothetical prote	390	6	1.1	140	2	AH0085	probable membrane
318	6	1.1	108	2	AE3388	heB protein (limp	391	6	1.1	141	2	S15145	hypothetical prote
319	6	1.1	109	2	UH0335	T-cell receptor al	392	6	1.1	141	2	E83345	hypothetical prote
320	6	1.1	109	2	C53302	hemf 3'-region hyp	393	6	1.1	141	2	AB3373	hypothetical prote
321	6	1.1	109	2	A10812	probable membrane	394	6	1.1	141	2	I39059	hypothetical prote

395	6	1.1	141	2	S15785	heat-stable antigen
396	1.1	142	2	JT0573	retinoic acid-indu	
397	6	1.1	143	1	FOBOGM	granulocyte-macrop
398	6	1.1	143	2	E30338	DNA transport mach
399	6	1.1	143	2	F84390	hypothetical prote
400	6	1.1	143	2	T36978	probable transpos
401	6	1.1	143	2	A53045	translocation initia
402	6	1.1	144	1	FOHUGM	granulocyte-macrop
403	6	1.1	144	2	S74059	hypothetical prote
404	6	1.1	144	2	A75369	conserved hypotet
405	6	1.1	144	2	C53045	translocation initia
406	6	1.1	145	2	A32537	T-cell receptor al
407	6	1.1	145	2	F75337	transposase - Dein
408	6	1.1	145	2	D84458	probable translati
409	6	1.1	145	2	T08000	translocation initia
410	6	1.1	146	2	I40443	hypothetical prote
411	6	1.1	147	2	T35696	xylanase A - Strep
412	6	1.1	147	2	B36529	hemoglobin P3 - po
413	6	1.1	147	2	S13157	hemoglobin - polyc
414	6	1.1	147	2	G71282	hypothetical prote
415	6	1.1	147	2	T17958	hypothetical prote
416	6	1.1	150	2	C84371	hypothetical prote
417	6	1.1	151	2	D75347	hypothetical prote
418	6	1.1	152	2	E71645	single-strand bind
419	6	1.1	152	2	G97861	glycine-rich bind
420	6	1.1	152	2	T07858	interleukin-4 prec
421	6	1.1	153	1	A25946	granulocyte-macrop
422	6	1.1	153	1	FQMSGM	hypothetical prote
423	6	1.1	153	2	T09981	tumor related prot
424	6	1.1	154	2	T01983	hypothetical prote
425	6	1.1	154	2	D71071	probable ATPase, c
426	6	1.1	154	2	C71379	probable ATPase, c
427	6	1.1	154	2	F82632	NADH2 dehydrogen
428	6	1.1	155	2	S59155	hypothetical prote
429	6	1.1	155	2	E97507	hypothetical prote
430	6	1.1	155	2	A12725	conserved hypotet
431	6	1.1	155	2	AEO048	hypothetical prote
432	6	1.1	156	1	JN0456	H+-exporting ATPas
433	6	1.1	156	2	A56680	H+-exporting ATPas
434	6	1.1	156	2	AF0222	flagellar protein
435	6	1.1	157	2	T16066	hypothetical prote
436	6	1.1	157	2	S58020	probable olfactory
437	6	1.1	157	2	AG1312	chlorodioxin homo
438	6	1.1	158	2	S57779	oleosin 2 - barley
439	6	1.1	158	2	G87623	chemotaxis protein
440	6	1.1	158	2	C71406	hypothetical prote
441	6	1.1	158	2	G83438	probable transcrip
442	6	1.1	158	2	A69178	conserved hypotet
443	6	1.1	158	2	C96005	conserved hypotet
444	6	1.1	159	1	S42878	H+-exporting ATPas
445	6	1.1	160	1	A61088	plastoquinol-plast
446	6	1.1	160	2	UC5205	sulfur-rich protei
447	6	1.1	160	2	S56214	apoptosis inducer
448	6	1.1	160	2	T02151	hypothetical prote
449	6	1.1	160	2	AF3517	lacyoylglyuathione
450	6	1.1	161	1	S43893	H+-exporting ATPas
451	6	1.1	161	2	AB2583	conserved hypotet
452	6	1.1	162	2	T50253	Vacuolar ATP synth
453	6	1.1	163	2	A29674	phycocyanin alpha
454	6	1.1	163	2	AH1872	phycocyanin alpha
455	6	1.1	163	2	S66795	probable membrane
456	6	1.1	164	2	B72364	funarate hydratase
457	6	1.1	164	2	T07759	disease resistance
458	6	1.1	164	2	T23249	hypothetical prote
459	6	1.1	164	2	T00891	hypothetical prote
460	6	1.1	165	2	JC2081	granulocyte colony
461	6	1.1	166	2	S52308	pall protein - Pae
462	6	1.1	166	2	T21142	hypothetical prote
463	6	1.1	167	2	T36290	probable integral
464	6	1.1	167	2	AH2173	hypothetical prote
465	6	1.1	168	2	D95349	protein (imported
466	6	1.1	168	2	A12865	transcription regu
467	6	1.1	168	2	G97642	hypothetical prote
468	6	1.1	170	2	T03018	glycine-rich prote
469	6	1.1	170	2	E81662	Holliday junction
470	6	1.1	170	2	D71504	crossover junction
471	6	1.1	170	2	C71024	hypothetical prote
472	6	1.1	171	2	G90077	conserved hypotet
473	6	1.1	171	2	AD3400	N utilization subu
474	6	1.1	172	2	T02230	NBS-LRR type resis
475	6	1.1	172	2	AC3176	conserved hypotet
476	6	1.1	173	2	D58893	NADH2 dehydrogen
477	6	1.1	173	2	E90623	NADH dehydrogen
478	6	1.1	173	2	D83298	hypothetical prote
479	6	1.1	174	2	F72607	probable heterocys
480	6	1.1	176	2	C82816	limbrial assembly
481	6	1.1	176	2	H75332	ankyrin-related pr
482	6	1.1	176	2	C82797	hypothetical prote
483	6	1.1	176	2	H69166	conserved hypotet
484	6	1.1	178	1	RB585F	ribosomal protein
485	6	1.1	179	1	AE4551	hypothetical prote
486	6	1.1	179	2	D71957	hypothetical prote
487	6	1.1	179	2	H66211	protein F2489.22 f
488	6	1.1	180	2	H95334	Tapo Tryptophan ri
489	6	1.1	180	2	H75418	hypothetical prote
490	6	1.1	180	2	H66311	FlaA6.4 protein -
491	6	1.1	181	2	B82908	inorganic pyrophos
492	6	1.1	182	2	F83378	hypothetical prote
493	6	1.1	182	2	T44654	nosL protein (limp
494	6	1.1	182	2	A64007	hypothetical prote
495	6	1.1	182	2	E82967	hypothetical prote
496	6	1.1	182	2	C90936	hypothetical prote
497	6	1.1	182	2	G85784	hypothetical prote
498	6	1.1	183	2	A64935	hypothetical prote
499	6	1.1	183	2	S53143	core antigen - hep
500	6	1.1	185	2	JC4085	glycine-rich cutic
501	6	1.1	185	2	T15399	hypothetical prote
502	6	1.1	186	2	AH2898	ATP Synthase delta
503	6	1.1	186	2	T15368	hypothetical prote
504	6	1.1	186	2	T41601	hypothetical prote
505	6	1.1	186	2	H90788	probable major pil
506	6	1.1	186	2	A85649	probable pilin sub
507	6	1.1	187	1	A41654	superoxide dismuta
508	6	1.1	187	1	G69308	probable 2-oxogluc
509	6	1.1	187	2	T30679	probable DNA-direc
510	6	1.1	187	2	F65009	hypothetical prote
511	6	1.1	188	2	A97674	ATP synthase delta
512	6	1.1	188	2	D87705	intracellular sept
513	6	1.1	188	2	AD0525	probable fibrillar
514	6	1.1	189	1	IVB011	interferon alpha-I
515	6	1.1	189	1	IVB01D	interferon alpha-I
516	6	1.1	189	2	AE1316	GTP cyclohydrolyse
517	6	1.1	189	2	G70485	hypothetical prote
518	6	1.1	189	2	E84314	hypothetical prote
519	6	1.1	190	2	S15275	cutis protein - Str
520	6	1.1	190	2	AD3413	hypothetical membr
521	6	1.1	191	2	A75518	guanylyl-specific ri
522	6	1.1	191	2	H97364	hypothetical prote
523	6	1.1	192	2	S76506	hypothetical prote
524	6	1.1	192	2	B81911	probable molybdopt
525	6	1.1	193	2	S32992	hypothetical prote
526	6	1.1	193	2	B95340	hypothetical prote
527	6	1.1	194	2	AG1145	limdazoleglycerol-
528	6	1.1	194	2	A43858	alanyl hydroperoxid
529	6	1.1	195	2	D82313	2-amino-4-hydroxy-
530	6	1.1	196	2	T01982	tumor related prot
531	6	1.1	197	2	A53126	syndecan-4 precurs
532	6	1.1	198	2	A12622	conserved hypotet
533	6	1.1	198	2	A75270	conserved hypotet
534	6	1.1	198	2	S14456	XA-1 protein precu
535	6	1.1	200	2	H90477	hypothetical prote
536	6	1.1	201	2	S57712	krig protein - hum
537	6	1.1	202	2	D96962	probable metal-dep
538	6	1.1	202	2	H95329	protein (imported
539	6	1.1	203	2	T25222	hypothetical prote
540	6	1.1	204	2	F83306	hypothetical prote

541	6	1.1	205	2	S37804	614	6	1.1	230	2	A75260	hypothetical prote
542	6	1.1	205	2	S55670	615	6	1.1	230	2	AC0888	probable membrane
543	6	1.1	205	2	A48929	616	6	1.1	231	2	S11429	nitrate reductase
544	6	1.1	205	2	B97302	617	6	1.1	231	2	E90887	cryptic nitrate re
545	6	1.1	206	2	T07797	618	6	1.1	231	2	D85730	cryptic nitrate re
546	6	1.1	206	2	S72581	619	6	1.1	231	2	AH0671	respiratory nitrat
547	6	1.1	207	2	D90526	620	6	1.1	231	2	F69977	two-component resp
548	6	1.1	207	2	AG0055	621	6	1.1	231	2	H81698	hypothetical prote
549	6	1.1	207	2	AE0632	622	6	1.1	231	2	E96555	unknown protein (i
550	6	1.1	209	2	C69783	623	6	1.1	233	1	S13625	eosinophil major b
551	6	1.1	210	2	G71685	624	6	1.1	233	1	S71464	ribonuclease (EC 3
552	6	1.1	210	2	D93606	625	6	1.1	233	2	T21494	hypothetical prote
553	6	1.1	211	2	H64961	626	6	1.1	233	2	T00566	hypothetical prote
554	6	1.1	211	2	F90967	627	6	1.1	233	2	A12442	hypothetical prote
555	6	1.1	211	2	E85815	628	6	1.1	234	1	S15102	eosinophil major b
556	6	1.1	211	2	D82600	629	6	1.1	235	1	CTMSP	corticotropin / li
557	6	1.1	212	2	H83305	630	6	1.1	235	1	CTRP	corticotropin / li
558	6	1.1	213	2	D70972	631	6	1.1	236	2	D72556	hypothetical prote
559	6	1.1	214	2	A87276	632	6	1.1	237	2	A90529	potassium uptake p
560	6	1.1	214	2	T34856	633	6	1.1	237	2	T26660	hypothetical prote
561	6	1.1	214	2	G95391	634	6	1.1	237	2	AG3474	carbamoyl-phosphat
562	6	1.1	215	2	S25358	635	6	1.1	238	2	I52638	neuronal growth-re
563	6	1.1	216	2	A54305	636	6	1.1	238	2	F70107	hypothetical prote
564	6	1.1	216	2	B87342	637	6	1.1	239	1	Q0BEG5	HMLF2 protein - hu
565	6	1.1	217	2	A97405	638	6	1.1	240	2	A39842	insulin-like growt
566	6	1.1	217	2	T04580	639	6	1.1	240	2	S75017	hypothetical prote
567	6	1.1	218	2	C86337	640	6	1.1	240	2	B82833	conserved hypotet
568	6	1.1	218	2	G70438	641	6	1.1	241	1	R7HS45	ribosomal protein
569	6	1.1	218	2	AC3537	642	6	1.1	241	1	RKN218	phosphoprotein p -
570	6	1.1	219	2	AG2036	643	6	1.1	241	1	B69885	transcription regu
571	6	1.1	219	2	C65074	644	6	1.1	242	2	S60143	cellulase (EC 3.2.
572	6	1.1	219	2	C91100	645	6	1.1	243	2	A25037	afes regulatory pr
573	6	1.1	219	2	G85945	646	6	1.1	244	1	JN0703	carboxyl reductase
574	6	1.1	219	2	AG0872	647	6	1.1	244	1	A28053	phosphoribosylamin
575	6	1.1	219	2	AG2124	648	6	1.1	245	1	AE2089	phospholipid protei
576	6	1.1	220	2	I50588	649	6	1.1	245	2	A12126	hypothetical prote
577	6	1.1	220	2	F83159	650	6	1.1	245	2	A12126	hypothetical prote
578	6	1.1	220	2	F64327	651	6	1.1	245	2	F71887	hypothetical prote
579	6	1.1	220	2	H87695	652	6	1.1	246	2	D83540	probable sulfate u
580	6	1.1	220	2	D84420	653	6	1.1	246	2	B95144	amino acid ABC tra
581	6	1.1	220	2	A12910	654	6	1.1	246	2	B48350	infected-cell prot
582	6	1.1	220	2	G97685	655	6	1.1	246	2	S23538	hypothetical prote
583	6	1.1	221	2	S51868	656	6	1.1	246	2	T36203	probable integral
584	6	1.1	221	2	T50665	657	6	1.1	246	2	T04765	hypothetical prote
585	6	1.1	221	2	JC7587	658	6	1.1	246	2	H98011	hypothetical prote
586	6	1.1	222	1	JL0085	659	6	1.1	248	2	T14002	aquaporin TIP7 - c
587	6	1.1	222	1	E71024	660	6	1.1	248	2	T14001	aquaporin TIP8 - c
588	6	1.1	222	2	B90669	661	6	1.1	248	2	T12632	water channel prot
589	6	1.1	222	2	B85519	662	6	1.1	248	2	T01648	probable tonoplast
590	6	1.1	223	1	K1HUA3	663	6	1.1	248	2	T07819	probable water cha
591	6	1.1	223	2	H83462	664	6	1.1	248	2	T48885	water channel prot
592	6	1.1	223	2	AB0161	665	6	1.1	248	2	C83431	type III export pr
593	6	1.1	223	2	A29770	666	6	1.1	248	2	B90890	hypothetical prote
594	6	1.1	224	2	AB3127	667	6	1.1	248	2	A98235	ferredoxin-NADP re
595	6	1.1	224	2	G98160	668	6	1.1	248	2	A86082	ferredoxin-NADP re
596	6	1.1	225	1	RDEGNG	669	6	1.1	248	2	AD3456	phosphoglycolate p
597	6	1.1	225	2	D90845	670	6	1.1	248	2	S40867	ferredoxin-NADP re
598	6	1.1	225	2	C85703	671	6	1.1	249	1	A61087	myelin P0 glycopro
599	6	1.1	225	2	D95016	672	6	1.1	249	1	B64571	probable neuraminy
600	6	1.1	225	2	F97889	673	6	1.1	249	2	E71865	probable neuraminy
601	6	1.1	226	2	T14960	674	6	1.1	250	2	F71442	probable membrane
602	6	1.1	226	2	T49807	675	6	1.1	250	2	J01012	Tob87-18C protein
603	6	1.1	226	2	CA2124	676	6	1.1	250	2	S13719	probable membrane
604	6	1.1	227	1	S68150	677	6	1.1	250	2	S51781	integral membrane
605	6	1.1	227	2	T46456	678	6	1.1	250	2	T48884	membrane channel p
606	6	1.1	228	2	S48116	679	6	1.1	250	2	H96521	protein F21D18.8 l
607	6	1.1	228	2	D36914	680	6	1.1	250	2	T26010	hypothetical prote
608	6	1.1	228	2	T22259	681	6	1.1	251	2	B83413	polydate-binding
609	6	1.1	229	2	E90058	682	6	1.1	251	2	AP1665	hypothetical prote
610	6	1.1	229	2	T06204	683	6	1.1	251	2	AH1293	hypothetical prote
611	6	1.1	229	2	F97367	684	6	1.1	251	2	D69363	conserved hypotet
612	6	1.1	229	2	AG2585	685	6	1.1	251	2	C83987	ABC transporter (A
613	6	1.1	229	2	F84370	686	6	1.1	252	2	G70967	probable clpx' pro

687	6	1.1	252	2	H72469	hypotheoretical prote
688	6	1.1	253	2	C72758	probable enoyl-CoA
689	6	1.1	253	2	AH2107	hypotheoretical prote
690	6	1.1	253	2	C87589	conserved hypotnet
691	6	1.1	254	2	A12802	hypotheoretical prote
692	6	1.1	254	2	B97582	phosphoribosylamin
693	6	1.1	254	2	T33021	hypotheoretical prote
694	6	1.1	255	2	C95411	probable GntR-fam1
695	6	1.1	256	1	MGMSA	7S nerve growth fa
696	6	1.1	256	1	T11233	H+-transporting tw
697	6	1.1	256	2	A54322	corticotropin / 11
698	6	1.1	256	2	A10267	probable membrane
699	6	1.1	256	2	AE2019	hypotheoretical prote
700	6	1.1	256	2	C90443	hypotheoretical prote
701	6	1.1	256	2	D87681	hypotheoretical prote
702	6	1.1	256	2	G70830	hypotheoretical prote
703	6	1.1	257	2	AH1865	hypotheoretical prote
704	6	1.1	257	2	S24812	minor fibrial pro
705	6	1.1	258	2	I40374	N-acetylglutamate
706	6	1.1	258	2	G83069	probable oxidoredu
707	6	1.1	260	2	T35293	probable cobalamn
708	6	1.1	260	2	T16909	hypotheoretical prote
709	6	1.1	260	2	D84568	hypotheoretical prote
710	6	1.1	260	2	F69278	conserved hypotnet
711	6	1.1	260	2	T40430	conserved hypotnet
712	6	1.1	261	2	A25606	tissue kallikrein
713	6	1.1	261	2	G64373	procaseome alpha s
714	6	1.1	263	2	T28146	class II histocomp
715	6	1.1	263	2	A13629	taurine transport
716	6	1.1	264	1	CTMKP	corticotropin / 11
717	6	1.1	264	2	S22090	catechol O-methyl
718	6	1.1	265	1	CTBOP	corticotropin / 11
719	6	1.1	265	2	S16592	chlorophyll a/b-bi
720	6	1.1	265	2	H71105	hypotheoretical prote
721	6	1.1	265	2	B95988	hypotheoretical prote
722	6	1.1	265	2	D69263	conserved hypotnet
723	6	1.1	266	2	T09570	carbonate dehydrat
724	6	1.1	266	2	C90257	translation initia
725	6	1.1	266	2	G64022	hypotheoretical prote
726	6	1.1	267	1	CTHOP	corticotropin / 11
727	6	1.1	267	2	A34078	prolactin-related
728	6	1.1	267	2	T22978	hypotheoretical prote
729	6	1.1	267	2	F87665	hypotheoretical prote
730	6	1.1	267	2	H69373	hypotheoretical prote
731	6	1.1	267	2	AC2493	hypotheoretical prote
732	6	1.1	268	2	S67583	KMn protein - yea
733	6	1.1	268	2	C90709	thiol disulfide in
734	6	1.1	268	2	G85559	thiol, disulfide in
735	6	1.1	268	2	B64794	hypotheoretical prote
736	6	1.1	268	2	AB2498	hypotheoretical prote
737	6	1.1	269	1	T35532	probable dihem cy
738	6	1.1	269	1	S74490	type IV prepilin p
739	6	1.1	269	2	AD3051	hypotheoretical prote
740	6	1.1	269	2	B69180	conserved hypotnet
741	6	1.1	269	2	E72808	gp69 protein - MYC
742	6	1.1	269	2	G96925	bicin-lacetyl-CoA
743	6	1.1	270	2	C86838	hypotheoretical prote
744	6	1.1	270	2	B88734	protein F32E10.2 l
745	6	1.1	270	2	G72390	dihydroorotate deh
746	6	1.1	271	2	D82924	conserved hypotnet
747	6	1.1	271	2	E81384	prolipoprotein dia
748	6	1.1	271	2	A11102	dihydroorotate sy
749	6	1.1	271	2	G83554	hypotheoretical prote
750	6	1.1	272	2	I48268	bilary glycoprote
751	6	1.1	272	2	C75137	hypotheoretical prote
752	6	1.1	272	2	H98234	ferichrome transp
753	6	1.1	273	1	R5EC2	ribosomal protein
754	6	1.1	273	2	B85997	SOS ribosomal subu
755	6	1.1	273	2	P91151	SOS ribosomal subu
756	6	1.1	273	2	AB1172	probable lipoprote
757	6	1.1	273	2	AF1110	probable lipoprote
758	6	1.1	273	2	AF3210	ABC transporter, m
759	6	1.1	273	2	F86665	ABC transporter pe
760	6	1.1	274	2	C82059	ribosomal protein
761	6	1.1	274	2	UC2474	glutamate-cysteine
762	6	1.1	274	2	S44616	CO8C.2 protein -
763	6	1.1	275	2	S77388	nitrate transport
764	6	1.1	275	2	G64368	hypotheoretical prote
765	6	1.1	277	2	A37416	bloodstream-specif
766	6	1.1	277	2	UC7903	collectin liver 1
767	6	1.1	278	1	S57643	stearyl-CoA 9-des
768	6	1.1	278	2	AF2699	conserved hypotnet
769	6	1.1	278	2	P97481	probable integral
770	6	1.1	278	2	D70504	hypotheoretical prote
771	6	1.1	278	2	D83080	hypotheoretical prote
772	6	1.1	278	2	T15461	hypotheoretical prote
773	6	1.1	279	2	S73526	probable lipoprote
774	6	1.1	279	2	T33771	hypotheoretical prote
775	6	1.1	279	2	D82243	transcription regu
776	6	1.1	280	1	C70784	probable dihem cy
777	6	1.1	280	2	AD1109	B. subtilis ComEC
778	6	1.1	280	2	E89981	hypotheoretical prote
779	6	1.1	281	2	S37541	H+-transporting tw
780	6	1.1	282	2	G64479	hypotheoretical prote
781	6	1.1	282	2	B95138	conserved hypotnet
782	6	1.1	282	2	B97999	conserved hypotnet
783	6	1.1	282	2	H65116	hypotheoretical prote
784	6	1.1	282	2	T13526	hypotheoretical prote
785	6	1.1	282	2	D97138	DNA replication pr
786	6	1.1	282	2	AF2672	conserved hypotnet
787	6	1.1	282	2	D97454	hypotheoretical prote
788	6	1.1	283	2	F72476	hypotheoretical prote
789	6	1.1	284	1	H69355	conserved hypotnet
790	6	1.1	284	2	H69277	branched-chain ami
791	6	1.1	284	2	S52003	major intrinac pr
792	6	1.1	284	2	H68898	undecaprenol kinas
793	6	1.1	284	2	S08385	nodo protein - Rhi
794	6	1.1	284	2	A43721	nodule formation p
795	6	1.1	285	2	H69369	branched-chain ami
796	6	1.1	285	2	S74771	hypotheoretical prote
797	6	1.1	285	2	H83733	RNA polymerase ECF
798	6	1.1	285	1	QOEC4A	hypotheoretical 30.9K
799	6	1.1	286	2	T38888	probable oxidoredu
800	6	1.1	286	2	C91103	mechanosensitive c
801	6	1.1	286	2	F85948	probable transport
802	6	1.1	286	2	A10874	probable membrane
803	6	1.1	287	2	A82318	conserved hypotnet
804	6	1.1	287	2	A82519	hypotheoretical prote
805	6	1.1	287	2	G69766	conserved hypotnet
806	6	1.1	288	1	B36961	type IV prepilin p
807	6	1.1	288	2	T31087	probable dTP-L-tn
808	6	1.1	288	2	S75324	aspartoacylase (EC
809	6	1.1	289	2	F65129	phosphoribulokinas
810	6	1.1	289	2	F91154	probable phosphori
811	6	1.1	289	2	C66000	probable phosphori
812	6	1.1	289	2	A11002	phosphoribulokinas
813	6	1.1	289	2	AH0112	probable membrane
814	6	1.1	289	2	T41846	HE65 ori105 - Bomb
815	6	1.1	289	2	AG3353	hypotheoretical prote
816	6	1.1	289	2	AH1723	hypotheoretical prote
817	6	1.1	290	2	T03552	maltoase transport
818	6	1.1	290	2	A82946	hypotheoretical prote
819	6	1.1	290	2	H98336	maltoase transport
820	6	1.1	290	2	S48301	geranylgeranyl tra
821	6	1.1	291	2	I48602	insulin-like growt
822	6	1.1	291	2	E71491	probable geranyl t
823	6	1.1	291	2	D90491	ABC transporter, A
824	6	1.1	291	2	AB3235	nitrioltriacetate
825	6	1.1	291	2	A13092	hypotheoretical prote
826	6	1.1	292	2	E81650	geranylgeranyl pyr
827	6	1.1	292	2	AB2893	metal dependant by
828	6	1.1	292	2	E97668	hypotheoretical prote
829	6	1.1	292	2	H82214	conserved hypotnet
830	6	1.1	293	2	AE1927	3-ketoacyl-acyl ca
831	6	1.1	293	2	AB3051	hypotheoretical prote
832	6	1.1	293	2	H82184	glycerol-3-phospha

833	6	1.1	293	2	A87473	Smp-30/Cgr1 family	906	6	1.1	313	2	D85855	probable kinase, ye
834	6	1.1	293	2	H70713	hypothetical prote	907	6	1.1	313	2	A75256	conserved hypothet
835	6	1.1	294	2	S72897	pyrroline-5-carbox	908	6	1.1	313	2	A89971	cmp-binding-factor
836	6	1.1	294	2	JC5305	hypothetical prote	909	6	1.1	314	2	C70562	probable DTP-Gluc
837	6	1.1	294	2	T05028	nodulin-26-like pr	910	6	1.1	314	2	S66274	annexin - pepper
838	6	1.1	294	2	S52426	s-SNAP protein-1	911	6	1.1	314	2	T02961	annexin p33 - maize
839	6	1.1	294	2	D87691	ABC transporter, A	912	6	1.1	314	2	AD0482	sugar-binding tran
840	6	1.1	295	2	G70745	probable proc prot	913	6	1.1	315	1	JC0503	ribose-phosphate d
841	6	1.1	295	2	E95200	fructokinase [impo	914	6	1.1	315	2	T06164	peroxidase (EC 1.1
842	6	1.1	295	2	D98067	fructokinase (EC 2	915	6	1.1	315	2	T06172	peroxidase (EC 1.1
843	6	1.1	295	2	D75010	UDP-N-acetylglucos	916	6	1.1	315	2	T29258	hypothetical prote
844	6	1.1	295	2	B86742	amino acid ABC tra	917	6	1.1	315	2	AH3567	permease, imported
845	6	1.1	296	2	B83384	conserved hypothet	918	6	1.1	316	2	T50027	annexin-like prote
846	6	1.1	296	2	C82645	transcription regu	919	6	1.1	316	2	T52464	hypothetical prote
847	6	1.1	296	2	S72444	DNA-binding protei	920	6	1.1	316	2	AB0669	probable virulence
848	6	1.1	296	2	A87311	hypothetical prote	921	6	1.1	317	1	E69763	probable ferrichro
849	6	1.1	297	1	WZECN	N-acetylneuraminat	922	6	1.1	317	2	S16916	plastoquinol plast
850	6	1.1	297	2	E85986	N-acetylneuraminat	923	6	1.1	317	2	E83344	probable adhesion
851	6	1.1	297	2	B91141	N-acetylneuraminat	924	6	1.1	318	2	T50026	annexin-like prote
852	6	1.1	297	2	AB0908	N-acetylneuraminat	925	6	1.1	318	2	I59301	bone marrow stroma
853	6	1.1	298	2	A87147	methyl mycolic aci	926	6	1.1	318	2	C83062	hypothetical prote
854	6	1.1	298	2	E82157	probable N-acetyl	927	6	1.1	319	2	E89872	hypothetical prote
855	6	1.1	298	2	B64180	arac-like transcri	928	6	1.1	319	2	JC5624	olfactory receptor
856	6	1.1	298	2	AC3617	oligopeptide trans	929	6	1.1	319	2	JC4350	bone marrow stroma
857	6	1.1	299	2	E90573	methyltransferase	930	6	1.1	319	2	G75106	hypothetical prote
858	6	1.1	299	2	B69155	hypothetical prote	931	6	1.1	319	2	G75628	hypothetical prote
859	6	1.1	299	2	H87567	hypothetical prote	932	6	1.1	319	2	T47852	hypothetical prote
860	6	1.1	299	2	AE0461	probable membrane	933	6	1.1	320	2	C87657	alcohol dehydrogen
861	6	1.1	300	1	A69444	thioredoxin-disulf	934	6	1.1	320	2	T31130	hypothetical prote
862	6	1.1	300	2	B98235	fnud protein (Au00	935	6	1.1	320	2	C72862	hypothetical prote
863	6	1.1	300	2	T47460	hypothetical prote	936	6	1.1	321	2	H82540	conserved hypothet
864	6	1.1	300	2	S36430	hypothetical prote	937	6	1.1	321	2	S65551	hypothetical prote
865	6	1.1	300	2	AE9329	transcription regu	938	6	1.1	322	2	G72421	hypothetical prote
866	6	1.1	300	2	AE0535	hypothetical prote	939	6	1.1	322	2	AB1851	iron(III) ABC tran
867	6	1.1	301	2	T27648	hypothetical prote	940	6	1.1	322	2	A37759	hypothetical prote
868	6	1.1	301	2	G84053	hypothetical prote	941	6	1.1	322	2	D72289	piv protein - Mora
869	6	1.1	302	2	T29321	hydrid-endo-beta-1	942	6	1.1	323	2	A72508	oligopeptide ABC t
870	6	1.1	303	2	A97383	hypothetical prote	943	6	1.1	323	2	C84961	probable cobalamin
871	6	1.1	303	2	AH2600	hypothetical prote	944	6	1.1	323	2	E86935	lipote acid synthe
872	6	1.1	304	2	C83891	hypothetical prote	945	6	1.1	324	2	E87196	conserved hypothet
873	6	1.1	304	2	T23801	hypothetical prote	946	6	1.1	324	2	G69515	probable hydrolase
874	6	1.1	305	1	H75285	probable phosphos	947	6	1.1	324	2	G90856	transcription regu
875	6	1.1	305	2	B69548	molybdopterin oxid	948	6	1.1	324	2	H90269	probable transcrip
876	6	1.1	305	2	B84413	hypothetical prote	949	6	1.1	325	2	C82251	GDEF family prote
877	6	1.1	305	2	A38422	insulin-like prote	950	6	1.1	325	2	B31595	hypothetical prote
878	6	1.1	306	2	H97007	probable permease	951	6	1.1	325	2	I52998	interferon regulat
879	6	1.1	306	2	T19934	hypothetical prote	952	6	1.1	325	2	A10715	interferon regulat
880	6	1.1	306	2	T52340	cell wall-plasma m	953	6	1.1	326	2	B71681	probable inner mem
881	6	1.1	306	2	T06607	hypothetical prote	954	6	1.1	326	2	T36497	pyruvate dehydroge
882	6	1.1	308	1	AE2684	conserved hypothet	955	6	1.1	326	2	D97743	probable branched-
883	6	1.1	309	1	S51356	olfactory receptor	956	6	1.1	326	2	T08849	hypothetical prote
884	6	1.1	309	1	FOVVF	gag polypeptin -	957	6	1.1	326	2	G85727	alternative respir
885	6	1.1	309	2	I51900	carbonic anhydrase	958	6	1.1	326	2	T30166	probable transport
886	6	1.1	309	2	H89832	hypothetical prote	959	6	1.1	326	2	H95984	hypothetical prote
887	6	1.1	310	1	T38493	hypothetical prote	960	6	1.1	327	2	B82918	probable transcrip
888	6	1.1	310	1	VAZ031	300K antigen Ag231	961	6	1.1	327	2	T04004	DNA-directed RNA p
889	6	1.1	310	1	B69475	conserved hypothet	962	6	1.1	327	2	T35482	hypothetical prote
890	6	1.1	310	1	A70481	acetoin utilizatio	963	6	1.1	327	2	E69430	hypothetical prote
891	6	1.1	310	2	S67181	hypothetical prote	964	6	1.1	327	2	F71497	hypothetical prote
892	6	1.1	310	2	T55976	conserved hypothet	965	6	1.1	327	2	H85720	hypothetical prote
893	6	1.1	310	2	T37824	hypothetical prote	966	6	1.1	328	2	A95897	probable UDPglucos
894	6	1.1	311	2	JC2541	bone marrow stroma	967	6	1.1	328	2	A13600	UDPglucose 4-epime
895	6	1.1	311	2	C84101	hypothetical prote	968	6	1.1	328	2	AC0750	probable deaminase
896	6	1.1	311	2	D95076	peptide methionin	969	6	1.1	328	2	T07610	W6176 protein - ri
897	6	1.1	312	2	C82356	peptide ABC transp	970	6	1.1	328	2	S32369	gamma-SNAP protein
898	6	1.1	312	2	F81279	enterohelein uptak	971	6	1.1	328	2	A36330	interferon regulat
899	6	1.1	312	2	G69423	branched-chain ami	972	6	1.1	328	2	A13017	enhanced entry pro
900	6	1.1	312	2	H84153	hypothetical prote	973	6	1.1	329	2	A12023	protochlorophyllid
901	6	1.1	312	2	C87562	conserved hypothet	974	6	1.1	329	2	A48715	gal-beta(1-3/-4)G
902	6	1.1	312	2	A56911	TRAD protein - hu	975	6	1.1	329	2	T17033	lucine rich repea
903	6	1.1	313	2	H95158	probable ABC trans	976	6	1.1	329	2	T22221	hypothetical prote
904	6	1.1	313	2	B64985	hypothetical 33.6K	977	6	1.1	329	2	T44459	arginine metabolis
905	6	1.1	313	2	B91011	probable kinase [1	978	6	1.1	329	2	B41344	lutropin-choriogon

979 6 1.1 329 2 D41344
 980 6 1.1 329 2 A31595
 981 6 1.1 329 2 A72990
 982 6 1.1 329 2 C98293
 983 6 1.1 330 1 C69042
 984 6 1.1 330 2 JQ2262
 985 6 1.1 330 2 AB0225
 986 6 1.1 330 2 T46994
 987 6 1.1 330 2 A10239
 988 6 1.1 330 2 T30238
 989 6 1.1 331 2 C69376
 990 6 1.1 331 2 T51899
 991 6 1.1 331 2 E88991
 992 6 1.1 331 2 C41344
 993 6 1.1 332 2 AC0158
 994 6 1.1 332 2 S75621
 995 6 1.1 332 2 A49879
 996 6 1.1 332 2 T42370
 997 6 1.1 332 2 B95978
 998 6 1.1 333 1 HLHUC
 999 6 1.1 333 1 H87220
 1000 6 1.1 333 2 A83797

ALIGNMENTS

RESULT 1

E83679
 multidrug-efflux transporter BH0237 [imported] - Bacillus halodurans (strain C-125)
 C.Species: Bacillus halodurans
 C.Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001

C/Accession: E83679
 R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Maeni, N.; Fujii, F.; Hira
 Nucleic Acids Res. 28, 4317-4331, 2000
 A.Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and
 A.Reference number: A83650, PMID:20512582; PMID:11058132
 A.Accession: E83679
 A.Status: preliminary
 A.Molecule type: DNA
 A.Residues: 1-387 <STO>
 A.Cross-references: GB:AP001507; GB:BA000004; NID:G10172612; PIDN:BA803956.1; GSPDB:GN00
 A.Experimental source: strain C-125
 C.Genetics:
 A:Gene: BH0237

Query Match 1.7%; Score 9; DB 2; Length 387;
 Best Local Similarity 100.0%; Pred. No. 1.4;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 461 LAGGVLL 469
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 DB 73 LAGGVLL 81

RESULT 2

G87364
 conserved hypothetical protein CC0931 [imported] - Caulobacter crescentus
 C.Species: Caulobacter crescentus
 C.Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001

C/Accession: G87364
 R/Nierman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eissen, J.; Heidelberg, J.
 B.; Laub, M.T.; Deboy, R.T.; Dodson, R.U.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kolon
 N.; J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
 Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001
 A.Title: Complete Genome Sequence of Caulobacter crescentus.
 A.Reference number: A87249; PMID:21173698; PMID:11259647

A.Accession: G87364
 A.Status: preliminary
 A.Molecule type: DNA
 A.Residues: 1-401 <STO>
 A.Cross-references: GB:AE005673; NID:G13422203; PIDN:AAK22915.1; GSPDB:GN00148
 C.Genetics:

A:Gene: CC0931

Query Match 1.7%; Score 9; DB 2; Length 401;
 Best Local Similarity 100.0%; Pred. No. 1.5;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 455 TALAGLAV 463
 |||||
 DB 36 TALAGLAV 44

RESULT 3

G90656
 hypothetical protein EC60223 [imported] - Escherichia coli (strain O157:H7, substrain RT
 C.Species: Escherichia coli
 C.Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001

C/Accession: G90656
 R/Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
 gasawara, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hatlori, M.; Shinagawa, H.
 DNA Res. 8, 11-22, 2001

A.Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and geno
 A.Reference number: A89629; PMID:21156231; PMID:11258796

A.Accession: G90656
 A.Status: preliminary
 A.Molecule type: DNA
 A.Residues: 1-923 <HAY>
 A.Cross-references: GB:BA000007; PIDN:BA833646.1; PID:G13359679; GSPDB:GN00154
 A.Experimental source: strain O157:H7, substrain RMD 0509952
 C.Genetics:
 A:Gene: EC60223
 C:Superfamily: endopeptidase Clp ATP-binding chain

Query Match 1.7%; Score 9; DB 2; Length 923;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 464 GGVLLALL 472
 |||||
 DB 114 GGVLLALL 122

RESULT 4

G85507
 probable proteinase Z0254 [imported] - Escherichia coli (strain O157:H7, substrain EDL93
 C.Species: Escherichia coli
 C.Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001

C/Accession: G85507
 R/Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glaeser, J.D.; Rose, D.J.; Mayhew
 Iller, L.; Grobeck, E.J.; Davis, N.W.; Lam, A.; Dimalanta, E.; Potamousis, K.; Apodaca,
 Nature 409, 529-533, 2001

A.Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
 A.Reference number: A85480; PMID:21074935; PMID:11206551

A.Accession: G85507
 A.Status: preliminary
 A.Molecule type: DNA
 A.Residues: 1-923 <STO>
 A.Cross-references: GB:AE005174; NID:G12512960; PIDN:AG54523.1; GSPDB:GN00145; UMGF:202
 A.Experimental source: strain O157:H7, substrain EDL933
 C.Genetics:
 A:Gene: Z0254
 C:Superfamily: endopeptidase Clp ATP-binding chain

Query Match 1.7%; Score 9; DB 2; Length 923;
 Best Local Similarity 100.0%; Pred. No. 3;
 Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 464 GGVLLALL 472
 |||||
 DB 114 GGVLLALL 122

RESULT 5

S52116

transforming protein ski - axolotl (fragment)
N/Alternate names: proto-oncogene ski

C/Species: Ambystoma mexicanum (axolotl)

C/Date: 14-Jul-1995 #sequence_revision 14-Feb-1997 #text_change 20-Jun-2000

C/Accession: S52116

R/Ludolph, D.C.; Neff, A.W.; Parker, M.A.; Mescher, A.L.; Smith, R.C.; Malacinski, G.M.

Biochim. Biophys. Acta 1260, 102-104, 1995

A/Title: Cloning and expression of the axolotl proto-oncogene ski.

A/Reference number: S52116; MUID:95092782; PMID:7999783

A/Accession: S52116

A/Molecule type: mRNA

A/Residues: 1-130 <LUD>

A/Cross-references: EMBL:D28907; NID:9762853; PIDN:BA18908.1; PID:92160486

C/Genetics:

A/Gene: ski

C/Superfamily: ski transforming protein

C/Keywords: oncogene; transforming protein

Query Match 1.5%; Score 8; DB 2; Length 130;
Best Local Similarity 100.0%; Pred. No. 5.6;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 470 ALLGGGCT 477

DB 36 ALLGGGCT 43

RESULT 6

D70718 hypothetical protein RV0966c - Mycobacterium tuberculosis (strain H37RV)

C/Species: Mycobacterium tuberculosis

C/Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 02-Sep-2000

C/Accession: D70718

R/Cole, S.T.; Broesch, R.; Parkhill, J.; Garner, T.; Churcher, C.; Harris, D.; Gordon, S.

; Connor, R.; Davies, R.; Devlin, K.; Felwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.

; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skellon, S.; Squares, S.

Nature 393, 537-544, 1998

A/Authors: Sgarbes, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.

A/Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome

A/Reference number: A70500; MUID:98295987; PMID:9634230

A/Accession: D70718

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Molecule type: DNA

A/Residues: 1-230 <COL>

A/Cross-references: GB:Z79700; GB:AL123456; NID:93261628; PIDN:CAB01985.1; PID:e264092;

C/Genetics:

A/Experimental source: strain H37RV

C/Superfamily: Mycobacterium tuberculosis hypothetical protein RV2862c

Query Match 1.5%; Score 8; DB 2; Length 230;
Best Local Similarity 100.0%; Pred. No. 9.2;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 467 LLLALLGG 474

DB 118 LLLALLGG 125

RESULT 7

A60643 antigen 5401 - Elmeria tenella (fragment)

C/Species: Elmeria tenella

C/Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 18-Jun-1993

C/Accession: A60643

R/Danforth, H.D.; Augustine, P.C.; Ruff, M.D.; McCandless, R.; Strausberg, R.L.; Likel,

Poult. Sci. 68, 1643-1652, 1989

A/Title: Genetically engineered antigen confers partial protection against avian coccidia

A/Reference number: A60643; MUID:90160107; PMID:2622819

A/Accession: A60643

A/Status: not compared with conceptual translation

A/Molecule type: mRNA

A/Residues: 1-287 <DAN>

F,11-120/Region: 22-residue repeats (A-G-X-X-G-G-S-G-G-X-A-E-E-L-P-G-E-G-G-A-G)

Query Match 1.5%; Score 8; DB 2; Length 287;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 463 VGGVLLLA 470

DB 219 VGGVLLLA 226

RESULT 8

AF3503

benzoate membrane transport protein [imported] - Brucella melitensis (strain 16M)

C/Species: Brucella melitensis

C/Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 01-Feb-2002

C/Accession: AF3503

R/DelVecchio, V.G.; Kapetral, V.; Redkar, R.J.; Patra, G.; Mujer, C.; Los, T.; Ivanova, P.

; Mazur, M.; Goldsman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Leteser,

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A/Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis

A/Reference number: AD3252; PMID:11756688

A/Accession: AF3503

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-383 <KUR>

A/Cross-references: GB:AE008917; PIDN:AL53193.1; PID:917984067; GSPDB:GN00190

A/Experimental source: strain 16M

C/Genetics:

A/Gene: BMEI2012

A/Map position: 1

Query Match 1.5%; Score 8; DB 2; Length 383;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 456 ALIAGLAV 463

DB 364 ALIAGLAV 371

RESULT 9

AF1903

hypothetical protein alr0776 [imported] - Nostoc sp. (strain PCC 7120)

C/Species: Nostoc sp. PCC 7120

A/Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C/Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

C/Accession: AF1903

R/Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriuchi,

Nakazaki, N.; Shimo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S.

DNA Res. 8, 205-213, 2001

A/Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena

A/Reference number: AB1807; MUID:21595285; PMID:11759840

A/Accession: AF1903

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-396 <KUR>

A/Cross-references: GB:BA000019; PIDN:BA872733.1; PID:917130121; GSPDB:GN00179

A/Experimental source: strain PCC 7120

C/Genetics:

A/Gene: alr0776

Query Match 1.5%; Score 8; DB 2; Length 396;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 GLSSSTRS 29

DB 266 GLSSSTRS 273

RESULT 10

AH0189

Amino acid permease [imported] - *Yersinia pestis* (strain CO92)
C:Species: *Yersinia pestis*
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Nov-2001
C:Accession: AF0189
R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Tilball, R.W.; Holden, M.T.G.; Prentice, M.B.; deno-Tarragga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; 11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrall, Nature 413, 523-527, 2001
A:Title: Genome sequence of *Yersinia pestis*, the causative agent of plague.
A:Reference number: AF0001; MUID:21470413; PMID:11586360
A:Accession: AF0189
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-463 <KID>
A:Cross-references: GB:AL590842; PIDN:CA90379.1; PID:G15979598; GSPDB:GN00175
C:Genetics:
A:Gene: YPO1557
C:Superfamily: arginine permease

Query Match 1.5%; Score 8; DB 2; Length 463;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 380 SUSEPTPN 387
|||||||
DB 230 SUSEPTPN 237

RESULT 11
J02263
glutamate-1-semialdehyde 2,1-aminomutase (EC 5.4.3.8) precursor - soybean
C:Species: Glycine max (soybean)
C:Date: 30-Sep-1993 #sequence_revision 20-Aug-1994 #text_change 24-Nov-1999
C:Accession: J02263
R:Sangwan, I.; O'Brian, M.R.
Plant Physiol. 102, 829-834, 1993
A:Title: Expression of the soybean (Glycine max) glutamate 1-semialdehyde aminotransferase
A:Reference number: J02263; MUID:94105311; PMID:8278535
A:Accession: J02263
A:Molecule type: mRNA
A:Residues: 1-466 <SAN>
A:Cross-references: GB:U12453; NID:G310566; PIDN:AAA3968.1; PID:G310567
C:Comment: This enzyme catalyzes delta-aminolevulinic acid synthesis from glutamate 1-semialdehyde.
C:Function: porphyrin biosynthesis
A:Pathway: porphyrin biosynthesis
C:Superfamily: ornithine-oxo-acid aminotransferase
C:Keywords: intramolecular transference; isomerase; phosphoprotein; pyridoxal phosphate
F:1-28/Domain: signal sequence #status predicted <SIG>
F:29-466/Product: glutamate 1-semialdehyde aminotransferase #status predicted <MAT>
F:306/Binding site: pyridoxal phosphate (Lys) (covalent) #status predicted

Query Match 1.5%; Score 8; DB 2; Length 466;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 LSSSTRSR 30
|||||||
DB 17 LSSSTRSR 24

RESULT 12
F70785
hypothetical protein RV2205C - *Mycobacterium tuberculosis* (strain H37RV)
C:Species: *Mycobacterium tuberculosis*
C:Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 22-Oct-1999
C:Accession: F70785
R:Cole, S.T.; Broesch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.; Connor, R.; Davies, R.; Devlin, K.; Feltham, T.; Gentles, S.; Hamlin, N.; Holroyd, S.; Rajandream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S. Nature 393, 537-544, 1998
A:Authors: Sgarbes, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrall, B.G.
A:Title: Deciphering the biology of *Mycobacterium tuberculosis* from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230

A:Accession: F70785
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-480 <COL>
A:Cross-references: GB:F70283; GB:AL123456; NID:G3261561; PIDN:CAA94248.1; PID:G233581;
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: RV2205C

Query Match 1.5%; Score 8; DB 2; Length 480;
Best Local Similarity 100.0%; Pred. No. 17;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 398 PPTPTAL 405
|||||||
DB 223 PPTPTAL 230

RESULT 13
T01491
ubiquitin-protein ligase homolog F1707.15 - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 04-Mar-2000
C:Accession: T01491
R:Vysotskaya, V.S.; Schwartz, J.R.; Toriumi, M.; Yu, G.; Kwan, A.; Oji, O.; Liu, S.; Li, rtz, D.; Li, Y.; Palm, C.J.; Shinn, P.; Sun, H.; Davis, R.W.; Ecker, J.R.; Federspiel, N. submitted to the EMBL Data Library, June 1998
A:Description: *Arabidopsis thaliana* chromosome 1 BAC F1707 sequence.
A:Reference number: Z14334
A:Accession: T01491
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-1126 <VYS>
A:Cross-references: EMBL:AC003671; NID:G2833627; PID:G3176690; GSPDB:GN00059; ATSP:F1707
A:Experimental source: cytovar Columbia
C:Genetics:
A:Gene: ATSP:F1707.15
A:Map position: 1
A:Intron: 118/3; 224/3; 292/1; 373/3; 457/2; 826/3; 875/3; 902/3; 1057/3; 1093/2
C:Superfamily: ubiquitin-protein ligase homolog
F:756-1120/Domain: ubiquitin-protein ligase homolog <UBI>

Query Match 1.5%; Score 8; DB 2; Length 1126;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 ASGUSST 27
|||||||
DB 492 ASGUSST 499

RESULT 14
S52781
neurocan - mouse
C:Species: *Mus musculus* (house mouse)
C:Date: 19-May-1995 #sequence_revision 21-Jul-1995 #text_change 04-Feb-2000
C:Accession: S52781
R:Rauch, U.; Foreberg, N.; Kulbe, G.; Arnold-Ammer, I.; Feeseler, R. submitted to the EMBL Data Library, February 1995
A:Description: Amino acid sequence of mouse neurocan and brevican and their different ex
A:Reference number: S52781
A:Accession: S52781
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-1268 <RAU>
A:Cross-references: EMBL:X84727; NID:G758629; PIDN:CAA59226.1; PID:G758630
C:Superfamily: aggrecan; C-type lectin homolog; complement factor H repeat homolog; EG
F:176-253/Domain: link protein repeat homolog <LNK1>
F:274-355/Domain: link protein repeat homolog <LNK2>
F:364-955/Domain: EGF lectin homolog <EGF>
F:1040-1160/Domain: C-type lectin homolog <LCH>
F:1167-1223/Domain: complement factor H repeat homolog <FHD>

Query March 1.5%; Score 8; DB 2; Length 1266;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 218 GEPDLTW 225
 Db 413 GEPDLTW 420

RESULT 15
 SS1656
 Vascular endothelial growth factor receptor - Japanese quail
 N:Alternate names: quail endothelial kinase 1 (Quek 1); vascular endothelial growth factor
 C:Species: Coturnix coturnix japonica (Japanese quail)
 C>Date: 07-May-1995 #sequence revision 01-Sep-1995 #text_change 08-Dec-2000
 C:Accession: J04953; A56598; I51162; S51656
 R:Elchmann, A.; Marcelle, C.; Breant, C.; Le Douarin, N.M.
 Gene 17, 3-8, 1996
 A>Title: Molecular cloning of Quek 1 and 2, two quail vascular endothelial growth factor
 A:Reference number: J04953; MUID:97017121; PMID:8863722
 A:Accession: J04953
 A:Status: nucleic acid sequence not shown
 A:Molecule type: mRNA
 A:Residues: 1-1348 <E1C1>
 A:Cross-references: EMBL:X83288; NID:G603523; PIDN:CAA58268.1; PID:G603524
 A>Note: submitted to the EMBL Data Library, December 1994
 R:Elchmann, A.; Marcelle, C.; Breant, C.; Le Douarin, N.M.
 Mech. Dev. 42, 33-48, 1993
 A>Title: Two molecules related to the VEGF receptor are expressed in early endothelial
 A:Reference number: A56598; MUID:93378866; PMID:8396413
 A:Accession: A56598
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 910-1348 <E1C2>
 A:Cross-references: GB:S65205; NID:G410680; PIDN:AAE28127.1; PID:G410681
 A>Note: sequence extracted from NCBI backbone (NCBI:137162; NCBI:P.137163)
 R:Marcelle, C.; Elchmann, A.
 Oncogene 7, 2479-2487, 1992
 A>Title: Molecular cloning of a family of protein kinase genes expressed in the avian
 A:Reference number: 150595; MUID:93096482; PMID:1281306
 A:Accession: 151162
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1023-1079 <MAR>
 A:Cross-references: EMBL:X65994; NID:G395226; PIDN:CAA9364.1; PID:G395278
 A>Note: the species is not identified by the authors; the most probable species is shown
 C:Comment: This protein is an endothelial-specific receptor and binds vascular endothelial
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
 C:Keywords: ATP; embryo; growth factor receptor; transmembrane protein
 F:1-19/Domain: signal sequence #status predicted <SIG>
 F:20-1138/Product: vascular endothelial growth factor receptor 1 #status predicted <NAT>
 F:766-777/Domain: transmembrane #status predicted <TM>
 F:833-1160/Domain: protein kinase homology <KIN>
 F:831-839/Region: protein kinase ATP-binding motif

Query March 1.5%; Score 8; DB 2; Length 1348;
 Best Local Similarity 100.0%; Pred. No. 42;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 405 LQCTADKF 412
 Db 559 LQCTADKF 566

RESULT 16
 GNMVWV
 genome polyprotein - West Nile virus
 N:Contains: core protein V2; membrane-associated glycoprotein NV2 precursor; membrane-as-
 sociated glycoprotein NV5
 C:Species: West Nile virus
 C>Date: 30-Sep-1987 #sequence_revision 30-Sep-1987 #text_change 19-Jan-2001
 C:Accession: A25256

R:Gaetle, E.; Leidner, U.; Nowak, T.; Wengler, G.; Wengler, G.
 Virology 149, 10-26, 1986
 A>Title: Primary structure of the West Nile flavivirus genome region coding for all non-
 A:Reference number: A25256; MUID:66124703; PMID:3753811
 A:Accession: A25256
 A:Molecule type: genomic RNA
 A:Residues: 1-3430 <CAS>
 A:Cross-references: GB:M10103; GB:M12294; NID:G336167; PIDN:AAA48498.1; PID:G336168
 A>Note: parts of this sequence, including the amino ends of the mature proteins, were de-
 C:Superfamily: yellow fever virus genome polyprotein
 C:Keywords: ATP; core protein; glycoprotein; membrane-associated protein; nucleotide bin-
 F:1-92/Product: core protein V2 #status predicted <CV2>
 F:105-233/Product: membrane-associated glycoprotein NV2 precursor #status predicted <NV2>
 F:105-123/Domain: nonterminal signal sequence #status predicted <SS>
 F:124-233/Product: membrane-associated glycoprotein NV2 #status predicted <NV2>
 F:275-287/Product: membrane-associated glycoprotein NV3 precursor #status predicted <NV3>
 F:275-280/Domain: nonterminal signal sequence #status predicted <SS>
 F:291-787/Product: membrane-associated glycoprotein NV3 #status predicted <NV3>
 F:788-2109/Product: nonstructural protein NV4 #status predicted <NV4>
 F:1695-1702/Region: nucleotide-binding motif A (P-loop)
 F:1782-1787/Region: nucleotide-binding motif B
 F:1786-1789/Region: DBAH motif
 F:2580-2427/Product: nonstructural protein NV5 #status predicted <NV5>
 F:138,917,962,994,1289,1659,1966,2336,2459,2489,2573,2739,2759,2864,2902/Binding site: C

Query March 1.5%; Score 8; DB 1; Length 3430;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 461 LAVGVLL 468
 Db 772 LAVGVLL 779

RESULT 17
 GNMVWV
 genome polyprotein - Kunjin virus (strain MRM61C)
 N:Contains: capsid protein C; envelope protein E; membrane protein M; nonstructural pro-
 in NS4a; nonstructural protein NS4b; nonstructural protein NS5
 C:Species: Kunjin virus
 C>Date: 30-Sep-1989 #sequence_revision 30-Sep-1989 #text_change 19-Jan-2001
 C:Accession: A28697
 R:Coia, G.; Parker, M.D.; Speight, G.; Byrne, M.E.; Westaway, E.G.
 J. Gen. Virol. 69, 1-21, 1988
 A>Title: Nucleotide and complete amino acid sequences of Kunjin virus: definitive gene o-
 A:Reference number: A28697; MUID:88089524; PMID:2826659
 A:Accession: A28697
 A:Molecule type: genomic RNA
 A:Residues: 1-3433 <COI>
 A:Cross-references: GB:D00246; NID:G221966; PIDN:BA00176.1; PID:G221967
 C:Superfamily: yellow fever virus genome polyprotein
 C:Keywords: ATP; capsid protein C; envelope protein E; membrane protein; nonstructural prote-
 C:Superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolog
 C:Keywords: ATP; embryo; growth factor receptor; transmembrane protein
 F:1-215/Domain: nonterminal signal sequence #status predicted <SIG>
 F:216-290/Product: membrane protein M #status predicted <MP>
 F:291-791/Product: envelope protein E #status predicted <EP>
 F:792-1143/Product: nonstructural protein NS1 #status predicted <NS1>
 F:1144-1374/Product: nonstructural protein NS2a #status predicted <NS2a>
 F:1375-1505/Product: nonstructural protein NS2b #status predicted <NS2b>
 F:1506-2124/Product: nonstructural protein NS3 #status predicted <NS3>
 F:1699-1706/Region: nucleotide-binding motif A (P-loop)
 F:1786-1791/Region: nucleotide-binding motif B
 F:1790-1793/Region: DBAH motif
 F:2125-2273/Product: nonstructural protein NS4a #status predicted <NS4a>
 F:2274-2528/Product: nonstructural protein NS4b #status predicted <NS4b>
 F:2529-3433/Product: nonstructural protein NS5 #status predicted <NS5>

Query March 1.5%; Score 8; DB 1; Length 3433;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 461 LAVGSVLL 468
 Db 776 LAVGSVLL 783

RESULT 18

GNMWV
 genome polypeptide - Murray Valley encephalitis virus (strain Australia)
 N:Contains: capsid protein; envelope protein; membrane protein; nonstructural protein NS
 a; nonstructural protein NS4b; nonstructural protein NS5
 C:Species: Murray Valley encephalitis virus
 C:Date: 30-Jun-1988 #sequence_revision 17-Feb-1994 #text_change 19-Jan-2001
 C:Accession: A24635; A60288
 R:Daigarno, L.; Trent, D.W.; Strauss, J.H.; Rice, C.M.
 J. Mol. Biol. 187, 309-323, 1986
 A:Title: Partial nucleotide sequence of the Murray Valley encephalitis virus genome: com
 A:Reference number: A24635; MUID:86200215; PMID:3009829
 A:Accession: A24635
 A:Molecule type: genomic RNA
 A:Residues: 1-1780 <DAL>
 A:Cross-references: GB:X03467; NID:959329; PIDN:CAA27184.1; PID:9755731
 R:Lee, E.; Fernon, C.; Simpson, R.; Weir, R.C.; Rice, C.M.; Daigarno, L.
 Virus Genes 4, 197-213, 1990
 A:Title: Sequence of the 3' half of the Murray Valley encephalitis virus genome and map
 A:Reference number: A60288; MUID:91102934; PMID:1702914
 A:Accession: A60288
 A:Molecule type: genomic RNA
 A:Residues: 1504-1778, 'V', 1780-3434 <LEB>
 C:Superfamily: yellow fever virus genome polypeptide; glycoprotein; nonstructural protein;
 C:Keywords: ATP; capsid protein; envelope protein; glycoprotein; nonstructural protein;
 F.1126-292/Product: capsid protein #status predicted <CAP>
 F.1126-292/Product: membrane protein #status predicted <GLM>
 F.1126-292/Product: nonterminal signal sequence #status predicted <SIG>
 F.1218-292/Product: transmembrane protein #status predicted <TM1>
 F.1218-292/Product: transmembrane protein #status predicted <TM2>
 F.293-793/Product: envelope protein #status predicted <ENV>
 F.773-791/Product: transmembrane protein #status predicted <TM2>
 F.794-1205/Product: nonstructural protein NS1 #status predicted <NS1>
 F.1206-1372/Product: nonstructural protein NS2a #status predicted <NS2a>
 F.1306-1503/Product: nonstructural protein NS2b #status predicted <NS2b>
 F.1504-2122/Product: nonstructural protein NS3 #status predicted <NS3>
 F.1697-1704/Product: nucleotide-binding motif A (P-loop)
 F.1788-1789/Product: nucleotide-binding motif B
 F.1788-1791/Product: DEAH motif
 F.2123-2414/Product: nonstructural protein NS4a #status predicted <NS4a>
 F.2415-2529/Product: nonstructural protein NS4b #status predicted <NS4b>
 F.2530-3434/Product: nonstructural protein NS5 #status predicted <NS5>
 F.73,140,446/Product: carbohydrate (Aam) (covalent) #status predicted

Query Match 1.5%; Score 8; DB 1; Length 3434;
 Best Local Similarity 100.0%; Pred. No. 95;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 465 GVLLALL 472
 Db 2228 GVLLALL 2235

RESULT 19

A60996
 Complement C3 - bovine (fragment)
 N:Contains: alternative-complement-pathway C3/C5 convertase (EC 3.4.21.47) C3b subunit;
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 31-Dec-1993 #sequence_revision 03-Feb-1994 #text_change 07-Oct-1994
 C:Accession: A60996
 R:Anwar, H.
 FEWS Microbiol. Lett. 71, 305-310, 1990
 A:Title: Association of a 36 kDa bovine serum protein with the outer membrane of Bordet
 A:Reference number: A60996
 A:Accession: A60996
 A:Molecule type: protein
 A:Residues: 1-23 <ANW>
 A>Note: this protein was purified from Bordetella pertussis outer membranes after exposu

ected after exposure to human serum
 C:Comment: Complement C3 contains two chains, formed by removal of four residues and lin
 alternative complement pathways, releases the C3a anaphylatoxin from the amino end of t
 native-complement-pathway C3/C5 convertase.
 C:Comment: C3a anaphylatoxin is a vasoactive peptide and a mediator of inflammation.
 C:Comment: C3b, with its highly reactive thiol group, binds to the surface of foreign pa
 e classical-complement-pathway C3/C5 convertase. The activity of C3b is regulated by pro
 C:Comment: The major site of synthesis of this plasma protein is the liver.
 C:Superfamily: alpha-2-macroglobulin
 C:Keywords: acute phase; complement alternate pathway; complement pathway; glycoprotein;

Query Match 1.3%; Score 7; DB 2; Length 23;
 Best Local Similarity 100.0%; Pred. No. 13;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 358 LSDQVPD 364
 Db 6 LSDQVPD 12

RESULT 20

hypothetical protein B15120.60 [imported] - Neurospora crassa
 C:Species: Neurospora crassa
 C:Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 08-Sep-2000
 R:Schulte, U.; Aign, V.; Hohenseil, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura,
 submitted to the Protein Sequence Database, July 2000
 C:Accession: T51036
 A:Reference number: Z55286
 A:Accession: T51036
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-122 <SCH>
 A:Cross-references: EMBL:AL389900; GSPDB:GN00116; NCSP:B15120.60
 A:Experimental source: BAC clone B15120; strain OR74A
 C:Genetics:
 A:Gene: NCSP:B15120.60
 C:Superfamily: Neurospora crassa hypothetical protein B15120.60

Query Match 1.3%; Score 7; DB 2; Length 122;
 Best Local Similarity 100.0%; Pred. No. 54;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 36 SASISGN 42
 Db 89 SASISGN 95

RESULT 21

G64863
 ycgK protein precursor - Escherichia coli (strain K-12)
 C:Species: Escherichia coli
 C:Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002
 R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co
 A.; Rose, D.J.; Mau, B.; Shao, Y.
 Science 277, 1453-1462, 1997
 A:Title: The complete genome sequence of Escherichia coli K-12.
 A:Reference number: A64720; MUID:97426617; PMID:9278503
 A:Accession: G64863
 A:Molecule type: DNA
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Cross-references: GB:AE000216; GB:U00096; NID:91787417; PIDN:AACT4262.1; PID:91787426;
 A:Experimental source: strain K-12, substrain MG1655
 C:Genetics:
 A:Gene: ycgK
 C:Superfamily: Escherichia coli ycgK protein
 F.1-22/Domain: signal sequence #status predicted <SIG>
 F.23-133/Product: ycgK protein #status predicted <MAT>

Best Local Similarity 100.0%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 466 VLLALL 472
|||||
Db 10 VLLALL 16

RESULT 22
H90837
hypothetical protein Ecol672 (imported) - Escherichia coli (strain O157:H7, substrain R1)
C:Species: Escherichia coli
C>Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text_change 03-Aug-2001
C:Accession: H90837
R:Hayashi, T.; Makino, K.; Ohnishi, M.; Kurokawa, K.; Ishii, K.; Yokoyama, K.; Han, C.G.
Gasaawa, N.; Yasunaga, T.; Kuhara, S.; Shiba, T.; Hattori, M.; Shinagawa, H.
DNA Res. 8, 11-22, 2001
A:Title: Complete genome sequence of enterohemorrhagic Escherichia coli O157:H7 and gene
A:Reference number: A59629; MUID:21156231; PMID:11258796
A:Accession: H90837
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-133 <HAV>
A:Cross-references: GB:BA000007; PIDN:BA85095.1; PID:g13361136; GSPDB:GN00154
A:Experimental source: strain O157:H7, substrain RMD 050952
C:Genetics:
A:Gene: Ecol672
C:Superfamily: Escherichia coli ycgK protein

Query Match 1.3%; Score 7; DB 2; Length 133;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 466 VLLALL 472
|||||
Db 10 VLLALL 16

RESULT 23
A85696
hypothetical protein ycgK (imported) - Escherichia coli (strain O157:H7, substrain EDL93)
C:Species: Escherichia coli
C>Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 14-Sep-2001
C:Accession: A85696
R:Perna, N.T.; Plunkett III, G.; Burland, V.; Mau, B.; Glaeser, J.D.; Rose, D.J.; Mayhew
Miller, L.; Grobeck, B.J.; Davis, N.W.; Lm, A.; Dimalanta, E.; Potamoudis, K.; Apodaca,
Nature 409, 529-533, 2001
A:Title: Genome sequence of enterohemorrhagic Escherichia coli O157:H7.
A:Reference number: A85480; MUID:21074935; PMID:11206551
A:Accession: A85696
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-133 <STO>
A:Cross-references: GB:AE005174; NID:g12514875; PIDN:AAG56029.1; GSPDB:GN00145; UWGP:Z18
A:Experimental source: strain O157:H7, substrain EDL933
C:Genetics:
A:Gene: ycgK
C:Superfamily: Escherichia coli ycgK protein

Query Match 1.3%; Score 7; DB 2; Length 133;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 466 VLLALL 472
|||||
Db 10 VLLALL 16

RESULT 24
J01561
hypothetical 15.3k protein - Lymantria dispar nuclear polyhedrosis virus
N:Alternate names: hypothetical protein 5
C:Species: Lymantria dispar nuclear polyhedrosis virus, LdMNPV

C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 20-Sep-1999
C:Accession: J01561
R:Bjornson, R.M.; Rohmann, G.F.
J. Gen. Virol. 73, 1499-1504, 1992
A:Title: Nucleotide sequence of the polyhedron envelope protein gene region of the Lymantria
A:Reference number: F00359; MUID:92300345; PMID:1607868
A:Accession: J01561
A:Molecule type: DNA
A:Residues: 1-141 <BJO>
A:Cross-references: DDBJ:D10836
A>Note: the authors translated the codon TAT for residue 19 as Thr, and TAT for residue
C:Superfamily: Lymantria dispar nuclear polyhedrosis virus hypothetical 15.3k protein

Query Match 1.3%; Score 7; DB 2; Length 141;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 376 TAAGSL 382
|||||
Db 121 TAAGSL 127

RESULT 25
AG1972
hypothetical protein alr1330 (imported) - Nostoc sp. (strain PCC 7120)
C:Species: Nostoc sp. PCC 7120
A>Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120
C>Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002
C:Accession: AG1972
R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi
Nakazaki, N.; Shimp, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S
DNA Res. 8, 205-213, 2001
A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena
A:Reference number: AB1807; MUID:21595285; PMID:11759840
A:Accession: AG1972
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-151 <KUR>
A:Cross-references: GB:BA000019; PIDN:BA873287.1; PID:g17130677; GSPDB:GN00179
A:Experimental source: strain PCC 7120
C:Genetics:
A:Gene: alr1330

Query Match 1.3%; Score 7; DB 2; Length 151;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 384 ETPNFI 390
|||||
Db 71 ETPNFI 77

RESULT 26
C70513
hypothetical protein Rv2120c - Mycobacterium tuberculosis (strain H37RV)
C:Species: Mycobacterium tuberculosis
C>Date: 17-Jul-1998 #sequence_revision 17-Jul-1998 #text_change 28-Jul-2000
C:Accession: C70513
R:Cole, S.T.; Brosch, R.; Parkhill, J.; Garnier, T.; Churcher, C.; Harris, D.; Gordon, S.
Comor, R.; Davies, R.; Devlin, K.; Fellwell, T.; Gentles, S.; Hamlin, N.; Holroyd, S.
Rajadream, M.A.; Rogers, J.; Rutter, S.; Seeger, K.; Skelton, S.; Squares, S.
Nature 393, 537-544, 1998
A:Authors: Sgares, R.; Sultston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.
A:Title: Deciphering the biology of Mycobacterium tuberculosis from the complete genome
A:Reference number: A70500; MUID:98295987; PMID:9634230
A:Accession: C70513
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-160 <COL>
A:Cross-references: GB:Z97559; GB:AL123456; NID:g3261820; PIDN:CA810716.1; PID:e328401;
A:Experimental source: strain H37RV
C:Genetics:
A:Gene: Rv2120c

C:Superfamily: Mycobacterium tuberculosis hypothetical protein RV2120c

Query Match 1.3%; Score 7; DB 2; Length 160;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 466 VLLALL 472
DB 6 VLLALL 12

RESULT 27

Conserved hypothetical protein VC0439 [imported] - Vibrio cholerae (strain N16961 serogz

C:Species: Vibrio cholerae
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001

C:Accession: F82322
R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.J.; Chardson, D.; Ermolaeva, M.D.; Vamathevan, J.; Bass, S.; Qin, H.; Dragol, I.; Sellers, F.

1, R.R.; Mekalanos, J.U.; Venter, J.C.; Fraser, C.M.
Nature 406, 477-483, 2000
A:Title: DNA Sequence of both chromosomes of the cholera pathogen Vibrio cholerae.

A:Reference number: A82035; MUID:20406833; PMID:10952301

A:Accession: F82322

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-161 <HEI>

A:Cross-references: GB:AE004311; GB:AE003852; NID:g9654856; PIDN:AAF93612.1; GSPDB:GN001

A:Experimental source: serogroup O1, strain N16961; biotype El Tor

C:Genetics:

A:Gene: VC0439

A:Map position: 1
C:Superfamily: primosomal operon 14K protein

Query Match 1.3%; Score 7; DB 2; Length 161;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 458 IAGLAVG 464
DB 140 IAGLAVG 146

RESULT 28

H87591
Hypothetical protein CC2768 [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus

C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001

C:Accession: H87591

R:Heiman, W.C.; Feldblyum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwinn, M.L.; Haft, D.H.; Kojima, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.
Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A:Title: Complete Genome Sequence of Caulobacter crescentus.

A:Reference number: A87249; MUID:21173698; PMID:11259647

A:Accession: H87591

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-169 <STO>

A:Cross-references: GB:AE005673; NID:G13424364; PIDN:AAK24732.1; GSPDB:GN00148

C:Genetics:

A:Gene: CC2768

Query Match 1.3%; Score 7; DB 2; Length 169;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 466 VLLALL 472
DB 46 VLLALL 52

RESULT 29

B83411
Hypothetical protein PA1867 [imported] - Pseudomonas aeruginosa (strain PA01)

C:Species: Pseudomonas aeruginosa

C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000

C:Accession: B83411
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizioch, S.D.; Warren, P.; Hickey, M.J.; Bradman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho

A:Reference number: A82950; MUID:20437337; PMID:10584043

A:Accession: B83411

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-175 <STO>

A:Cross-references: GB:AE004613; GB:AE004091; NID:g9947856; PIDN:AG05256.1; GSPDB:GN001

A:Experimental source: strain PA01

C:Genetics:

A:Gene: PA1867

Query Match 1.3%; Score 7; DB 2; Length 175;
Best Local Similarity 100.0%; Pred. No. 73;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 466 VLLALL 472
DB 37 VLLALL 43

RESULT 30

AG2369
Cytochrome b6/f-complex iron-sulfur protein [imported] - Nostoc sp. (strain PCC 7120)

C:Species: Nostoc sp. PCC 7120

A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Dec-2002

C:Accession: AG2369

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Matanabe, A.; Iriyuchi, Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata, S.

DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Anabaena

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: AG2369

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-178 <KDB>

A:Cross-references: GB:BA000019; PIDN:BA876210.1; PID:G17133647; GSPDB:GN00179

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: petC

C:Superfamily: ubiquinol-cytochrome-c reductase iron-sulfur protein; Rieske [2Fe-2S] hom

Query Match 1.3%; Score 7; DB 2; Length 178;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 456 ALIAGLA 462
DB 78 ALIAGLA 84

RESULT 31

T16472
Hypothetical protein F56C9.8 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 20-Sep-1999

C:Accession: T16472

R:Du, Z.

submitted to the EMBL Data Library, May 1994

A:Description: The sequence of C. elegans coemid F56C9.

A:Reference number: S46729

A:Accession: T16472

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: DNA

A:Residues: 1-182 <DUZ>
A:Cross-references: EMBL:U00063; NID:G488186; PID:G488194; PIDN:AA08717.1; CESP:F56C9.8
A:Experimental source: strain Bristol N2
C:Genetics:
A:Gene: CESP:F56C9.8
A:Introns: 19/3; 48/3; 74/2; 93/2

Query Match
Best Local Similarity 1.3%; Score 7; DB 2; Length 182;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 464 GCVLLA 470
29 GGVLLA 35

RESULT 32
T36745
Probable RNA polymerase sigma factor - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 21-Jan-2000
C:Accession: T36745
R:Saunders, D.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
submitted to the EMBL Data Library, July 1999
A:Reference number: Z21613
A:Accession: T36745
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-185 <SAN>
A:Cross-references: EMBL:AL096849; PIDN:CAB50938.1; GSPDB:GN00070; SCOEDB:SC11.12C
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SC11.12C
C:Superfamily: transcription initiation factor sigma E

Query Match
Best Local Similarity 1.3%; Score 7; DB 2; Length 185;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 9 LTVLVAD 15
11 LTVLVAD 17

RESULT 33
C81224
conserved hypothetical protein NMB0215 [imported] - Neisseria meningitidis (strain MC58
C:Species: Neisseria meningitidis
C:Date: 31-Mar-2000 #sequence_revision 31-Mar-2000 #text_change 19-Jan-2001
C:Accession: C81224
R:Tettelin, H.; Saunders, N.J.; Heidelberg, J.; Jeffries, A.C.; Nelson, K.E.; Eisen, J.A.
Hickey, E.K.; Haft, D.H.; Salzberg, S.L.; White, O.; Fleischmann, R.D.; Dougherty, B.A.;
ri, H.; Qin, H.; Yamachyan, U.; Gill, J.; Scarlato, V.; Massignani, V.; Pizza, M.
Science 287, 1809-1815, 2000
A:Authors: Grandi, G.; Sun, L.; Smith, H.O.; Fraser, C.M.; Moxon, E.R.; Rappuoli, R.; Ve
A:Title: Complete genome sequence of Neisseria meningitidis serogroup B strain MC58.
A:Reference number: AB1000; MUID:2017555; PMID:10710307
A:Accession: C81224
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-188 <TER>
A:Cross-references: GB:AE002379; GB:AE002098; NID:G7225435; PIDN:AAF40671.1; PID:G722543
A:Experimental source: serogroup B, strain MC58
C:Genetics:
A:Gene: NMB0215
C:Superfamily: Escherichia coli conserved hypothetical protein b1821

Query Match
Best Local Similarity 1.3%; Score 7; DB 2; Length 186;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 164 GRCAEPA 170
|||||||

Db 161 GRCAEPA 167
|||||||

RESULT 34
D83334
conserved hypothetical protein PA2484 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: D83334
R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mitsuuchi, S.D.; Warriner, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathog
A:Reference number: AB2950; MUID:2043737; PMID:10984043
A:Accession: D83334
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-204 <STO>
A:Cross-references: GB:AE004676; GB:AE004091; NID:G9948532; PIDN:AA05872.1; GSPDB:GN001.
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA2484

Query Match
Best Local Similarity 1.3%; Score 7; DB 2; Length 204;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 370 SAAVSAT 376
93 SAAVSAT 99

RESULT 35
A40305
biliary glycoprotein - mouse (fragment)
C:Species: Mus musculus (house mouse)
C:Date: 03-Apr-1992 #sequence_revision 03-Apr-1992 #text_change 23-Jul-1999
C:Accession: A40305
R:Robbins, J.; Robbins, P.F.; Kozak, C.A.; Callahan, R.
Genomics 10, 583-587, 1991
A:Title: The mouse biliary glycoprotein gene (Bgp): partial nucleotide sequence, express
A:Reference number: A40305; MUID:91365364; PMID:1653760
A:Accession: A40305
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-206 <ROB>
A:Cross-references: GB:M61907; GB:M73534; NID:G192197; PIDN:AAA7298.1; PID:G192198
C:Superfamily: carcinoembryonic antigen; carcinoembryonic antigen precursor amino-termin
C:Keywords: glycoprotein
F:2-51/Domain: immunoglobulin homology <IMM1>
F:87-144/Domain: immunoglobulin homology <IMM2>

Query Match
Best Local Similarity 1.3%; Score 7; DB 2; Length 206;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Db 456 ALTAGLA 462
186 ALTAGLA 192

RESULT 36
C82979
hypothetical protein PA5341 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: C82979
R:Stover, C.K.; Pham, X.O.; Erwin, A.L.; Mitsuuchi, S.D.; Warriner, P.; Hickey, M.J.; Br
adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic patho

A:Reference number: A82950; MUID:20437337; PMID:10984043
 A:Accession: C82979
 A:Status: Preliminary
 A:Molecule type: DNA
 A:Residues: 1-206 <STO>
 A:Cross-references: GB:A8004946; GB:A8004091; NID:g9951650; PIDN:AAG08726.1; GSPDB:GN001
 A:Experimental source: strain P801
 C:Genetics:
 A:Gene: PAS341
 C:Superfamily: hypothetical protein b1798

Query Match 1.3%; Score 7; DB 2; Length 206;
 Best Local Similarity 100.0%; Pred. No. 84;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 465 GVLTLAL 471
 |||||
 DB 191 GVLTLAL 197

RESULT 37
 F84563
 hypothetical protein At2g18380 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C:Accession: F84563
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.;
 Ems, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: F84563
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-207 <STO>
 A:Cross-references: GB:A8002093; NID:g4309729; PIDN:AAD15499.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: At2g18380
 A:Map position: 2

Query Match 1.3%; Score 7; DB 2; Length 207;
 Best Local Similarity 100.0%; Pred. No. 85;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 438 STSVDC 444
 |||||
 DB 34 STSVDC 40

RESULT 38
 JX0244
 pyroglutamy1-peptidase I (EC 3.4.19.3) - Bacillus amyloliquefaciens
 N:Alternate names: 5-oxopropyl-peptidase; pyroglutamy1 aminopeptidase
 C:Species: Bacillus amyloliquefaciens
 C>Date: 10-Jun-1993 #sequence_revision 10-Jun-1993 #text_change 18-Aug-2000
 C:Accession: JX0244
 R:Yoshimoto, T.; Shimoda, T.; Kitazono, A.; Kabashima, T.; Ito, K.; Tsuru, D.
 J. Biochem. 113, 67-73, 1993
 A>Title: Pyroglutamy1 peptidase gene from Bacillus amyloliquefaciens: Cloning, sequencin
 A:Reference number: JX0244; MUID:93203177; PMID:8095933
 A:Accession: JX0244
 A:Molecule type: DNA
 A:Residues: 1-215 <YOS>
 A:Cross-references: DBJ:D11035; NID:g216315; PIDN:BA01791.1; PID:g216316
 C:Superfamily: Bacillus subtilis pyroglutamy1-peptidase I pcg
 C:Keywords: hydrolase; omega peptidase

Query Match 1.3%; Score 7; DB 2; Length 215;
 Best Local Similarity 100.0%; Pred. No. 88;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 371 AAVSYTA 377

DB 133 AAVSYTA 139
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RESULT 39
 S23432
 pyroglutamy1-peptidase I (EC 3.4.19.3) pcg - Bacillus subtilis
 N:Alternate names: 5-oxopropyl-peptidase; pyroglutidone-carboxylate peptidase pcg
 C:Species: Bacillus subtilis
 C>Date: 03-May-1994 #sequence_revision 20-Feb-1995 #text_change 18-Aug-2000
 C:Accession: S23432; G69673
 R:Awade, A.; Cleuziat, P.; Gonzales, T.; Robert-Baudouy, J.
 FEBS Lett. 305, 67-73, 1992
 A>Title: Characterization of the pcg gene encoding the pyroglutidone carboxyl peptidase of
 A:Reference number: S23432; MUID:9233527; PMID:1353026
 A:Accession: S23432
 A:Molecule type: DNA
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 A:Cross-references: EMBL:X66034; NID:g40036; PIDN:CAA46833.1; PID:g40037
 A:Experimental source: strain 168
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Bertier
 C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Cho
 A.; Ehrlich, S.D.; Emmeron, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
 Nature 390, 249-256, 1997
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Gallier
 lech, J.; Harwood, C.R.; Henauf, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M.F.
 Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois,
 A:Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauel
 Y. M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portecelle
 Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon,
 A:Authors: Schleich, S.; Schroeder, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror
 Akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpet, P.; Tognoni, A.; Tosato, V.; Uchiyama,
 T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamano, K.; Yasumoto, K.; Yata, K.; Yoshida, K
 A:Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.
 A>Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
 A:Reference number: A69580; MUID:98044033; PMID:9364377
 A:Accession: G69673
 A:Status: nucleic acid sequence not shown; translation not shown
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 A:Residues: 1-215 <KUN>
 A:Cross-references: GB:259105; GB:AL009126; NID:g2632457; PIDN:CAB12059.1; PID:g2632551
 A:Experimental source: strain 168
 C:Genetics:
 A:Gene: pcg
 C:Superfamily: Bacillus subtilis pyroglutamy1-peptidase I pcg
 C:Keywords: hydrolase; omega peptidase

Query Match 1.3%; Score 7; DB 2; Length 215;
 Best Local Similarity 100.0%; Pred. No. 88;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 371 AAVSYTA 377
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 DB 133 AAVSYTA 139

RESULT 40
 AG3100
 replicative DNA helicase [imported] - Agrobacterium tumefaciens (strain C58, Dupont)
 C:Species: Agrobacterium tumefaciens
 C>Date: 11-Jan-2002 #sequence_revision 11-Jan-2002 #text_change 18-Nov-2002
 C:Accession: AG3100
 R:Wood, D.W.; Setubal, J.C.; Kaul, R.; Monks, D.; Chen, L.; Wood, G.E.; Chen, Y.; Woo, L
 erage, G.; Gillet, W.; Grant, C.; Guenheuer, D.; Kurayarin, T.; Levy, R.; Li, M.; McClell
 Science 294, 2317-2323, 2001
 A:Authors: Yoo, H.; Tao, Y.; Biddle, P.; Jung, M.; Krepan, W.; Perry, M.; Gordon-Kamm,
 ster, E.W.
 A>Title: The Genome of the Natural Genetic Engineer Agrobacterium tumefaciens C58.
 A:Reference number: A82577; MUID:21608550; PMID:11743193
 A:Accession: AG3100
 A:Status: preliminary
 A:Molecule type: DNA

A:Residues: 1-217 <KUR>
 A:Cross-references: GB:AE008689; PIDN:AAL45221.1; PID:gi7742902; GSPDB:GN00187
 A:Experimental source: strain C58 (Dupont)
 C:Genetics:
 A:Gene: Atu4427
 A:Map position: linear chromosome

Query Match 1.3% Score 7; DB 2; Length 217;
 Best Local Similarity 100.0%; Pred.No. 88;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 377 AAGSLSE 383
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 Db 33 AAGSLSE 39

Search completed: October 2, 2003, 16:06:29
 Job time : 63 secs

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OM protein - protein search, using sw model

Run on: October 2, 2003, 15:53:10 / Search time 25 Seconds
(without alignments)
1017.658 million cell updates/sec

Title: US-10-039-770A-1
Perfect score: 541
Sequence: 1 MGWGVQVLLVTVADCTIFA.....EAEENIEQDETHVMEGDEY 541

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 127863 seqs, 47026705 residues

Word size: 0

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database: SwissProt_41.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8	1.5	200	Y966_MYCTU	P71544 mycobacteri
2	8	1.5	358	YM05_MYCTU	Q10394 mycobacteri
3	8	1.5	466	GSA_SOYBN	P45621 glycine max
4	8	1.5	1268	PCGN_MOUSE	P55066 mus musculu
5	8	1.5	1348	VGR2_COTJA	P55583 coturnix co
6	8	1.5	3430	POLG_COTJA	P06935 w genome po
7	8	1.5	3433	POLG_KUNM	P14335 k genome po
8	8	1.5	114	YCGK_ECOLI	P76002 escherichia
9	7	1.3	133	YCGK_ECOLI	Q94287 mus musculu
10	7	1.3	137	GILZ_MOUSE	P24481 escherichia
11	7	1.3	205	HYPA_ECOLI	P46107 bacillus am
12	7	1.3	215	PCP_BACAM	P28618 bacillus su
13	7	1.3	215	PCP_BACAM	Q94087 homo sapien
14	7	1.3	217	CLD9_HUMAN	P45275 haemophilus
15	7	1.3	217	YGI8_HAEIN	O51353 borrelia bu
16	7	1.3	217	YGI8_HAEIN	P35898 rattus norv
17	7	1.3	226	RL1_BORBU	P13319 homo sapien
18	7	1.3	234	GU45_RAT	Q09262 p phosphadi
19	7	1.3	257	FCEA_HUMAN	O56137 methanococ
20	7	1.3	263	YOD1_CABEL	Q8165 yersinia pe
21	7	1.3	271	CD5A_PSEAE	O8165 yersinia pe
22	7	1.3	272	UPK_YERPE	P09391 escherichia
23	7	1.3	276	GRPG_ECOLI	O8165 yersinia pe
24	7	1.3	284	DAPE_BUCAP	O8165 yersinia pe
25	7	1.3	289	AROK_METH	O8165 yersinia pe
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32	7	1.3	335	BTUC_YERPE	O8165 yersinia pe
33	7	1.3	352	Z185_MOUSE	O62394 mus musculu

34	7	1.3	376	YQCB_ERWCA	Q47417 erwinia car
35	7	1.3	399	GALI_LACTA	Q97471 lactococcus
36	7	1.3	399	GALI_LACTA	Q9662 lactococcus
37	7	1.3	408	PGK_THFAC	O9195 thermoplas
38	7	1.3	424	YKJ6_BPPFI	P2511 bacterioph
39	7	1.3	430	YKJ5_STRCO	Q9460 streptomyce
40	7	1.3	431	NMTH_CLOAB	Q9745 clostridium
41	7	1.3	432	OAT_DROAN	P49724 drosophila
42	7	1.3	436	NMTH_DEIRA	Q9745 clostridium
43	7	1.3	450	FOKP_CHIMU	O9268 deincoccus
44	7	1.3	462	US29_HCMVA	P82602 c foliate sy
45	7	1.3	481	BIND_STRPN	P09705 human cyto
46	7	1.3	485	BIND_STRPN	P06651 strongyloce
47	7	1.3	499	NU4C_MARPO	P23118 strongyloce
48	7	1.3	508	GATB_BOWMO	P06263 marchantia
49	7	1.3	521	CEAL_MOUSE	P52167 bombyx mori
50	7	1.3	526	ASPA_CORGL	P21809 mus musculu
51	7	1.3	563	CYB_SULAC	Q99200 corynebacte
52	7	1.3	570	MKKS_HUMAN	P39480 sulfolobus
53	7	1.3	589	C49A_DROME	Q9npj1 homo sapien
54	7	1.3	600	SP96_DICDI	Q9v513 drosophila
55	7	1.3	602	DCP1_ORRSA	P14338 dicyosteli
56	7	1.3	608	UL27_HCMVA	P51847 cryza sativ
57	7	1.3	643	GAG_SFV3L	P16763 human cyto
58	7	1.3	665	TKT_BUCAI	P27400 stimian foa
59	7	1.3	693	PERO_DROME	P57195 buchiera ap
60	7	1.3	723	PAB5_STRGR	Q01603 drosophila
61	7	1.3	727	PILOI_HUMAN	P32483 streptomyce
62	7	1.3	738	GCP4_ARATH	Q02809 homo sapien
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64	7	1.3	802	FGR4_HUMAN	Q9sc88 medicago tr
65	7	1.3	887	UFO_HUMAN	P22455 homo sapien
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67	7	1.3	994	PROL_DROME	O06998 bluetongue
68	7	1.3	1009	M2B2_HUMAN	P35875 drosophila
69	7	1.3	1093	RNT1_NEUCR	Q9245 homo sapien
70	7	1.3	1104	COLA_CLOPE	Q9heh1 neurospora
71	7	1.3	1174	NIFU_ECOLI	P3153 clostridium
72	7	1.3	1191	NIFU_RHORI	P52647 escherichia
73	7	1.3	1199	NIFU_ANASP	O53046 rhodospirill
74	7	1.3	1199	NIFU_STNY3	Q06879 anabena ap
75	7	1.3	1202	YE01_SCHPO	P22965 eynecocyst
76	7	1.3	1663	CO3_HUMAN	O13788 schizosach
77	7	1.3	1663	CO3_MOUSE	P01024 homo sapien
78	7	1.3	1663	CO3_RAT	P01027 mus musculu
79	7	1.3	1666	CO3_CAVPO	P01026 rattus norv
80	7	1.3	1857	FAS2_PENPA	P12387 cavia porce
81	7	1.3	1964	NTC4_MOUSE	P15368 p fatty aci
82	7	1.3	2337	TOR2_SCHPO	P21695 mus musculu
83	7	1.3	6486	TYCC_BREPA	Q97782 schizosach
84	6	1.1	38	DCH5_MTCSP	O30409 b tyrocidin
85	6	1.1	62	GBG_CABEL	P00863 micrococcus
86	6	1.1	64	LAP_BOVIN	P54406 caenorhabdi
87	6	1.1	64	TAP_BOVIN	Q28880 bos taurus
88	6	1.1	67	YFUB_BACSU	P25068 dos taurus
89	6	1.1	69	GRK_BACCE	P51511 bacillus su
90	6	1.1	75	YA26_STPAE	Q9y311 bacillus ce
91	6	1.1	76	CD24_MOUSE	O8c983 streptoloco
92	6	1.1	76	CD24_RAT	P24887 mus musculu
93	6	1.1	80	CD24_HUMAN	Q07490 rattus norv
94	6	1.1	80	COXK_MOUSE	P25063 mus sapien
95	6	1.1	81	ATPH_ARATH	P56392 mus musculu
96	6	1.1	81	ATPH_TORTA	P57670 arabidopsis
97	6	1.1	81	ATPH_MARPO	P12231 lotus japon
98	6	1.1	81	ATPH_PEA	P06287 marchantia
99	6	1.1	81	ATPH_SPIOI	P08212 pisum sativ
100	6	1.1	81	ATPH_TOBAC	P08433 spinacia ol
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103	6	1.1	82	ATPH_CHLRE	O02861 antihuman
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P23118	strongyloce
P06263	marchantia
P52167	bombyx mori
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Q9npj1	homo sapien
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P51847	cryza sativ
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P27400	stimian foa
P57195	buchiera ap
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Q9sc88	medicago tr
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P52647	escherichia
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P15368	p fatty aci
P21695	mus musculu
Q97782	schizosach
O30409	b tyrocidin
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Q28880	bos taurus
P25068	dos taurus
P51511	bacillus su
Q9y311	bacillus ce
O8c983	streptoloco
P24887	mus musculu
Q07490	rattus norv
P25063	mus sapien
P56392	mus musculu
P57670	arabidopsis
P12231	lotus japon
P06287	marchantia
P08212	pisum sativ
P08433	spinacia ol
P06286	nicotiana t
Q03131	rattus norv
O02861	antihuman
Q27304	chlamydomon
P56297	chlorella v
Q9tcm0	cyanidium c
Q9tcm0	mesocistigma

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108	6	1.1	82	1	ATPH_PORPU	P51246	porphyra pu	181	6	1.1	153	1	IL4_HUMAN	P05112	homo sapien
109	6	1.1	82	1	YBDJ_KLEPN	O48414	klebsiella	182	6	1.1	153	1	IL4_MACPA	P79339	macaca fasc
110	6	1.1	83	1	ATPH_GALSU	P35013	galdieria s	183	6	1.1	153	1	IL4_MACMU	P51492	macaca mula
111	6	1.1	83	1	N19M_BOVIN	Q02371	bos taurus	184	6	1.1	153	1	YD03_MYCLE	P53431	mycobacteri
112	6	1.1	83	1	YK76_MYCTU	Q10684	mycobacteri	185	6	1.1	155	1	NU6M_ALBIO	P48922	albimaria c
113	6	1.1	90	1	GON3_DICLA	Q91409	dicentrarchi	186	6	1.1	156	1	VATL_HELVI	P55277	heliobla v
114	6	1.1	90	1	GON3_HABPU	P45652	haplochromi	187	6	1.1	156	1	VATL_MANSE	P13403	mundaica sex
115	6	1.1	90	1	GON3_PAGMA	P51921	pagrus majo	188	6	1.1	157	1	VATL_AEDAE	O16110	aedes aegyp
116	6	1.1	90	1	GON3_SPAU	P51923	sparus aua	189	6	1.1	159	1	VATL_DROME	P23380	drosophila
117	6	1.1	92	1	SFSB_ECOLI	P18837	escherichia	190	6	1.1	160	1	BIK_HUMAN	Q13322	homo sapien
118	6	1.1	92	1	YO18_BACAN	Q99114	bacillus an	191	6	1.1	160	1	PETD_SYNY3	P27589	synecocyst
119	6	1.1	97	1	FER COLES	P00222	colocaccia e	192	6	1.1	161	1	VATL_NEUCR	P14113	neurospora
120	6	1.1	98	1	FER2_PHYAM	P00231	phytolacca	193	6	1.1	162	1	Y79A_METJA	P13131	methanococ
121	6	1.1	98	1	FER2_PHYES	P00332	phytolacca	194	6	1.1	163	1	PHCA_ANASP	P07121	anaeana sp
122	6	1.1	98	1	FERB_ALOMA	P81373	alocasia ma	195	6	1.1	163	1	SR19_DROME	P49963	drosophila
123	6	1.1	99	1	NLT4_ORYSA	Q42976	oryza sativ	196	6	1.1	165	1	NRG7_HUMAN	Q16617	homo sapien
124	6	1.1	101	1	NU1C_OENHO	Q9M410	oenothera h	197	6	1.1	166	1	PAL_PSEPK	P43036	pseudomonas
125	6	1.1	101	1	INSE_SPIOL	Q9M319	spinacia ol	198	6	1.1	169	1	GSHC_SCHMA	Q00277	schistosoma
126	6	1.1	102	1	INSE_ECOLI	P77681	escherichia	199	6	1.1	170	1	RUVIC_CHLMU	O9P199	chlamydia m
127	6	1.1	102	1	INSE_SHITL	P59445	shigella fl	200	6	1.1	170	1	RUVIC_CHLTR	O84510	chlamydia t
128	6	1.1	103	1	FTSB_SALTY	O8X6P2	salmoneila	201	6	1.1	171	1	NU5B_BRUME	O8Y2K1	telosonia b
129	6	1.1	105	1	YPPK_SALTY	Q9EY33	klebsiella	202	6	1.1	171	1	Y134_RALSO	O03175	latimeria c
130	6	1.1	109	1	INS_SPEPR	Q9Z1X3	salmomeila	203	6	1.1	173	1	NU6M_LATCH	P14348	epstein-bar
131	6	1.1	110	1	INS_SPEPR	Q45972	caulobacter	204	6	1.1	176	1	YFDR_ECOLI	P6514	escherichia
132	6	1.1	112	1	INS_VERMO	O9W1R2	verasper mo	205	6	1.1	178	1	IL22_HUMAN	O9G2X6	homo sapien
133	6	1.1	115	1	INS_LOPPI	P01341	lophius pis	206	6	1.1	179	1	IL22_HUMAN	P08895	bacillus st
134	6	1.1	116	1	VAG2_HUMAN	O9S670	homo sapien	207	6	1.1	179	1	RUS_BACST	O9P9H6	ureaplasma
135	6	1.1	118	1	GSPI_AERHY	P31377	aeromonas h	208	6	1.1	181	1	IPYR_UREPA	O88593	mus muscicu
136	6	1.1	119	1	IAAT_ELECO	P01087	eleusine co	209	6	1.1	182	1	PERP_MOUSE	P43992	haemophilus
137	6	1.1	122	1	YK63_MYCTU	Q10674	mycobacteri	210	6	1.1	182	1	Y391_HAEIN	P76222	escherichia
138	6	1.1	122	1	SVS5_RAT	P04812	rattus norv	211	6	1.1	182	1	YVJA_ECOLI	O29179	archaeoglob
139	6	1.1	123	1	MAO5_HUMAN	P43359	homo sapien	212	6	1.1	187	1	KORC_ARCFU	P25841	haemophilus
140	6	1.1	124	1	ANFC_BOVIN	P52306	bos taurus	213	6	1.1	187	1	SODC_HAEIN	O9A288	caulobacter
141	6	1.1	126	1	ANFC_BOVIN	O61839	mus muscicu	214	6	1.1	188	1	ISPP_CAUCR	GCHI_LISMO	liesteria mo
142	6	1.1	126	1	ANFC_MOUSE	P55207	rattus norv	215	6	1.1	189	1	INAI_BOVIN	P05101	bos taurus
143	6	1.1	126	1	ANFC_MOUSE	P48750	rattus norv	216	6	1.1	189	1	INAD_BOVIN	P49876	bos taurus
144	6	1.1	127	1	CSF2_RAT	O05377	mycobacteri	217	6	1.1	189	1	INAF_BOVIN	P49877	bos taurus
145	6	1.1	128	1	VG64_BPML5	O64449	mycobacteri	218	6	1.1	189	1	INAG_BOVIN	O67915	aquifex aeo
146	6	1.1	129	1	VG58_BPMD2	Q74124	human immun	219	6	1.1	189	1	Y164_AOUDE	P13661	bos taurus
147	6	1.1	130	1	TAT1_HVZK	Q05371	mycobacteri	220	6	1.1	190	1	BCT7_BOVIN	O91U45	neisseria m
148	6	1.1	130	1	VG58_BPML5	P56783	saccharomyc	221	6	1.1	190	1	MOBA_NEIMA	P56747	neisseria m
149	6	1.1	130	1	YHL9_YEAST	P33494	desulfotibir	222	6	1.1	192	1	LEXA_LEPIN	O01151	homo sapien
150	6	1.1	131	1	AGSR_MOUSE	P42302	equus caball	223	6	1.1	192	1	HIS7_LISMO	P70444	mus muscicu
151	6	1.1	132	1	IL4_HORSE	P38877	saccharomyc	224	6	1.1	194	1	BID_MOUSE	P49415	gallus gall
152	6	1.1	133	1	CTFE_YEAST	P28164	chlamydia p	225	6	1.1	195	1	SOC4_CHICK	P23507	xenopus lae
153	6	1.1	134	1	SRP_CHLPS	P54308	agrobacteri	226	6	1.1	197	1	XAI_XENLA	O81663	leptospira
154	6	1.1	134	1	TRBC_AGRUV	P33394	desulfotibir	227	6	1.1	198	1	CD83_HUMAN	O01151	homo sapien
155	6	1.1	138	1	RRFI_DESVH	P22618	myxine glut	228	6	1.1	205	1	YK07_YEAST	P36061	saccharomyc
156	6	1.1	139	1	IGF_MYXGL	P43769	haemophilus	229	6	1.1	205	1	GPBB_MOUSE	P56400	mus muscicu
157	6	1.1	139	1	TOLE_HAEIN	O60481	cavia porce	230	6	1.1	206	1	LPCA_CHLRE	O8Kaw3	chlorobium
158	6	1.1	140	1	CSF2_CAVPO	P50777	human papil	231	6	1.1	209	1	YDGI_BACSU	P66707	bacillus su
159	6	1.1	141	1	VE6_HPV24	P01587	mus muscicu	232	6	1.1	209	1	YR47_CAUCR	Q94413	caulobacter
160	6	1.1	141	1	CSF2_MOUSE	P24052	gallus gall	233	6	1.1	210	1	Y433_CABEL	Q11071	caenorhabdi
161	6	1.1	142	1	MK_CHICK	P25566	gallus gall	234	6	1.1	210	1	Y433_CABEL	O8Xb73	escherichia
162	6	1.1	143	1	CMGD_BACSU	P11052	bos taurus	235	6	1.1	211	1	YEDZ_BCOS7	P76343	escherichia
163	6	1.1	143	1	CSF2_BOVIN	P47815	tritricum ae	236	6	1.1	211	1	YEDZ_BCOS7	O04041	prunus pers
164	6	1.1	143	1	IF1A_WHEAT	O75642	homo sapien	237	6	1.1	214	1	AS20_PRUPE	P23341	saccharomyc
165	6	1.1	143	1	IF1H_HUMAN	P47813	homo sapien	238	6	1.1	215	1	WM12_YEAST	O63147	mus muscicu
166	6	1.1	143	1	IF1X_HUMAN	O14602	homo sapien	239	6	1.1	216	1	SSPN_MOUSE	O56827	escherichia
167	6	1.1	143	1	IF1Y_HUMAN	O07103	enterococcu	240	6	1.1	216	1	YQFA_ECOLI	O57674	methanococ
168	6	1.1	143	1	MRAR_ENTFA	O51699	paracoccu	241	6	1.1	220	1	ATPL_METJA	P48801	gallus gall
169	6	1.1	143	1	NIRI_PARDE	P04141	homo sapien	242	6	1.1	220	1	FGF3_CHICK	O9Pcn8	homo sapien
170	6	1.1	144	1	CSF2_HUMAN	P56331	onodrychis	243	6	1.1	221	1	SDPL_HUMAN	P13727	homo sapien
171	6	1.1	144	1	IF1A_ONOVI	Q9DE32	bungaricus ca	244	6	1.1	222	1	EMBP_HUMAN	P51861	homo sapien
172	6	1.1	145	1	PA2K_BUNCE	O76095	homo sapien	245	6	1.1	223	1	CDR1_HUMAN	O61878	mus muscicu
173	6	1.1	146	1	YTAB_HUMAN	P37523	bacillus su	246	6	1.1	223	1	EMBP_MOUSE	P27144	homo sapien
174	6	1.1	146	1	YTAB_BACSU	P21660	glycera dib	247	6	1.1	223	1	KAD4_HUMAN	P11350	escherichia
175	6	1.1	147	1	GLP3_GLYDI	O83761	treponema p	248	6	1.1	225	1	NARI_ECOLI	O63189	rattus norv
176	6	1.1	147	1	Y782_TREPA	O9K537	mycobacteri	249	6	1.1	227	1	EMBP_RAT	O08382	rhodobacter
177	6	1.1	151	1	Y000_MYCPA	O14880	homo sapien	250	6	1.1	228	1	MODB_RHOCA	P19317	escherichia
178	6	1.1	152	1	GST3_HUMAN	Q9ZCC2	rickettsia	251	6	1.1	231	1	NARW_ECOLI		
179	6	1.1	152	1	SSB_RICPR			252	6	1.1	231	1	NARW_ECOLI		

253	6	1.1	231	1	YRKP_BACSU	P54443 bacillus su	326	6	1.1	279	1	V43D_MYCPN	P75155 mycoplasma
254	6	1.1	233	1	EMBI_CAVPO	P22032 cavia porce	327	6	1.1	280	1	QCRC_MYCTU	Q10386 mycobacteri
255	6	1.1	234	1	A29B_DROME	Q46197 drosophila	328	6	1.1	281	1	ATPE_STRLI	P50012 streptomyce
256	6	1.1	234	1	EMB2_CAVPO	P35079 cavia porce	329	6	1.1	282	1	AROK_METYA	Q56833 methanococc
257	6	1.1	235	1	COLI_MOUSE	P01193 m corticotr	330	6	1.1	282	1	YHDR_ECOLI	P46476 escherichia
258	6	1.1	235	1	COLI_MOUSE	P01194 r corticotr	331	6	1.1	284	1	KDQA_PASHA	P95514 pasteurella
259	6	1.1	238	1	NEUM_HUMAN	P17677 homo sapien	332	6	1.1	284	1	NODO_RHLIV	P15728 rhizobium l
260	6	1.1	238	1	SSPN_RABIT	P82352 oryctolagus	333	6	1.1	284	1	UPK_IACUA	Q9cdm7 lactococcus
261	6	1.1	238	1	Y062_BORBU	O51089 borrella bu	334	6	1.1	285	1	T13B_HUMAN	Q9y275 homo sapien
262	6	1.1	239	1	US21_HCMVA	P09723 human cycom	335	6	1.1	286	1	VAV8_SCHPO	O10216 schizosacch
263	6	1.1	240	1	IBP6_HUMAN	P24592 homo sapien	336	6	1.1	286	1	YVGB_ECOLI	P11666 escherichia
264	6	1.1	240	1	IBP6_HUMAN	P24592 homo sapien	337	6	1.1	286	1	YVGB_ECOLI	P11666 escherichia
265	6	1.1	241	1	RKRP_HRSVA	P24567 human reepi	338	6	1.1	287	1	YCXE_BACSU	O52401 edwardsiell
266	6	1.1	241	1	YVFC_BACSU	O31761 bacillus su	339	6	1.1	288	1	LEP4_PSEPU	P40420 bacillus su
267	6	1.1	242	1	GUNS_TIRIE	P43317 trichoderma	340	6	1.1	288	1	UBIA_PROST	P36642 pseudomonas
268	6	1.1	242	1	NAGB_MYCPE	O8em7 mycoplasma	341	6	1.1	289	1	KPRP_ECOLI	O53366 providencia
269	6	1.1	243	1	SSPN_HUMAN	Q14714 homo sapien	342	6	1.1	290	1	BET4_YEAST	P73307 escherichia
270	6	1.1	244	1	CBR2_MOUSE	P08074 mus musculu	343	6	1.1	291	1	IBP3_MOUSE	Q00618 s type ii p
271	6	1.1	244	1	CBR2_PIG	Q29529 sus scrofa	344	6	1.1	293	1	YF09_MYCTU	P47878 mus musculu
272	6	1.1	245	1	COMB_ANASP	O8ytc25 anabaena sp	345	6	1.1	294	1	PROC_MYCLE	P71788 mycobacteri
273	6	1.1	245	1	DMA_SQUAC	P36963 squaalus aca	346	6	1.1	295	1	DUSF_HUMAN	P46725 mycobacteri
274	6	1.1	245	1	PUR7_ANASP	O8yur7 anabaena sp	347	6	1.1	295	1	PROC_HUMAN	O9h1r2 homo sapien
275	6	1.1	246	1	CYS2_PSEAE	Q91595 pseudomonas	348	6	1.1	296	1	NAAI_ECOLI	O11141 mycobacteri
276	6	1.1	246	1	PRTP_HSV2	P36385 herpes simp	349	6	1.1	296	1	NAAI_ECOLI	O8td58 escherichia
277	6	1.1	246	1	YU54_CORGL	P94338 corynebacte	350	6	1.1	297	1	KHSE_PYRAE	P06995 escherichia
278	6	1.1	247	1	FENR_ECOLI	P28861 escherichia	351	6	1.1	297	1	NANA_SALTI	O8azx3 pyrobaculum
279	6	1.1	247	1	MPUI_CRIGR	O60441 cricetulus	352	6	1.1	297	1	NANA_SALTI	O8z1f6 salmoneilla
280	6	1.1	247	1	STCI_HUMAN	P52823 homo sapien	353	6	1.1	298	1	VAS2_HARIN	P45008 hemophilus
281	6	1.1	248	1	DSBG_ECOS7	P58320 escherichia	354	6	1.1	299	1	NRAM_MYCTU	Q98q75 mycoplasma
282	6	1.1	248	1	DSBG_ECOLI	P77202 escherichia	355	6	1.1	300	1	DAPA_METYA	Q8uq45 methanopyru
283	6	1.1	248	1	FENR_SHIFL	P28901 shigella fl	356	6	1.1	300	1	Y270_BUCAP	P42390 buchnera ap
284	6	1.1	249	1	MYPO_CHICK	P37301 gallus gall	357	6	1.1	301	1	KLF7_MOUSE	Q993b0 mus musculu
285	6	1.1	250	1	DIP_ANTMA	P33560 antirrhinum	358	6	1.1	302	1	KLF7_HUMAN	O97540 mus musculu
286	6	1.1	250	1	TIP1_TOBAC	P21653 nicotiana t	359	6	1.1	305	1	CAH4_MOUSE	O64444 mus musculu
287	6	1.1	250	1	TIP2_TOBAC	P24422 nicotiana t	360	6	1.1	305	1	ILP_ERACL	P22334 brachioleto
288	6	1.1	252	1	Y067_MYCTU	P71964 mycobacteri	361	6	1.1	305	1	NAA2_ECOLD	Q8tdu7 escherichia
289	6	1.1	254	1	PUR7_AGR75	Q8ueb7 agrobacteri	362	6	1.1	305	1	YN45_DEIRA	Q9tr7y deinococcus
290	6	1.1	256	1	COLI_CAVPO	P15402 c corticotr	363	6	1.1	309	1	CAH4_RAT	P48284 rattus norv
291	6	1.1	256	1	HYPA_HYPLI	P35587 hypodermia l	364	6	1.1	309	1	GAG_FUJUV	P03326 fujinami sa
292	6	1.1	257	1	KLK4_MOUSE	P00757 mus musculu	365	6	1.1	309	1	O7A1_HUMAN	O96100 homo sapien
293	6	1.1	257	1	PAEJ_ECOLI	P33784 escherichia	366	6	1.1	309	1	T13B_MOUSE	Q9nu72 mus musculu
294	6	1.1	258	1	ARGB_BACSU	P36840 bacillus su	367	6	1.1	310	1	FIRA_PLAUF	P69616 plasmodium
295	6	1.1	260	1	Y230_ARCFU	O30009 archaeglob	368	6	1.1	310	1	RFMI_YEAST	Q12192 saccharomyc
296	6	1.1	261	1	KLK1_MOUSE	P15947 mus musculu	369	6	1.1	310	1	YE99_SCHPO	O43771 schizosacch
297	6	1.1	261	1	PSMA_METYA	Q60177 methanococ	370	6	1.1	310	1	YS19_STRCO	Q9zbl5 streptomyce
298	6	1.1	264	1	COLI_MACNE	P01201 m corticotr	371	6	1.1	311	1	MAB2_MOUSE	O64277 mus musculu
299	6	1.1	264	1	COMT_RAT	P22734 rattus norv	372	6	1.1	311	1	MAB2_STRPN	Q97rx3 s peptide m
300	6	1.1	264	1	PUR7_RHIL0	Q98hm8 rhizobium l	373	6	1.1	312	1	CAH4_BOVIN	O95323 bos taurus
301	6	1.1	265	1	CB23_PEA	P27520 pisum sativ	374	6	1.1	312	1	CELF_PRYVA	O85230 pseudorabie
302	6	1.1	265	1	COLI_BOVIN	P01190 b corticotr	375	6	1.1	312	1	TRAD_HUMAN	O15628 homo sapien
303	6	1.1	265	1	CYSH_RHIME	P56891 rhizobium m	376	6	1.1	313	1	YEIC_ECOLI	P30235 escherichia
304	6	1.1	265	1	KXHI_CANGA	O74684 candida gla	377	6	1.1	314	1	TEST_HUMAN	Q9y6m0 homo sapien
305	6	1.1	265	1	Y108_ARCFU	O30128 archaeglob	378	6	1.1	315	1	KERS_BACCL	P42816 bacillus ca
306	6	1.1	266	1	IT2A_SULSO	Q97279 sulfolobus	379	6	1.1	315	1	PERI_HORVU	P27337 hordeum vul
307	6	1.1	266	1	YC41_HAEIN	P44133 haemophilus	380	6	1.1	317	1	CYF_CHLRE	P23577 chlamydomon
308	6	1.1	267	1	COLI_HUMAN	P01189 h corticotr	381	6	1.1	318	1	BSTI_HUMAN	O10588 homo sapien
309	6	1.1	267	1	PRR2_BOVIN	P12401 bos taurus	382	6	1.1	319	1	BSTI_RAT	Q63072 rattus norv
310	6	1.1	267	1	YGR4_CAEEL	Q09952 caenorhabdi	383	6	1.1	319	1	O7A5_HUMAN	Q15622 homo sapien
311	6	1.1	268	1	KXHI_YEAST	P50112 saccharomyc	384	6	1.1	319	1	Y597_CAEEL	Q09966 caenorhabdi
312	6	1.1	269	1	LEB4_SYNY3	P76640 synchocyst	385	6	1.1	320	1	KITH_PRYVA	P27363 pseudorabie
313	6	1.1	269	1	VG69_BPMD2	O64262 mycobacteri	386	6	1.1	320	1	Y098_NPVAC	P47465 autographa
314	6	1.1	270	1	PNK1_UREPA	Q9pqw6 ureaplasma	387	6	1.1	321	1	RLPA_SYNY3	O55755 synchocyst
315	6	1.1	270	1	PYRD_THEMA	O9yvg8 thermotoga	388	6	1.1	322	1	PIV_MORO	P00666 moraxella b
316	6	1.1	270	1	REP8_HUMAN	O00124 homo sapien	389	6	1.1	322	1	PIV_MORA	P19251 moraxella l
317	6	1.1	272	1	R1Z2_ECOLI	P03387 escherichia	390	6	1.1	323	1	COBD_AERPE	Q9yaa0 aeropyrum p
318	6	1.1	273	1	GRF4_RAT	Q9ep12 rattus norv	391	6	1.1	323	1	LIPA_BUCAI	P57357 buchnera ap
319	6	1.1	274	1	GSHO_HUMAN	P48507 homo sapien	392	6	1.1	323	1	Y0C5_MYCLE	O69538 mycobacteri
320	6	1.1	274	1	GSHO_MOUSE	O09172 mus musculu	393	6	1.1	324	1	PHT2_PSEPU	O05182 pseudomonas
321	6	1.1	274	1	YKXZ_CAEEL	P34324 caenorhabdi	394	6	1.1	325	1	IRF1_HUMAN	P16594 rana catesb
322	6	1.1	275	1	NRTB_SYNY3	P73451 synchocyst	395	6	1.1	325	1	NIUM_RANCA	O03376 glycine max
323	6	1.1	275	1	Y5S1_METYA	Q57971 methanococc	396	6	1.1	326	1	KOX3_SOYBN	Q9zbt3 rickettsia
324	6	1.1	278	1	UPK2_AGR75	P58741 agrobacteri	397	6	1.1	326	1	ODPB_RICPR	Q8xbct escherichia
325	6	1.1	278	1	YNPI_CAEEL	Q99q60 caenorhabdi	398	6	1.1	327	1	DCYD_ECOS7	

399	1.1	327	1	DCYD_BCOL6	P59329 escherichia	472	1.1	372	1	GDF1_HUMAN	P27539 homo sapien
400	1.1	327	1	DCYD_ECOL1	P76316 escherichia	473	1.1	372	1	LIG6_PHACH	P06622 panerochae
401	1.1	327	1	DCYD_SALT1	O85589 salmonella	474	1.1	375	1	RAPE_BACSU	P45943 bacillus su
402	1.1	327	1	DCYD_SALT1	O85287 salmonella	475	1.1	375	1	YCDO_ECOL1	P75902 escherichia
403	1.1	327	1	DCYD_SHIFL	P59330 shigella fl	476	1.1	376	1	AROC_ECOLI	O9wy12 thermotoga
404	1.1	327	1	RPOA_UREPA	O9pqn4 ureaplasma	477	1.1	376	1	GBAS_LYMTS	P30684 lymnaea sca
405	1.1	327	1	Y8A6_ARCFU	O28826 archaeoglob	478	1.1	377	1	Y392_CHLTR	P64627 chlamydia t
406	1.1	327	1	IRP1_RAT	P23570 rattus norv	479	1.1	378	1	CARA_RALSO	O8x288 ralestonia s
407	1.1	329	1	HEM1_FUSNN	O85687 fusobacteri	480	1.1	378	1	CYB_ELEMA	O47885 elephas max
408	1.1	329	1	IRP1_MOUSE	P15314 mus musculu	481	1.1	378	1	CYB_LOXAP	P24958 loxodonta a
409	1.1	330	1	DCYD_YERPE	O8x713 yerishia pe	482	1.1	378	1	CYB_WAMPR	P22658 mammutus p
410	1.1	330	1	PGIP_PYRGO	O05091 pyrus commu	483	1.1	378	1	RAPA_BACSU	P00828 bacillus su
411	1.1	331	1	LDHD_LEUMC	P51011 leuconostoc	484	1.1	378	1	SLGI_YEAST	O54803 mus musculu
412	1.1	333	1	CDIC_HUMAN	P29017 homo sapien	485	1.1	379	1	P2X6_MOUSE	P1579 rattus norv
413	1.1	333	1	STAC_HUMAN	O11206 h cmp-n-ace	486	1.1	379	1	P2X6_RAT	P1579 rattus norv
414	1.1	336	1	VG27_BPM2	O64221 mycobacteri	487	1.1	380	1	CAIA_ECOLI	O8gb20 proteus gp.
415	1.1	336	1	VG27_BPM2	O05534 mycobacteri	488	1.1	380	1	CAIA_PROSL	O82912 salmonella
416	1.1	336	1	YDPR_ECOL1	P77308 escherichia	489	1.1	380	1	CAIA_SALT1	O82912 salmonella
417	1.1	344	1	DCUP_BACHD	O9kd10 bacillus ha	490	1.1	380	1	CAIA_SALT1	O82912 salmonella
418	1.1	344	1	DFPB_MOUSE	O54788 mus musculu	491	1.1	380	1	CYB_VERRU	O82912 salmonella
419	1.1	344	1	RL3_AERPE	O9yfm2 aeropyrum p	492	1.1	381	1	CYB_PARP	O82912 salmonella
420	1.1	344	1	SP12_VARV	P33830 variola vir	493	1.1	382	1	NUSA_BACHD	O35377 parantechin
421	1.1	345	1	GAG1_HUMAN	P54826 homo sapien	494	1.1	384	1	GALI_ACTPL	O9ka74 bacillus ha
422	1.1	345	1	HIOM_BOVIN	P10950 bos taurus	495	1.1	384	1	GALI_HABIN	P34169 actinobacil
423	1.1	345	1	RECA_AQUAE	O67905 aquifex aeo	496	1.1	385	1	TPST_DROME	O9yvb7 haemophilus
424	1.1	345	1	SP12_RABPU	P42926 rabdipox v	497	1.1	386	1	LMPI_EBV	O9yvb7 haemophilus
425	1.1	346	1	NRU1_ARATH	P32861 arabidopsis	498	1.1	386	1	LMPI_EBV	O9yvb7 haemophilus
426	1.1	346	1	YR24_CAEEL	O09341 caenorhabdi	499	1.1	387	1	DADR_MOUSE	P31398 epstein-bar
427	1.1	348	1	FEN_METKA	O8rxu4 methanopyru	500	1.1	387	1	DADR_MOUSE	P31398 epstein-bar
428	1.1	348	1	RECA_AQUAP	P33542 aquifex pyr	501	1.1	387	1	RU3A_SCHPO	P10729 rattus norv
429	1.1	348	1	Y567_HELPY	O25291 hellicobacte	502	1.1	387	1	RU3A_SCHPO	P40372 schizosacch
430	1.1	348	1	Y735_STRFR	P20186 streptococce	503	1.1	387	1	SCGA_RABIT	P26584 schizosacch
431	1.1	349	1	AOX1_SAUUG	P22185 sauromatum	504	1.1	387	1	GALI_LACHE	O8686 oryctolagus
432	1.1	349	1	CTGF_BOVIN	O18739 bos taurus	505	1.1	388	1	GALI_STRTR	O59043 methanococ
433	1.1	349	1	CTGF_PIG	O19113 sus scrofa	506	1.1	388	1	GALI_STRTR	O00052 lactobacill
434	1.1	350	1	Y567_HELPY	O9z1r4 hellicobacte	507	1.1	389	1	GALI_CLOAB	O92b10 streptococ
435	1.1	350	1	ACCO_PESH	P32021 pseudomonas	508	1.1	389	1	RU3B_ARATH	O92b10 streptococ
436	1.1	350	1	HYPE_RHIV	P40599 rhizobium l	509	1.1	389	1	YD22_DEIRA	O92b10 streptococ
437	1.1	350	1	PL6_MOUSE	O9wuh1 mus musculu	510	1.1	390	1	SH1B_RABIT	P49144 oryctolagus
438	1.1	351	1	IBHC_RAT	O9wuh1 mus musculu	511	1.1	390	1	GALI_STRMU	P96993 streptococ
439	1.1	351	1	IBHC_RAT	O9wuh1 mus musculu	512	1.1	390	1	YV18_SCHPO	O09895 echizosacch
440	1.1	351	1	PL6_HUMAN	O12893 homo sapien	513	1.1	390	1	YV18_SCHPO	O28406 archaeoglob
441	1.1	352	1	PLNC_PENCI	P47189 penicillium	514	1.1	391	1	TRBL_RHISN	O54402 rhizobium s
442	1.1	352	1	IBHC_MOUSE	P55104 mus musculu	515	1.1	391	1	CARA_THEMEA	O9w242 thermotoga
443	1.1	353	1	R8S1_ARATH	O9e808 arabidopsis	516	1.1	392	1	HISZ_LISMO	O8y9f9 listeria mo
444	1.1	353	1	EDG7_HUMAN	O9ubys homo sapien	517	1.1	393	1	SETB_ECOLI	P33026 escherichia
445	1.1	354	1	EDG7_MOUSE	O9eg31 mus musculu	518	1.1	393	1	SETB_SALT1	P33027 salmonella
446	1.1	354	1	OTC_HUMAN	O8K560 rattus norv	519	1.1	396	1	CATE_HUMAN	P14091 homo sapien
447	1.1	354	1	YCDH_BACSU	P00480 homo sapien	520	1.1	396	1	DH11_XENIA	O91610 xenopus lae
448	1.1	354	1	MLTC_HAEIN	O34538 bacillus su	521	1.1	396	1	PAS_XENIA	P31233 xenopus lae
449	1.1	357	1	MCAL_CRIGR	P44049 haemophilus	522	1.1	396	1	S1BL_HUMAN	O75177 homo sapien
450	1.1	357	1	FIXB_AZOVI	O54873 cricetulus	523	1.1	398	1	CATE_RAT	P16228 rattus norv
451	1.1	360	1	MTSB_IACLC	P53574 azobacter	524	1.1	398	1	DH12_XENIA	O91611 xenopus lae
452	1.1	360	1	Y503_CAEEL	P34878 lactococcus	525	1.1	398	1	GGST_PYRAB	O9uzp8 pyrococcus
453	1.1	361	1	SERC_WIGBR	O09358 caenorhabdi	526	1.1	399	1	TRMU_AGRYS	O8u9m5 agrobacteri
454	1.1	362	1	ALBU_HORVU	O8d68 wigglewort	527	1.1	399	1	CHS2_HORVU	O96562 hordaeum vul
455	1.1	362	1	LEU3_PICAN	P05167 hordaeum vul	528	1.1	399	1	CR05_MOUSE	O9y966 mus musculu
456	1.1	362	1	YE11_ECOLI	P34733 pichia angu	529	1.1	399	1	FRSW_BUCHI	P53132 buchnera ap
457	1.1	362	1	YLU3_CAEEL	P33020 escherichia	530	1.1	399	1	Y111_STRCL	O9y966 mus musculu
458	1.1	363	1	GALI_MYCTV	P96610 mycobacteri	531	1.1	400	1	CYH2_MOUSE	O99414 mus musculu
459	1.1	364	1	VM21_BORHE	P21875 borrelia he	532	1.1	400	1	CH2_MOUSE	P97695 mus musculu
460	1.1	365	1	P43_XENBO	P25066 xenopus bor	533	1.1	400	1	PKRY_TOBAC	P10667 xenopus lae
461	1.1	365	1	P43_XENIA	P25066 xenopus bor	534	1.1	401	1	PKRY_WHEAT	O42962 nicotiana t
462	1.1	365	1	VSX1_BOVIN	O9gma3 bos taurus	535	1.1	401	1	PKRY_WHEAT	P12783 triticum ae
463	1.1	366	1	BCPA_PROAB	P11741 prosthecoc	536	1.1	402	1	KLFC_MOUSE	O94344 mus sapien
464	1.1	368	1	CHEB_PYRAB	O9uyf3 pyrococcus	537	1.1	402	1	OXAI_YEAST	O35778 mus musculu
465	1.1	368	1	ID12_SUITSO	P95997 sulfolobus	538	1.1	402	1	ARGD_VIBVU	P33952 saccharomyc
466	1.1	368	1	YBX5_SCHPO	O10203 schizosacch	539	1.1	403	1	THII_LISIN	P59323 saccharomyc
467	1.1	368	1	YBX5_SCHPO	O10203 schizosacch	540	1.1	403	1	THII_LISIN	O92b66 listeria in
468	1.1	369	1	RADA_CERST	O93748 cenarchaeum	541	1.1	404	1	LMPI_EBVC	P29362 epstein-bar
469	1.1	370	1	YG26_YEAST	P53249 saccharomyc	542	1.1	404	1	OK1_HUMAN	P51810 homo sapien
470	1.1	371	1	NU1M_NEUCR	P08774 neurospora	543	1.1	405	1	AK_HELPY	O9zjz7 hellicobacte
471	1.1	371	1	TGT_NE1MB	O9K096 neisseria m	544	1.1	405	1	AK_HELPY	O25827 hellicobacte

545	6	1.1	405	1	OA1_MOUSE	P70259	mus musculus	618	6	1.1	461	1	YCUJ_ECOLI	P76037	escherichia
546	6	1.1	405	1	S3AE_BACSU	P49782	bacillus su	619	6	1.1	462	1	GIPR_MESAU	P43128	mesocricetu
547	6	1.1	408	1	ARGD_XANAC	O9h31	xanthomonas	620	6	1.1	462	1	PO22_MOUSE	O30196	mus musculus
548	6	1.1	408	1	ARGD_XANCP	O85q4	xanthomonas	621	6	1.1	462	1	SELA_YERPE	O82971	yersinia pe
549	6	1.1	410	1	ARPI_MOUSE	P70295	mus musculus	622	6	1.1	462	1	TPH4_HUMAN	O92759	homo sapien
550	6	1.1	411	1	ARGD_XYLFA	O9p4f2	xyella fas	623	6	1.1	463	1	TFH4_MOUSE	O70422	mus musculus
551	6	1.1	411	1	NORB_HAEIN	O05011	haemophilus	624	6	1.1	464	1	SRPX_RAT	O63769	rattus norv
552	6	1.1	411	1	PGK_METTH	O27121	metanobact	625	6	1.1	466	1	ANX7_HUMAN	P20073	homo sapien
553	6	1.1	414	1	CUTS_STRCO	O03757	streptomyce	626	6	1.1	466	1	GIPR_HUMAN	P48546	homo sapien
554	6	1.1	416	1	CHRA_PSEAB	P14285	pseudomonas	627	6	1.1	466	1	IMP2_DROME	P28605	synecococc
555	6	1.1	417	1	PKGB_LEIME	O27684	leishmania	628	6	1.1	467	1	D4DR_HUMAN	P21917	homo sapien
556	6	1.1	417	1	TKNS_MOUSE	O91w90	mus musculus	629	6	1.1	468	1	FIIB_BOVIN	P02676	bos taurus
557	6	1.1	418	1	CINA_STRPN	P51184	streptococc	630	6	1.1	468	1	MURD_XANCP	O9b775	xanthomonas
558	6	1.1	418	1	Y285_HELPY	O9mf0	helicobacte	631	6	1.1	469	1	MURD_XYLFA	O9p403	xyella fas
559	6	1.1	418	1	Y285_HELPY	P56130	helicobacte	632	6	1.1	469	1	NORM_XYLFA	O9p334	xyella fas
560	6	1.1	419	1	AROA_METTH	O26860	metanobact	633	6	1.1	470	1	CEBK_MOUSE	O63397	mus musculus
561	6	1.1	419	1	CHSD_PETRY	P22925	petunia hyb	634	6	1.1	470	1	KNIF_XENLA	P35617	xenopus lae
562	6	1.1	419	1	KDAP_MOUSE	O09043	mus musculus	635	6	1.1	471	1	HYDA_BACST	O45515	baecillus st
563	6	1.1	420	1	YHAP_BACSU	O07523	bacillus su	636	6	1.1	471	1	NORM_CAUCR	P28163	caulobacter
564	6	1.1	420	1	ALAU_HUMAN	P20848	homo sapien	637	6	1.1	472	1	VTDB_MOUSE	P21614	mus musculus
565	6	1.1	421	1	SHT2_APLCA	O16951	aplysia cal	638	6	1.1	473	1	GLNA_SYNP2	P28605	synecococc
566	6	1.1	421	1	CCG8_RAT	O8wh5	rattus norv	639	6	1.1	473	1	PHDK_MOCSK	O24723	nocardioid
567	6	1.1	421	1	HNDH_AERPE	O9a84	aetopyrum p	640	6	1.1	474	1	Y068_MYCCE	P47314	mycoplasma
568	6	1.1	423	1	CCG8_MOUSE	O8vhw2	mus musculus	641	6	1.1	476	1	VTDB_RAT	P04276	rattus norv
569	6	1.1	423	1	GATM_MOUSE	O9a964	mus musculus	642	6	1.1	477	1	XYNA_STRLI	P26514	streptomyce
570	6	1.1	423	1	GATM_RAT	P50442	rattus norv	643	6	1.1	478	1	PGKH_ARATH	P50318	arabidopsis
571	6	1.1	423	1	NSMA_HUMAN	O60906	homo sapien	644	6	1.1	478	1	PO22_HUMAN	P09086	homo sapien
572	6	1.1	424	1	ZP3_GALSO	P53786	callithrix	645	6	1.1	478	1	PO22_PIG	O29013	sus scrofa
573	6	1.1	425	1	CCG8_HUMAN	O8vxs	homo sapien	646	6	1.1	479	1	CBSA_SUISO	P56029	sulfolobus
574	6	1.1	425	1	ESC_DROME	O24338	drosophila	647	6	1.1	479	1	PKGC_LEIME	O27685	leishmania
575	6	1.1	425	1	SECY_ODOSI	P49461	odonteila s	648	6	1.1	480	1	HOGT_ARATH	O9n156	arabidopsis
576	6	1.1	425	1	YTR1_EBV	P30119	epstein-bar	649	6	1.1	480	1	YNAO_BACSU	P37536	bacillus su
577	6	1.1	426	1	APEB_MYCLE	O50022	mycobacteri	650	6	1.1	481	1	PGKH_TOBAC	O42961	nicotiana t
578	6	1.1	428	1	SVH_BUCAP	O8k9p3	buchnera ap	651	6	1.1	483	1	BIAR_MELGA	P07700	mellegria g
579	6	1.1	430	1	DRP1_RHIME	O9qgm8	rhizobium m	652	6	1.1	485	1	ZDH1_HUMAN	O8vtx9	homo sapien
580	6	1.1	431	1	ACRO_RABIT	P48038	oryctolagus	653	6	1.1	485	1	ZDH1_MOUSE	O870n9	mus musculus
581	6	1.1	431	1	HIX1_ANASP	O8vms8	anabaena sp	654	6	1.1	487	1	SECY_HALMA	P28542	haloarcula
582	6	1.1	431	1	MEVF_PASMU	O9cp15	pasteurella	655	6	1.1	488	1	SECY_HALVO	O97773	halobacteri
583	6	1.1	431	1	NOOE_THERM	O56229	thermus the	656	6	1.1	491	1	CPBI_RAT	P00176	rattus norv
584	6	1.1	431	1	KXP6_HUMAN	O15547	homo sapien	657	6	1.1	491	1	CPB2_RAT	P04167	rattus norv
585	6	1.1	432	1	KOTP_ECOLI	P17448	escherichia	658	6	1.1	492	1	DBP2_HUMAN	O9uh14	homo sapien
586	6	1.1	432	1	ORC4_XENLA	O93479	xenopus lae	659	6	1.1	493	1	FBL3_HUMAN	O12805	homo sapien
587	6	1.1	433	1	GP22_HUMAN	O99680	homo sapien	660	6	1.1	493	1	FBL3_RAT	O35568	rattus norv
588	6	1.1	433	1	PGKH_SPIOL	P29409	epinacia ol	661	6	1.1	494	1	CPBB_CANFA	P24460	canis famli
589	6	1.1	436	1	UL32_HSVSA	O01040	herpesviru	662	6	1.1	494	1	EXOT_RHIME	P33699	rhizobium m
590	6	1.1	443	1	CAR4_DICDI	O9vxs3	dictyostei	663	6	1.1	495	1	DHAL_ECOLI	P23883	escherichia
591	6	1.1	443	1	HXA3_MOUSE	P02831	mus musculus	664	6	1.1	495	1	YBFI_YEAST	P36622	saeccharomyc
592	6	1.1	446	1	YD85_PYRHO	O50093	pyrococcus	665	6	1.1	496	1	GALI_ARATH	O9e65	arabidopsis
593	6	1.1	447	1	YPEB_BACHD	O9vcm8	bacillus ha	666	6	1.1	496	1	GLK2_THEMA	O9x1e4	thermotoga
594	6	1.1	448	1	YAP1_CHICK	P46936	gallus gall	667	6	1.1	496	1	GLPK_THERO	O9vxs3	thermus agu
595	6	1.1	449	1	C13A_MYCTU	O08447	mycobacteri	668	6	1.1	496	1	GLPK_THERT	O66131	thermus the
596	6	1.1	449	1	COMB_STRPN	P36498	streptococc	669	6	1.1	497	1	SGK3_MOUSE	O9vcm8	mus musculus
597	6	1.1	449	1	COMB_STRPN	P36498	streptococc	670	6	1.1	497	1	GLPK_BACHD	O9vcm8	mus musculus
598	6	1.1	450	1	GNUT_PSEAB	P59654	streptococc	671	6	1.1	497	1	GLPK_FUSIN	O8vtx9	homo sapien
599	6	1.1	451	1	GPID_CHLMU	O9z1j1	pseudomonas	672	6	1.1	497	1	GLPK_LISIN	O8vtx9	homo sapien
600	6	1.1	452	1	NORM_BACSU	O46437	chlamydia m	673	6	1.1	497	1	GLPK_LISIN	O9b622	listeria mo
601	6	1.1	453	1	SHT1_APLCA	O31855	bacillus su	674	6	1.1	497	1	GLPK_THETN	O9x1e4	thermanaer
602	6	1.1	453	1	ALN_ECOLI	O16950	aplysia cal	675	6	1.1	498	1	GLPK_CLOB	O9j194	clostridium
603	6	1.1	454	1	IMDH_PNECA	O12658	pneumocysti	676	6	1.1	498	1	GLPK_LACTA	O9vcm8	lactococcus
604	6	1.1	454	1	TNNA_CHLTR	O84300	chlamydia t	677	6	1.1	498	1	GLPK_STAM	O9vcm8	staphylococ
605	6	1.1	454	1	TNNA_HROCA	O30971	rhodobacter	678	6	1.1	498	1	GLPK_STAM	O8vtx9	homo sapien
606	6	1.1	455	1	AROA_AGRSP	O9vcm8	agrobacteri	679	6	1.1	499	1	GLCD_ECOLI	P52075	escherichia
607	6	1.1	455	1	AROA_RHIME	O9vcm8	rhizobium m	680	6	1.1	500	1	CPBA_MOUSE	P12791	mus musculus
608	6	1.1	455	1	GIPR_RAT	P43219	rattus norv	681	6	1.1	500	1	GLPK_ANASP	O8vcm8	anabaena sp
609	6	1.1	455	1	PHR_STRGR	P12768	streptomyce	682	6	1.1	500	1	GLPK_CLOPE	O8vcm8	clostridium
610	6	1.1	456	1	YMS8_ANASP	O52750	anabaena sp	683	6	1.1	500	1	GLPK_ENTFA	O34154	enterococcu
611	6	1.1	457	1	MMBI_METAC	P58865	methanosarc	684	6	1.1	500	1	GLPK_SALTI	O8vcm8	salmonella
612	6	1.1	458	1	BFJA_ASHGO	P41752	asbhyia goe	685	6	1.1	500	1	PCLI_ARATH	O8vcm8	arabidopsis
613	6	1.1	458	1	BFJA_YEAST	P02994	saccharomyc	686	6	1.1	501	1	GLPK_DEIRA	O9vcm8	deinococcus
614	6	1.1	458	1	GL2_HUMAN	O01451	homo sapien	687	6	1.1	501	1	GLPK_ECOLI	O9vcm8	escherichia
615	6	1.1	460	1	BNV_HV123	P12491	human immun	688	6	1.1	501	1	GLPK_SALTY	O8vcm8	salmonella
616	6	1.1	461	1	CSBC_BACSU	P46333	bacillus su	689	6	1.1	501	1	KEPL_DROME	O05652	drosophila
617	6	1.1	461	1	SILC_SALTY	O9zhd2	salmonella	690	6	1.1	501	1	YN57_CORGL	P46584	corynebacte

691	1.1	502	1	66P1_XYLRP	O99r6 xyella fas	764	552	1	K2C6 MOUSE	P5046 mus musculus
692	1.1	502	1	G6P1_XYLRP	O87av7 xyella fas	765	554	1	G6P1_PSEPK	O881w9 pseudomonas
693	1.1	503	1	YE10_YEAST	P39941 saccharomyc	766	554	1	G6P2_PSEPK	O88d7 pseudomonas
694	1.1	502	1	PUR8_STRLP	P42670 streptomyce	767	554	1	G6P1_PSSSM	O888q7 pseudomonas
695	1.1	504	1	C341_MOUSE	O9jma7 mus musculu	768	557	1	G6P1_MOUSE	P68745 mus musculus
696	1.1	504	1	YBLH_SCHPO	O10341 schizosacch	769	557	1	G6P1_PIG	P68059 sus scrofa
697	1.1	505	1	GLPK_ENTCA	O34153 entrococcc	770	557	1	MCP5_ENTAE	P21822 enterobacte
698	1.1	505	1	GLPK_VIBCH	O9k1j9 vibrio chol	771	558	1	G6P1_CRIGR	P50309 citreulbac
699	1.1	505	1	GLPK_VIBPA	O87n72 vibrio para	772	558	1	G6P1_HUMAN	P66744 homo sapien
700	1.1	505	1	GLPK_VIBVU	O88dm6 vibrio vuln	773	560	1	M4C2_ANASP	O8ym6 anabena sp
701	1.1	505	1	ICAI_PANTR	O28806 pan troglod	774	562	1	ATKA_ALIAC	OQxell1 alyciobac
702	1.1	505	1	KIR3_RAT	P80203 rattus norv	775	564	1	ATKA_PSEAE	P57683 pseudomonas
703	1.1	507	1	GLPK_MYCPU	O98cy9 mycoplasma	776	565	1	DEAF_HUMAN	O75398 homo sapien
704	1.1	507	1	NRRP_WOLSU	O9a1e5 wolfinella s	777	565	1	DEAF_PANTR	O77562 pan troglod
705	1.1	508	1	CPT7_CHICK	P12394 gallus gall	778	565	1	DEAF_RAT	O88450 rattus norv
706	1.1	508	1	GLPK_MYCLE	O9c8b1 mycobacteri	779	565	1	VPDA_ECOLI	P76523 escherichia
707	1.1	508	1	GLPK_STRP3	O8K65 streptococc	780	566	1	DEAF_MOUSE	O921e5 mus musculu
708	1.1	508	1	GLPK_STRP8	O8nw9 streptococc	781	566	1	MBHM_ECOLI	P37181 escherichia
709	1.1	508	1	GLPK_STRPY	O99y17 streptococc	782	567	1	CYDC_BACSU	P34366 bacillus su
710	1.1	509	1	PA23_HUMAN	O9m220 homo sapien	783	567	1	GSPE_XANCP	P31742 xanthomonas
711	1.1	510	1	GLPK_HALNT	O9hms halobacteri	784	568	1	VE1G_SCHPO	O33880 schizosacch
712	1.1	510	1	IAI_HUMAN	O01101 homo sapien	785	568	1	VE54_YEAST	P53309 saccharomyc
713	1.1	512	1	AWY1_DEBOC	P19269 debaryomyce	786	569	1	AAKH_HUMAN	O9ug10 homo sapien
714	1.1	512	1	G6PD_CHLPN	O928u6 chlamydia p	787	570	1	LKH1_SCHPO	O9j170 mus musculu
715	1.1	512	1	GLK1_STRCO	O9ada7 streptomyce	788	575	1	NRKS_MOUSE	O30156 schizosacch
716	1.1	512	1	LNT_ECOLI	P23330 escherichia	789	577	1	YG5U_YEAST	P53333 saccharomyc
717	1.1	512	1	LNT_SALTY	O87576 salmonella	790	579	1	YD49_MYCTU	O11019 mycobacteri
718	1.1	513	1	PDI_HORVU	P80284 hordium vul	791	580	1	SWTD_BOOMI	P53307 boophilus m
719	1.1	513	1	PDI_MALZE	P52588 zea mays (m	792	581	1	Z319_MOUSE	O9ert8 mus musculu
720	1.1	513	1	VL1_HPV48	P50817 human papil	793	582	1	ATKA_HALNT	P57684 halobacteri
721	1.1	515	1	PDI_WHEAT	P52589 triticum ae	794	582	1	Z319_HUMAN	O9p219 homo sapien
722	1.1	515	1	TLC1_CHLPN	O928j2 chlamydia p	795	585	1	RS01_LEPIN	P59117 leptospira
723	1.1	516	1	RS93_CHLRE	P12759 chlamydomo	796	586	1	YH09_YEAST	P38818 saccharomyc
724	1.1	516	1	Y107_YEAST	P40492 saccharomyc	797	586	1	HO_YEAST	P09932 saccharomyc
725	1.1	520	1	GLPK_MYCTU	O69644 mycobacteri	798	587	1	STD_STREN	O97nd6 streptococc
726	1.1	520	1	APH2_YEAST	P38207 saccharomyc	799	588	1	ATY1_MOUSE	O9ct9c mus musculu
727	1.1	520	1	PHO_DROME	O8e83 drosophila	800	590	1	OAM_ASCSU	O01456 acacaris suu
728	1.1	521	1	SVW_UREPA	O9pcu6 ureaplasma	801	591	1	DS01_PSEAE	O9nuw5 pseudomonas
729	1.1	521	1	Z286_HUMAN	O9huc8 homo sapien	802	591	1	FLGE_CAUCR	P35806 caulobacter
730	1.1	523	1	MP11_HUMAN	P30304 homo sapien	803	591	1	PAXI_HUMAN	P49023 homo sapien
731	1.1	524	1	HUTH_DEIRA	O9r206 deinococcus	804	592	1	ABP1_YEAST	P15891 saccharomyc
732	1.1	524	1	PP8T_BOVIN	P09487 bos taurus	805	593	1	PRTR_HUMAN	O03431 homo sapien
733	1.1	527	1	GALI_YEAST	P04855 saccharomyc	806	597	1	Y267_ARCPV	O29972 archaeoglyb
734	1.1	527	1	RBR1_CANAL	O00312 candida alb	807	598	1	TREZ_ARTSO	O8rv06 methanopyru
735	1.1	528	1	ICAI_CANPA	P33729 canis famli	808	598	1	MCD2_HUMAN	O44316 arthroacte
736	1.1	528	1	TLC1_CHLTR	O84068 chlamydia t	809	606	1	DNAK_LACIA	O9unf1 homo sapien
737	1.1	529	1	VL1_HPV34	P36738 human papil	810	607	1	DPOL_BPM02	P43368 lactococcus
738	1.1	529	1	TLC1_CHLMU	O9pkx5 chlamydia m	811	612	1	BIR2_MOUSE	O64235 mycobacteri
739	1.1	536	1	Y632_CHLTR	O84637 chlamydia t	812	612	1	YVW8_YEAST	O62210 mus musculu
740	1.1	530	1	Y921_CHLMU	O99b1 chlamydia m	813	613	1	ADAS_TRYAB	O03153 saccharomyc
741	1.1	530	1	YA9A_SCHPO	O09788 schizosacch	814	613	1	DEAD_HAEIN	O97157 trypanosoma
742	1.1	531	1	CHUB_NEPOL	O9t467 neptroleini	815	613	1	DNAD_PROAC	P44586 haemophilus
743	1.1	531	1	P111_MOUSE	O8i526 mus musculu	816	617	1	DP2S_PYRAB	O91791 proionibac
744	1.1	532	1	ACMS_MACMU	P56490 macaca mula	817	619	1	PM17_MOUSE	O92123 pyrococcus
745	1.1	532	1	EXU_DROME	P28750 drosophila	818	626	1	GIDA_AGR05	O66096 mus musculu
746	1.1	532	1	PPCK_ANASU	O09460 anaerobiop	819	627	1	KLH8_MOUSE	O8bm90 agrobacteri
747	1.1	532	1	YH87_YEAST	P38745 saccharomyc	820	629	1	RA21_XENLA	P59280 mus musculu
748	1.1	535	1	ICAI_BOVIN	O95132 bos tauru	821	629	1	FRSH_GUTHA	O93310 xenopus lae
749	1.1	535	1	PPCK_BACTN	O8a414 bacteroides	822	631	1	TAC3_MOUSE	O78516 guillardia
750	1.1	536	1	ARP_ARATH	P45951 arabidopsia	823	631	1	NIOL_MYCTU	O97111 mus musculu
751	1.1	536	1	YENT_SCHPO	O13695 schizosacch	824	633	1	SE69_BOVIN	O86330 mus musculu
752	1.1	537	1	AREH_SCHPO	O10269 schizosacch	825	633	1	SE6A_MOUSE	P28571 mus musculu
753	1.1	539	1	PCOB_HUMAN	P05166 homo sapien	826	633	1	SE6A_MOUSE	P28572 rattus norv
754	1.1	539	1	PCOB_PIG	P79384 sus scrofa	827	637	1	TETO_CAMBE	P10952 campylobact
755	1.1	540	1	TLC2_CHLTR	O84502 caenorhabd	828	638	1	PD41_LYNST	O77408 lymanaea sta
756	1.1	540	1	YTDC_CAEEL	P07633 rattus norv	829	638	1	PD41_LYNST	P08003 mus musculu
757	1.1	541	1	PCOB_RAT	O9p133 rattus norv	830	639	1	SE69_BOVIN	O28039 bos tauru
758	1.1	543	1	TLC2_CHLMU	O9p136 chlamydia m	831	639	1	TETO_CAMCO	P23835 campylobact
759	1.1	545	1	ICAI_RAT	O00238 rattus norv	832	639	1	TETO_STRPN	P20174 streptococc
760	1.1	547	1	USPA_AERHY	P45754 aeromonas h	833	643	1	PRIM_MYCLE	P75753 streptococc
761	1.1	550	1	USHA_SALPU	O9r137 salmonella	834	643	1	PD44_RAT	O9ccg2 mycobacteri
762	1.1	551	1	PODX_RABIT	O28645 oryctolagus	835	643	1	SL55_HUMAN	P38659 rattus norv
763	1.1	551	1	Y275_HAEIN	P43375 haemophilus	836	643	1	SL55_HUMAN	O92911 homo sapien

837	6	1.1	647	1	MAOC_FLAPR	P36444	flaveria pr	910	6	1.1	725	1	SP3_MOUSE	O70494	mus musculus
838	6	1.1	649	1	VE1_HPV6A	Q84293	human papil	911	6	1.1	727	1	BRCl_DROME	Q01295	drosophila
839	6	1.1	651	1	Q9NVC6	h cofactor	Q9NVC6	912	6	1.1	730	1	MMO1_MOUSE	P41245	mus musculus
840	6	1.1	652	1	PAB1_DROME	P10674	drosophila	913	6	1.1	736	1	PRX1_CHICK	Q91018	gallus gall
841	6	1.1	652	1	GR78_CHICK	Q90593	gallus gall	914	6	1.1	736	1	PRX1_HUMAN	Q92766	homo sapien
842	6	1.1	653	1	PRP1_HUMAN	Q14829	homo sapien	915	6	1.1	737	1	PRX1_MOUSE	P48437	mus musculus
843	6	1.1	654	1	HS10_HYDRA	Q05944	hydra magni	916	6	1.1	739	1	AD18_HUMAN	Q9Y397	homo sapien
844	6	1.1	654	1	PSTA_MYCGE	P47651	mycoplasma	917	6	1.1	741	1	CUL5_CAEEL	Q33639	caenorhabdi
845	6	1.1	656	1	ACSA_RHOCA	Q68040	rhodobacter	918	6	1.1	742	1	ZFA_MOUSE	P34607	mus musculus
846	6	1.1	656	1	PER_DROSI	Q03355	drosophila	919	6	1.1	743	1	ANAG_HUMAN	P54802	homo sapien
847	6	1.1	657	1	GRAD_TREPA	Q83062	treponema p	920	6	1.1	748	1	PA24_MOUSE	Q77733	mus musculus
848	6	1.1	659	1	NRPC_SYNP7	P38045	synecococc	921	6	1.1	749	1	PA24_HORSE	O77733	equus caball
849	6	1.1	660	1	PHUB_ECOLI	P08972	escherichia	922	6	1.1	749	1	PA24_HUMAN	P47712	homo sapien
850	6	1.1	661	1	PER_DROSE	Q03354	drosophila	923	6	1.1	752	1	DRS1_YEAST	P32892	saccharomyc
851	6	1.1	661	1	UAS3_HUMAN	P57075	homo sapien	924	6	1.1	752	1	PA24_RAT	P03391	rattus norv
852	6	1.1	662	1	GARP_HUMAN	Q14392	homo sapien	925	6	1.1	753	1	PPE2_HUMAN	Q04830	homo sapien
853	6	1.1	670	1	INVI_MAIZE	P49175	zea mays (m	926	6	1.1	754	1	PURL_MYCLE	O60023	homo sapien
854	6	1.1	670	1	PRCK_CUCSA	P42066	cucumis sat	927	6	1.1	754	1	PURL_MYCTU	P54876	mycobacteri
855	6	1.1	671	1	PRCK_ARATH	Q94074	arabidopsis	928	6	1.1	755	1	PPAX_CAEEL	Q9105	thermotoga
856	6	1.1	673	1	FLID_TREMA	Q94RW7	treponema m	929	6	1.1	757	1	MUS2_THEMEA	Q09549	caenorhabdi
857	6	1.1	673	1	YMS2_HUMAN	O60299	homo sapien	930	6	1.1	757	1	PPE2_MOUSE	O35385	mus musculus
858	6	1.1	673	1	YMS5_YEAST	P53918	saccharomyc	931	6	1.1	758	1	CLPA_ECOLI	P15716	escherichia
859	6	1.1	674	1	GLSK_RAT	P13264	rattus norv	932	6	1.1	759	1	HYPF_RALIV	P28155	rhizobium 1
860	6	1.1	675	1	YL10_VIBCH	Q94Q91	viديو chol	933	6	1.1	763	1	TSHR_BOVIN	Q27987	bos taurus
861	6	1.1	675	1	NUOG_RICER	Q94CF6	ricicetasia	934	6	1.1	764	1	TSHR_CANFA	P14763	canis famli
862	6	1.1	676	1	NUOG_RICCN	Q92992	ricicetasia	935	6	1.1	764	1	TSHR_HUMAN	P47750	homo sapien
863	6	1.1	676	1	PER_DROMA	Q03353	drosophila	936	6	1.1	764	1	TSHR_MOUSE	P47750	mus musculus
864	6	1.1	682	1	ATKB_XANAC	Q8PPC9	xanthomonas	937	6	1.1	767	1	TSHR_SHEEP	P66495	ovis aries
865	6	1.1	682	1	VG50_BPM15	Q05262	mycobacteri	938	6	1.1	767	1	ACBS_CHICK	P26196	gallus gall
866	6	1.1	683	1	CNG1_RAT	Q62927	r cgmip-gate	939	6	1.1	768	1	LEMS_MOUSE	Q01102	mus musculus
867	6	1.1	684	1	PMA_ARATH	P23974	m cgmip-gate	940	6	1.1	768	1	LEMS3_RAT	P818106	rattus norv
868	6	1.1	686	1	SYGB_FUSNN	Q94FV6	arabidopsis	941	6	1.1	768	1	SC23_YEAST	P51303	saccharomyc
869	6	1.1	686	1	SYGB_FUSNN	O84444	fuobacteri	942	6	1.1	769	1	TMEB_MOUSE	Q09268	mus musculus
870	6	1.1	687	1	CICK_RAT	O66393	rattus norv	943	6	1.1	771	1	XYKO_YEAST	Q02208	saccharomyc
871	6	1.1	692	1	SE69_HUMAN	P48067	homo sapien	944	6	1.1	772	1	EMAL_DROME	Q9VU13	drosophila
872	6	1.1	692	1	YFB3_YEAST	P43579	saccharomyc	945	6	1.1	772	1	PMIP_YEAST	P35999	saccharomyc
873	6	1.1	694	1	PRK_CAMCO	O33350	campylobact	946	6	1.1	775	1	YTX1_XENIA	P43380	xenopus lae
874	6	1.1	694	1	PRK_CAMJE	Q9PMU0	campylobact	947	6	1.1	776	1	YOK5_CAEEL	Q11177	caenorhabdi
875	6	1.1	696	1	LSHR_PIG	P16582	sus scrofa	948	6	1.1	780	1	PRTP_HSV1F	P06490	herpes simp
876	6	1.1	698	1	BFG_VIBCH	Q9KUZ7	vibrio chol	949	6	1.1	781	1	SP3_HUMAN	O02447	homo sapien
877	6	1.1	698	1	VANT_ENTGA	Q9X3P3	enterococcu	950	6	1.1	783	1	NOO3_THERT	Q66223	thermus the
878	6	1.1	699	1	BFG_HAEIN	P43925	haemophilus	951	6	1.1	785	1	K6P1_ASFOR	Q9HGZ1	aspergillus
879	6	1.1	699	1	BFG_VIBPA	Q87145	vibrio para	952	6	1.1	785	1	PRTP_HSV1A	P10212	herpes simp
880	6	1.1	699	1	BFG_VIBBU	Q86CQ8	vibrio vuln	953	6	1.1	785	1	PRTP_HSV1A	P12835	herpes simp
881	6	1.1	700	1	FRG2_RALSO	O8XRM7	raistocinia s	954	6	1.1	790	1	U84A_MOUSE	Q06666	mus musculus
882	6	1.1	700	1	BFG_PASMU	P57938	pasteurella	955	6	1.1	794	1	ZEY1_XENIA	O01611	xenopus lae
883	6	1.1	701	1	LSHR_BOVIN	Q28005	bos taurus	956	6	1.1	799	1	ZEY1_MOUSE	P17011	mus musculus
884	6	1.1	701	1	TBX2_MOUSE	Q60707	mus musculus	957	6	1.1	800	1	ARNT_RAT	P41739	rattus norv
885	6	1.1	702	1	BFG_BUCAI	P57593	buchnera ap	958	6	1.1	800	1	ZEY BOVIN	O62836	bos taurus
886	6	1.1	702	1	BFG_BUCAP	Q8K948	buchnera ap	959	6	1.1	801	1	CADR_HUMAN	Q9HBC6	homo sapien
887	6	1.1	702	1	BFG_THICU	O50565	thiobacillu	960	6	1.1	801	1	ZEY_HUMAN	P08048	homo sapien
888	6	1.1	702	1	BFG_YERPE	Q8XJ33	yersinia pe	961	6	1.1	803	1	CUL4_CAEEL	Q17392	caenorhabdi
889	6	1.1	703	1	TBX2_HUMAN	Q13207	homo sapien	962	6	1.1	805	1	ZFX_HUMAN	Q05144	homo sapien
890	6	1.1	703	1	BFG_ECOLI	P02996	escherichia	963	6	1.1	808	1	FGR4_MOUSE	Q03142	mus musculus
891	6	1.1	703	1	BFG_SALTY	P26229	salmonella	964	6	1.1	813	1	FGR2_XENIA	Q03364	xenopus lae
892	6	1.1	704	1	PBL1_CHICK	O73775	gallus gall	965	6	1.1	814	1	AD15_HUMAN	Q13444	homo sapien
893	6	1.1	704	1	LCRD_YERPE	P21210	yersinia en	966	6	1.1	819	1	LON_CHLTR	O84348	chlamydia t
894	6	1.1	704	1	LCRD_YERPE	P31487	yersinia pe	967	6	1.1	820	1	SYFB_DEIRA	Q9XRS5	deinococcus
895	6	1.1	704	1	NEUL_RABIT	P42675	oryctolagus	968	6	1.1	821	1	RBL1_ARATH	O04053	arabidopsis
896	6	1.1	704	1	NEUL_RAT	P42676	rattus norv	969	6	1.1	822	1	CAD3_MOUSE	P10287	mus musculus
897	6	1.1	705	1	BFG_XANAC	Q8N966	xanthomonas	970	6	1.1	824	1	JIP2_HUMAN	Q13387	homo sapien
898	6	1.1	705	1	BFG_XANCP	Q8PC52	xanthomonas	971	6	1.1	824	1	MULTI_HUMAN	Q9UDY8	homo sapien
899	6	1.1	705	1	BFG_XYLPF	Q9PAP0	xyliella fas	972	6	1.1	825	1	PBPA_VIBCH	Q9KUN5	vibrio chol
900	6	1.1	706	1	FRZ4_DROME	Q9DBW1	drosophila	973	6	1.1	834	1	IF2C_SCHPO	O74957	schizosacch
901	6	1.1	706	1	TREX_HORSE	P27425	equus caball	974	6	1.1	834	1	MPT5_YEAST	P39016	saccharomyc
902	6	1.1	708	1	NICA_MOUSE	P27716	mus musculus	975	6	1.1	837	1	XYNZ_CLOTT	P10478	clostridum
903	6	1.1	709	1	NICA_HUMAN	Q92542	homo sapien	976	6	1.1	839	1	ZFX2_MOUSE	P17012	mus musculus
904	6	1.1	710	1	BFG_BUCBP	P59451	buchnera ap	977	6	1.1	840	1	YA02_HUMAN	Q9ZK25	homo sapien
905	6	1.1	711	1	PRE2_YEAST	P36033	saccharomyc	978	6	1.1	842	1	LPFC_SALTY	P33622	salmonella
906	6	1.1	711	1	PRE3_YEAST	Q08905	saccharomyc	979	6	1.1	847	1	CD22_HUMAN	P20273	homo sapien
907	6	1.1	717	1	CU4B_HUMAN	Q13620	homo sapien	980	6	1.1	858	1	ALR2_YEAST	P43553	saccharomyc
908	6	1.1	719	1	CI1C_BACTU	O87404	bacillus th	981	6	1.1	860	1	CH12_COCPO	P4112	coccidioidide
909	6	1.1	723	1	S21C_RAT	Q99N01	rattus norv	982	6	1.1	861	1	GLND_SHEON	O9egh8	shewanella

ID	Y966_MYCTU	STANDARD	PRT	200 AA
983	6	1.1	863	1 AD17 DROME
984	6	1.1	867	1 V196 TRV1
985	6	1.1	872	1 STA_STRE
986	6	1.1	873	1 FAS2 DROME
987	6	1.1	873	1 VGLB_ILTV6
988	6	1.1	876	1 AREA_EMENT
989	6	1.1	877	1 PWT1 CANAL
990	6	1.1	878	1 OSB2 HUMAN
991	6	1.1	879	1 PRP2 HUMAN
992	6	1.1	879	1 PRP2 MOUSE
993	6	1.1	879	1 PRP2 RAT
994	6	1.1	879	1 MYSP ONCVO
995	6	1.1	882	1 AREA_ASPNG
996	6	1.1	883	1 VGLB_ILTV5
997	6	1.1	883	1 VGLB_ILTV7
998	6	1.1	883	1 RSC2 YEAST
999	6	1.1	893	1 BOSS_DROVI
1000	6	1.1	895	1 DAG1_RABIT

ALIGNMENTS

RESULT 1

Y966_MYCTU STANDARD; PRT; 200 AA.

AC P71544;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypothetical protein RV0966C.
 GN RV0966C OR MT0994 OR MTCY10D7.08.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
 CX NCBI_TaxID=1773;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eiglmeyer K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Felwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence.";
 RT Nature 393:537-544(1998).
 RL (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J.F., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
 RA Delcher A., Uterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains.";
 RT Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
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 DR EMBL: Z79700; CAB01985.1; ALT_INIT.
 DR EMBL: AE006984; AKK45243.1; ALT_INIT.

DR TIGR; MT0994; -;
 DR Tuberculist; RV0966C; -;
 KW Hypothetical protein; Complete proteome.
 FT CONFLICT 175 175 V > A (IN REF. 2).
 SQ SEQUENCE 200 AA; 22210 MW; 752F8CFB9B3C02 CRC64;
 Query Match 1.5%; Score 8; DB 1; Length 200;
 Best Local Similarity 100.0%; Pred. No. 3.7;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	467	LLALLGG 474
Db	88	LLALLGG 95

RESULT 2

Y05_MYCTU STANDARD; PRT; 358 AA.

AC Q10394;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 15-DEC-1998 (Rel. 37, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Hypothetical protein RV2205C.
 GN RV2205C OR MT261 OR MTCY190.16C.
 OS Mycobacterium tuberculosis.
 OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
 OC Corynebacteriaceae; Mycobacteriaceae; Mycobacterium.
 CX NCBI_TaxID=1773;
 RX MEDLINE=98295987; PubMed=9634230;
 RA Cole S.T., Brosch R., Parkhill J., Garnier T., Churcher C., Harris D.,
 RA Gordon S.V., Eiglmeyer K., Gas S., Barry C.E. III, Tekala F.,
 RA Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
 RA Davies R., Devlin K., Felwell T., Gentles S., Hamlin N., Holroyd S.,
 RA Hornsby T., Jagels K., Krogh A., McLean J., Moule S., Murphy L.,
 RA Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.,
 RA Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
 RA Sulston J.E., Taylor K., Whitehead S., Barrett B.G.;
 RT "Deciphering the biology of Mycobacterium tuberculosis from the
 RT complete genome sequence.";
 RT Nature 393:537-544(1998).
 RL (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=H37RV;
 RA Fleischmann R.D., Alland D., Eisen J.A., Carpenter L., White O.,
 RA Peterson J.F., Deboy R., Dodson R., Gwinn M.L., Haft D., Hickey E.,
 RA Kolonay J.F., Nelson W.C., Umayam L.A., Ermolaeva M.D., Salzberg S.L.,
 RA Delcher A., Uterback T., Weidman J., Khouri H., Gill J., Mikula A.,
 RA Bishai W.;
 RT "Whole genome comparison of Mycobacterium tuberculosis clinical and
 RT laboratory strains.";
 RT Submitted (Apr-2001) to the EMBL/GenBank/DBJ databases.
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 DR EMBL: Z70283; CA94248.1; ALT_INIT.
 DR EMBL: AE007072; AKK46547.1; ALT_INIT.
 DR TIGR; MT261; -;
 DR Tuberculist; RV2205C; -;
 DR InterPro: IPR004381; Cons_hypoch45.
 DR Pfam: PF02595; Gly_kinase_1.
 DR TIGRPFAMs: TIGR00045; TIGR00045; 1.
 DR Hypothetical protein; Transferrase; Kinase; Complete proteome.
 SQ SEQUENCE 358 AA; 35592 MW; ACTEDCSBFB8E41544 CRC64;

Query Match 1.5%; Score 8; DB 1; Length 358;
 Best Local Similarity 100.0%; Pred. No. 6.1;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

398 PPTPPTAL 405
 101 PPTPPTAL 108

RESULT 3
 GSA_SOYBN STANDARD; PRT; 466 AA.

ID_GSA_SOYBN STANDARD; PRT; 466 AA.
 AC P45621;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Glutamate-1-semialdehyde 2,1-aminomutase, chloroplast precursor
 (EC 5.4.3.8) (GSA) (Glutamate-1-semialdehyde aminotransferase) (GSA-AT)
 GN GSAI OR GSA.
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC Eusteroideae; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
 OX NCBI_TaxID=3847;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Root nodules;
 RX MEDLINE=94105311; PubMed=8278535;
 RA Sangwan I., O'Brian M.R.;
 RT "Expression of the soybean (Glycine max) glutamate-1-semialdehyde
 aminotransferase gene in symbiotic root nodules."
 RL Plant Physiol. 102:829-834(1993).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Essex;
 RX MEDLINE=95221396; PubMed=7706283;
 RA Frustaci J.M., Sangwan I., O'Brian M.R.;
 RT "gaal is a universal tetrahydropyridole synthesis gene in soybean and is
 regulated by a GAGA element."
 RL J. Biol. Chem. 270:7387-7393(1995).
 CC -1- CATALYTIC ACTIVITY: (S)-4-amino-5-oxopentanoate = 5-
 aminolevulinic acid.
 CC -1- COFACTOR: Pyridoxal phosphate.
 CC -1- PATHWAY: Porphyrin biosynthesis by the C5 pathway; second step.
 CC -1- INVOLVED in chlorophyll biosynthesis.
 CC -1- SUBUNIT: Homodimer (by similarity).
 CC -1- SUBCELLULAR LOCATION: Chloroplast.
 CC -1- TISSUE SPECIFICITY: STRONGLY EXPRESSED IN LEAVES OF ETIOLATED
 PLANTLETS INDEPENDENTLY OF LIGHT TREATMENT AND, TO A MUCH LESSER
 EXTENT, IN LEAVES OF MATURE PLANTS.
 CC -1- SIMILARITY: BELONGS TO CLASS-III OF PYRIDOXAL-PHOSPHATE-DEPENDENT
 aminotransferases.
 CC -----
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 CC -----
 CC EMBL: L12453; AAA33968.1; -
 CC EMBL: U20260; AAC48996.1; -
 CC PIR: J02263; J02263.
 CC HSSP: P24630; ZGSA.
 CC InterPro: IPR005814; Aminoctrans_3.
 CC InterPro: IPR004639; HemL.
 CC Pfam: PF00202; aminoctrans_3; 1.
 CC TIGRFAMs: TIGR00713; hemL; 1.
 CC PROSITE: PS00600; AA_TRANSFERRASE_CLASS_3; 1.
 CC Potphyrin biosynthesis; Chlorophyll biosynthesis; Isomerase;

KM Pyridoxal phosphate; Transic peptide; Chloroplast.
 FT TRANSIT 1 28 CHLOROPLAST (POTENTIAL).
 FT CHAIN 29 466 GLUTAMATE-1-SEMIALDEHYDE 2,1-AMINOMUTASE.
 FT BINDING 306 306 PYRIDOXAL PHOSPHATE (BY SIMILARITY).
 SQ SEQUENCE 466 AA; 49646 MM; 5523012AE808DF72 CXC64;

Query Match 1.5%; Score 8; DB 1; Length 466;
 Best Local Similarity 100.0%; Pred. No. 7.7;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

23 LSSSTRSR 30
 17 LSSSTRSR 24

RESULT 4
 PCGN_MOUSE STANDARD; PRT; 1268 AA.

ID_PCGN_MOUSE STANDARD; PRT; 1268 AA.
 AC P55066;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Neurocan core protein precursor (Chondroitin sulfate proteoglycan 3).
 GN CSFG3 OR NCAN.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Brain;
 RX MEDLINE=96039250; PubMed=7490074;
 RA Rauch U., Grimspe B., Kulbe G., Arnold-Ammer I., Beter D.,
 Faessler R.;
 RT "Structure and chromosomal localization of the mouse neurocan gene."
 RL Genomics 28:405-410(1995).
 CC -1- FUNCTION: May modulate neuronal adhesion and neurite growth during
 development by binding to neural cell adhesion molecules (NC-CAM
 and N-CAM). Chondroitin sulfate proteoglycan; binds to hyaluronic
 acid.
 CC -1- TISSUE SPECIFICITY: BRAIN.
 CC -1- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
 CC -1- SIMILARITY: Contains 2 EGF-like domains.
 CC -1- SIMILARITY: Contains 2 Igk domains.
 CC -1- SIMILARITY: Contains 1 C-type lectin family domain.
 CC -1- SIMILARITY: Contains 1 Sushi (SCR) domain.
 CC -1- SIMILARITY: BELONGS TO THE AGGRECAN/VERSICAN PROTEOGLYCAN FAMILY.
 CC -----
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 or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: X84727; CA59216.1; -
 CC PIR: S52781; S52781.
 CC HSSP: P00740; IEDM.
 CC MGD: MGI:104694; Cpg3.
 CC InterPro: IPR002353; Antifreeze2.
 CC InterPro: IPR000152; Asx hydroxyl.
 CC InterPro: IPR000742; EGF_2.
 CC InterPro: IPR001881; EGF_Ca.
 CC InterPro: IPR006209; EGF-like.
 CC InterPro: IPR007110; Ig-Ilike.
 CC InterPro: IPR003599; Ig.
 CC InterPro: IPR003006; Ig_MHC.
 CC InterPro: IPR001304; Lectin_C.
 CC InterPro: IPR000538; Link.
 CC InterPro: IPR000436; Sushi_SCR_CCP.
 CC Pfam: PF00008; EGF; 2.
 CC DR Pfam: PF00047; Ig; 1.

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DR Pfam; PF00059; lectin_c; 1.
DR Pfam; PF00084; sushi; 1.
DR Pfam; PF00193; xlink; 2.
DR PRINTS; PR01265; LINKMODULE.
DR PRINTS; PR00356; ANTIFREZEII.
DR ProDom; PD000918; Link; 2.
DR SMART; SM00032; CCE; 1.
DR SMART; SM00034; CCECT; 1.
DR SMART; SM00179; EGF_CA; 1.
DR SMART; SM00409; IG; 1.
DR SMART; SM00445; LINK; 2.
DR PROSITE; PS00010; ASX HYDROXYL; 1.
DR PROSITE; PS00615; C TYPE LECTIN 1; 1.
DR PROSITE; PS00041; C-TYPE LECTIN 2; 1.
DR PROSITE; PS00022; EGF_1; 3.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01187; EGF_CA; 1.
DR PROSITE; PS00835; IG LIKE; 1.
DR PROSITE; PS01241; LINK; 2.
DR Glycoprotein; Hyaluronic acid; Proteoglycan; Immunoglobulin domain;
KW EGF-like domain; Calcium; Repeat; Lectin; Sushi; Signal.
FT SIGNAL 1 22
FT CHAIN 23 1268
FT DOMAIN 37 157
FT DOMAIN 158 253
FT DOMAIN 259 355
FT DOMAIN 960 996
FT DOMAIN 1034 1165
FT DOMAIN 1166 1224
FT DOMAIN 139 158
FT DISULFID 181 252
FT DISULFID 205 226
FT DISULFID 279 354
FT DISULFID 303 324
FT DISULFID 964 975
FT DISULFID 964 984
FT DISULFID 986 995
FT DISULFID 1040 1051
FT DISULFID 1068 1160
FT DISULFID 1136 1152
FT DISULFID 1167 1210
FT DISULFID 1196 1223
FT CARBOHYD 121 121
FT CARBOHYD 339 339
FT CARBOHYD 742 742
FT CARBOHYD 978 978
FT CARBOHYD 1175 1175
SO SEQUENCE 1268 AA; 137200 MW; 3014EBE202A2FAEC CRC64;

Query Match 1.5%; Score 8; DB 1; Length 1268;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 218 GEPDPLTW 225
DB 413 GEPDPLTW 420

RESULT 5
VGR2_COTUA STANDARD; PRT; 1348 AA.
AC P52583;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Vascular endothelial growth factor receptor 2 precursor (EC 2.7.1.112)
DE (VGRFR-2) (endothelial kinase receptor EKI) (Quek 1) (Quek1).
GN KDR OR FLK-1 OR EKI.
OS Coturnix coturnix japonica (Japanese quail).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Coturnix.

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OX NCBI_TaxID=93934;
RN [1]
RN SEQUENCE FROM N.A.
RC TISSUE=Embryo;
RX MEDLINE=97017121; PubMed=8863722;
RA Eichmann A., Marcelle C., Breant C., Le Douarin N.M.;
RT "Molecular cloning of Quek 1 and 2, two quail vascular endothelial
RT growth factor (VEGF) receptor-like molecules.";
RL Gene 174:3-8(1996).

RN [2]
RN SEQUENCE OF 910-1348 FROM N.A.
RC TISSUE=Spinal cord;
RX MEDLINE=93378866; PubMed=8396413;
RA Eichmann A., Marcelle C., Breant C., Le Douarin N.M.;
RT "Two molecules related to the VEGF receptor are expressed in early
RT endothelial cells during avian embryonic development.";
RL Mech. Dev. 42:33-48(1993).

RN [3]
RN SEQUENCE OF 764-880 FROM N.A., AND CHARACTERIZATION.
RP TISSUE=Embryo;
RX MEDLINE=95301109; PubMed=7781909;
RA Flamme I., Breier G., Risau W.;
RT "Vascular endothelial growth factor (VEGF) and VEGF receptor 2 (Flk-1)
RT are expressed during vasculogenesis and vascular differentiation in
RT the quail embryo.";
RL Dev. Biol. 169:699-712(1995).

CC -1- FUNCTION: RECEPTOR FOR VEGF OR VEGF-C. HAS A TYROSINE-PROTEIN
CC KINASE ACTIVITY. THE VEGF-KINASE LIGAND/RECEPTOR SIGNALING SYSTEM
CC PLAYS A KEY ROLE IN VASCULAR DEVELOPMENT AND REGULATION OF
CC VASCULAR PERMEABILITY.
CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
CC tyrosine phosphate.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- TISSUE SPECIFICITY: IN ALL ENDOTHELIAL TISSUES DURING ONSET OF
CC VASCULARIZATION. IN LATER DEVELOPMENT, PRESENT IN LUNG, HEART,
CC INTESTINE AND SKIN.
CC -1- DEVELOPMENTAL STAGE: EXPRESSED IN WHOLE MESODERM AT ONSET OF
CC GASTRULATION. FROM DAY 2, CONFINED TO ENDOTHELIAL TISSUES AND
CC EXPRESSION CONTINUES TO BE WIDESPREAD THROUGHOUT VASCULARIZATION
CC UNTIL E9 WHERE IT BECOMES RESTRICTED TO SPECIFIC REGIONS SUCH AS
CC THE SPINAL CHORD AND HEART VALVES.
CC -1- INDUCTION: IN VITRO, VEGF IS INDUCED BY BASIC FIBROBLAST GROWTH
CC FACTOR (bFGF), UNIQUELY IN THE FIRST 24 H OF CELL CULTURE.
CC -1- SIMILARITY: BELONGS TO THE CSF-1/PDGF RECEPTOR FAMILY OF TYROSINE-
CC PROTEIN KINASES.
CC -1- SIMILARITY: Contains 7 immunoglobulin-like C2-type domains.
CC
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CC
CC EMBL, X83288; CAA58268.1; -.
CC EMBL, S65205; AAB28127.1; -.
CC EMBL, S78345; AAB34594.1; -.
CC PIR, JC4953; S51656.
CC HSP, P1362; 1FGK.
CC InterPro: IPR007110; IG-1like.
CC InterPro: IPR003598; IG_C2.
CC InterPro: IPR003006; IG_MHC.
CC InterPro: IPR000719; Prot_kinase.
CC InterPro: IPR001824; RTKinaseII.
CC InterPro: IPR001245; Tyr_kinase.
CC Pfam; PF00047; Ig; 6.
CC Pfam; PF00069; pkinase; 1.
CC ProDom; PD000001; Prot_kinase; 2.
CC SMART; SM00408; IGC2_1.
CC SMART; SM00219; TyKc; 1.
CC PROSITE; PS00835; IG LIKE; 5.
CC PROSITE; PS00107; PROTEIN_KINASE_ATP; 1.

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DR Pfam: PF00948; Flavi_N51; 1.
 DR Pfam: PF01005; Flavi_NS2A; 1.
 DR Pfam: PF01002; Flavi_NS2B; 1.
 DR Pfam: PF01350; Flavi_NS4A; 1.
 DR Pfam: PF01349; Flavi_NS4B; 1.
 DR Pfam: PF00972; Flavi_N5A; 1.
 DR Pfam: PF01570; Flavi_propep; 1.
 DR Pfam: PF01728; Flavi; 1.
 DR Pfam: PF00271; Helicase_C; 1.
 DR Pfam: PD001556; Flavi_glycoprote; 1.
 DR Pfam: PD001496; Flavi_N51; 1.
 DR SMART: SM00487; DEXDC; 1.
 DR SMART: SM00490; HELIC_C; 1.
 DR Polyprotein; Glycoprotein; Transferase; RNA-directed RNA polymerase;
 DR Core protein; Coat protein; Envelope protein; Hydrolase; Helicase;
 DR ATP-binding; Transmembrane; Nonstructural protein.
 DR INIT_MER 1 1
 FT CHAIN 1 123
 FT PROPEP 124 215
 FT CHAIN 216 290
 FT CHAIN 291 787
 FT CHAIN 788 1139
 FT CHAIN 1140 1370
 FT CHAIN 1371 1501
 FT CHAIN 1502 2120
 FT CHAIN 2121 2269
 FT CHAIN 2270 2525
 FT CHAIN 2526 3430
 FT CHAIN 3431 401
 FT NP_BIND 1695 1702
 FT SITE 1786 1789
 FT DISULFID 293 320
 FT DISULFID 350 406
 FT DISULFID 364 395
 FT DISULFID 382 411
 FT DISULFID 476 574
 FT DISULFID 591 622
 FT CARBOHYD 138 138
 FT CARBOHYD 917 917
 FT CARBOHYD 962 962
 FT CARBOHYD 994 994
 FT CARBOHYD 1289 1289
 FT CARBOHYD 2336 2336
 FT CARBOHYD 2489 2489
 SQ SEQUENCE 3430 AA; 379624 MW; 12EAA7E81F01CBEE C6C64;
 Query Match 1.5%; Score 8; DB 1; Length 3430;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 461 LAVGVLL 468
 Db 772 LAVGVLL 779
 RESULT 7
 POLG_KUNJM STANDARD; PRT; 3433 AA.
 ID POLG_KUNJM
 AC P1435; 082983;
 DT 01-JAN-1990 (Rel. 13, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Genome polyprotein [Contains: Capsid protein C (core protein); Matrix
 DE protein (Envelope protein M); Major envelope protein E; Nonstructural
 DE proteins NS1, NS2, NS4A and NS4B; Protease/helicase (EC 3.4.21.98)
 DE (NS3); RNA-directed RNA polymerase (EC 2.7.7.48) (NS5)].
 OS Kunjin virus (strain MR61C)
 OC Viruses; ssRNA positive-strand viruses, no DNA stage; Flaviviridae;
 OC NCBI_Taxid=11078;
 RN [1]
 RP SEQUENCE FROM N.A.

RX MEDLINE=88089524; PubMed=2826659;
 RA Coia G, Parker M.D., Speight G., Byrne M.E., Westaway E.G.;
 RT "Nucleotide and complete amino acid sequences of Kunjin virus:
 RT definitive gene order and characteristics of the virus-specified
 RT proteins";
 RL J. Gen. Virol. 69:1-21(1988).
 CC -1- FUNCTION: THE SMALL PROTEINS NS2A, NS2B, NS4A AND NS4B ARE
 CC HYDROPHOBIC, SUGGESTING A POSSIBLE MEMBRANE-RELATED FUNCTION.
 CC NS3 AND NS5 MAY PLAY A ROLE IN THE VIRAL RNA REPLICATION.
 CC -1- CATALYTIC ACTIVITY: Hydrolysis of four peptide bonds in the viral
 CC precursor polyprotein, commonly with Asp or Glu in the P6
 CC position, Cys or Thr in P1 and Ser or Ala in P1'.
 CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate +
 CC {RNA} (N).
 CC -1- SUBUNIT: THE VIRION OF THIS VIRUS IS A NUCLEOCAPSID COVERED BY A
 CC LIPOPROTEIN ENVELOPE. THE ENVELOPE CONSISTS OF TWO PROTEINS:
 CC PROTEIN M AND MNA.
 CC PROTEIN C AND MNA.
 CC -----
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 CC -----
 CC EMBL: D00246; BA00176.1; -.
 CC PIR: A28697; GNMVKV.
 CC HSP: P14336; ISVB.
 DR MEROPS: S07.001; -.
 DR InterPro: IPR001410; DEAD.
 DR InterPro: IPR001122; Flavi_capsidC.
 DR InterPro: IPR000336; Flavi_glycoprote.
 DR InterPro: IPR001850; Flavi_helicase.
 DR InterPro: IPR000069; Flavi_M.
 DR InterPro: IPR001157; Flavi_N51.
 DR InterPro: IPR000752; Flavi_NS2A.
 DR InterPro: IPR000487; Flavi_NS2B.
 DR InterPro: IPR000404; Flavi_NS4A.
 DR InterPro: IPR001528; Flavi_NS4B.
 DR InterPro: IPR000208; Flavi_N5B.
 DR InterPro: IPR002535; Flavi_N5S.
 DR InterPro: IPR002877; Flavi_propep.
 DR InterPro: IPR001650; Helicase_C.
 DR InterPro: IPR007095; RNA_pol_DS_PS.
 DR InterPro: IPR007094; RNA_pol_PS_vit.
 DR Pfam: PF01003; Flavi_capsid; 1.
 DR Pfam: PF02832; Flavi_glycop; 1.
 DR Pfam: PF00869; Flavi_glycoprote; 1.
 DR Pfam: PF00949; Flavi_helicase; 1.
 DR Pfam: PF01004; Flavi_M; 1.
 DR Pfam: PF00948; Flavi_N51; 1.
 DR Pfam: PF01005; Flavi_NS2A; 1.
 DR Pfam: PF01002; Flavi_NS2B; 1.
 DR Pfam: PF01350; Flavi_NS4A; 1.
 DR Pfam: PF01349; Flavi_NS4B; 1.
 DR Pfam: PF00972; Flavi_N5A; 1.
 DR Pfam: PF01570; Flavi_propep; 1.
 DR Pfam: PF01728; Flavi; 1.
 DR Pfam: PF00271; Helicase_C; 1.
 DR Pfam: PD001556; Flavi_glycoprote; 1.
 DR Pfam: PD001496; Flavi_N51; 1.
 DR SMART: SM00487; DEXDC; 1.
 DR SMART: SM00490; HELIC_C; 1.
 DR Polyprotein; Glycoprotein; Transferase; RNA-directed RNA polymerase;
 DR Core protein; Coat protein; Envelope protein; Hydrolase; Helicase;
 DR ATP-binding; Transmembrane; Nonstructural protein.
 DR INIT_MER 1 1
 FT CHAIN 1 123
 FT PROPEP 124 215
 FT CHAIN 216 290
 MEMBRANE PROTEIN M.

FT CHAIN 291 791 MAJOR ENVELOPE PROTEIN E.
 FT CHAIN 792 1143 NONSTRUCTURAL PROTEIN NS1.
 FT CHAIN 1144 1374 NONSTRUCTURAL PROTEIN NS2A.
 FT CHAIN 1375 1505 NONSTRUCTURAL PROTEIN NS2B.
 FT CHAIN 1506 2134 PROTEASE/HELICASE (NS3).
 FT CHAIN 2125 2273 NONSTRUCTURAL PROTEIN NS4A.
 FT CHAIN 2274 2528 NONSTRUCTURAL PROTEIN NS4B.
 FT CHAIN 2529 3433 RNA-DIRECTED RNA POLYMERASE (NS5).
 FT DOMAIN 388 401 INVOLVED IN FUSION.
 FT NP BIND 1639 1706 ATP (POTENTIAL).
 FT SITE 1790 1793 DEAD BOX.
 FT DISULFID 293 330 BY SIMILARITY.
 FT DISULFID 350 406 BY SIMILARITY.
 FT DISULFID 364 395 BY SIMILARITY.
 FT DISULFID 382 411 BY SIMILARITY.
 FT DISULFID 480 578 BY SIMILARITY.
 FT DISULFID 595 626 BY SIMILARITY.
 FT CARBOHYD 921 921 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 966 966 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 998 998 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 3433 AA; 381363 MW; EB4B88A7D040B99 CRC64;

Query Match 1.3%; Score 8; DB 1; Length 3433;
 Best Local Similarity 100.0%; Pred. No. 45;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 461 LAVGVLL 468
 |||||
 DB 776 LAVGVLL 783

RESULT 8
 RL22 PARAR STANDARD; PRT; 114 AA.

AC P41059;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last annotation update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE 60S acidic ribosomal protein P2.
 OS Parthenium argentatum (Guayule rubber plant).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 OC Asterales; Campanulids; Asteraceae; Asteroideae;
 OC Heliantheae; Parthenium.
 OC NCBI_TaxID=35935;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Line 11591; TISSUE=stem bark;
 RA MEDLINE=95062745; PubMed=7972523;
 RA Bachhaus R.A., Kuntz M., Camara B., Bouvier F., Pan Z.;
 RT "Nucleotide sequence of a cDNA for a P2 60S acidic ribosomal protein
 from Parthenium argentatum.";
 RL Plant Physiol. 106:395-395(1994).
 CC -1- FUNCTION: PLAYS AN IMPORTANT ROLE IN THE ELONGATION STEP OF
 CC PROTEIN SYNTHESIS.
 CC -1- SUBUNIT: P1 AND P2 EXIST AS DIMERS AT THE LARGE RIBOSOMAL
 CC SUBUNIT.
 CC -1- PTM: PHOSPHORYLATED (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE L12P FAMILY OF RIBOSOMAL PROTEINS.
 CC -----
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 CC -----
 CC EMBL; X78213; CAA55047.1; -;
 CC InterPro; IPR001813; 60S_ribosomal.
 DR Pfam; PF00428; 60S_ribosomal; 1.
 KW Ribosomal protein; Phosphorylation.

SQ SEQUENCE 114 AA; 11502 MW; 4C850A0AD572D1A0B CRC64;
 Query Match 1.3%; Score 7; DB 1; Length 114;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 468 LLALIGG 474
 |||||
 DB 8 LLALIGG 14

RESULT 9

YCGK_ECOLI
 ID YCGK_ECOLI STANDARD; PRT; 133 AA.
 AC P76002;
 DT 15-JUL-1998 (Rel. 36, Created)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Protein ycgK precursor.
 GN YCGK OR B1178.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
 OC Enterobacteriaceae; Escherichia.
 OC NCBI_TaxID=562;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12 / MG1655;
 RX MEDLINE=97426617; PubMed=9278503;
 RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
 RA Riley M., Collado-Valdes J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.;
 RT "The complete genome sequence of Escherichia coli K-12.";
 RL Science 277:1453-1474(1997).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=K12;
 RX MEDLINE=97061202; PubMed=8905232;
 RA Oshima T., Alba H., Baba T., Fujita K., Hayashi K., Honjo A.,
 RA Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
 RA Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
 RA Mori H., Motomura K., Nakamura Y., Nishimoto H., Nishio Y., Saito N.,
 RA Sampaio G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
 RA Yano M., Horuchi T.;
 RT "A 718-kb DNA sequence of the Escherichia coli K-12 genome
 corresponding to the 12.7-28.0 min region on the linkage map.";
 RL DNA Res. 3:137-155(1996).

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 CC -----

CC EMBL; AE000216; AAC74262.1; -;
 CC EMBL; D90751; BAA36012.1; -;
 CC EMBL; D90752; BAA36025.1; -;
 CC PIR; G64863; G64863.
 DR SWISS-2DPAGE; P76002; COLI.
 DR EcoGene; EG13892; YCGK.
 KW Signal; Complete proteome.
 FT SIGNAL 1 22
 FT CHAIN 23 133 POTENTIAL.
 FT SIGNAL 1 22 PROTEIN YCGK.
 SQ SEQUENCE 133 AA; 14906 MW; 54997548219541P1 CRC64;

Query Match 1.3%; Score 7; DB 1; Length 133;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 466 VLLALL 472
 |||||

Db 10 VLLALL 16

RESULT 10
GILZ_MOUSE STANDARD; PRT; 137 AA.

AC 092257;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Glucocorticoid-induced leucine zipper protein.
GN GILZ.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CH/HEM; PubMed=9430225;
RX MEDLINE=98090090; Moraca R., Ayroldi E., Bruscoli S., Bartoli A.,
RA D'Adamo F., Zollo O., Ricciardi C.,
RA Cannarile L., Migliorati G., Ricciardi C.,
RT "A new dexamethasone-induced gene of the leucine zipper family
protects T lymphocytes from TCR/CD3-activated cell death.";
RL Immunity 7:803-812(1997).
CC -1- FUNCTION: POTENTIAL CO-ACTIVATOR OF A TRANSCRIPTION FACTOR.
CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -1- SIMILARITY: BELONGS TO THE TSC-22/DIP/BUN FAMILY.

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DR EMBL; AF024519; AAD01789.1; -.
DR HSSP; P80220; IDIP.
DR MGD; MGI:1196284; Gilz.
DR GO; GO:0006916; P:anti-apoptosis; IDA.
DR InterPro: IPR000580; TSC-22_Dip_Bun.
DR Pfam; PF01166; TSC22_1; TSC22_Dip_Bun; 1.
DR ProDom; PD007152; TSC22_1; TSC22_Dip_Bun; 1.
DR PROSITE; PS01289; TSC22; 1.
DR KW Transcription regulation; Nuclear protein.
FT DOMAIN 76 LEUCINE-ZIPPER.
SQ SEQUENCE 137 AA; 15165 MW; F1007B609122A7C5 CRC64;

Query Match 13%; Score 7; DB 1; Length 137;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 149 ELEKNS 155
DB 82 ELEKNS 88

RESULT 11
HYPA_ECOLI STANDARD; PRT; 205 AA.

AC P23481; P76565;
DT 01-NOV-1991 (Rel. 20, Created)
DT 01-NOV-1991 (Rel. 20, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hydrogenase-4 component A (EC 1.-.-.-).
GN HYPA OR B2481.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN [1]
RP SEQUENCE FROM N.A.

RC STRAIN=K12;
RX MEDLINE=91202105; PubMed=2016588;
RA Andrews S.C., Harrison P.M., Guest J.R.;
RT "A molecular analysis of the 53.3 minute region of the Escherichia
coli linkage map.";
RL J. Gen. Microbiol. 137:361-367(1991).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Borne N.T., Burland V.,
RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12.";
RL Science 277:1453-1474(1997).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=97349980; PubMed=9205837;
RA Yamamoto Y., Alpa H., Baba T., Hayashi K., Inada T., Iseno K.,
RA Itoh T., Kimura S., Kitagawa M., Makino K., Miki T., Mitsunashi N.,
RA Mizobuchi K., Mori H., Nakade S., Nakamura Y., Nishimoto H.,
RA Oshima T., Oyama S., Saito N., Saito Y., Satoh Y., Sivasubram S.,
RA Tagami H., Takahashi H., Takeda J., Takemoto K., Uehara K., Wada C.,
RA Yamagata S., Horiuchi T.;
RT "Construction of a contiguous 874-kb sequence of the Escherichia coli
K-12 genome corresponding to 50.0-68.8 min on the linkage map and
analysis of its sequence features.";
RL DNA Res. 4:91-113(1997).
RN [4]
RP CHARACTERIZATION.
RA Andrews S.C.;
RT Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: PROBABLE ELECTRON TRANSPORT PROTEIN FOR HYDROGENASE 4.
CC -1- SIMILARITY: TO E. COLI DMSO REDUCTASE B SUBUNIT (DMSB).
CC -1- SIMILARITY: THE IRON-SULFUR CENTERS ARE SIMILAR TO THOSE OF
'BACTERIAL-TYPE; 4FE-4S FERREDOXINS'.

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DR EMBL; M63654; AAB88563.1; -.
DR EMBL; AE000335; AAC75534.1; ALT_INIT.
DR EMBL; D90876; BAA16359.1; -.
DR EMBL; D90877; BAA16369.1; -.
DR PIR; H65023; H65023.
DR HSSP; P00195; ICLF.
DR Ecogen; EG1150; hyFA.
DR InterPro: IPR001450; 4Fe4S_Ferredoxin.
DR Pfam; PF00037; fer4; 1.
DR PROSITE; PS00198; 4FE4S_FERREDOXIN; 1.
KW Oxidoreductase; Electron transport; 4Fe-4S; Iron-sulfur;
Complete proteome.
FT METAL 12
FT METAL 15
FT METAL 18
FT METAL 22
FT METAL 51
FT METAL 54
FT METAL 59
FT METAL 63
FT METAL 82
FT METAL 85
FT METAL 88
FT METAL 92
FT METAL 146
FT METAL 149
IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
IRON-SULFUR 1 (4FE-4S) (BY SIMILARITY).
IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
IRON-SULFUR 2 (4FE-4S) (BY SIMILARITY).
IRON-SULFUR 3 (4FE-4S) (BY SIMILARITY).
IRON-SULFUR 3 (4FE-4S) (BY SIMILARITY).
IRON-SULFUR 3 (4FE-4S) (BY SIMILARITY).
IRON-SULFUR 3 (4FE-4S) (BY SIMILARITY).
IRON-SULFUR 3 (4FE-4S) (BY SIMILARITY).
IRON-SULFUR 3 (4FE-4S) (BY SIMILARITY).
IRON-SULFUR 3 (4FE-4S) (BY SIMILARITY).
IRON-SULFUR 4 (4FE-4S) (BY SIMILARITY).
IRON-SULFUR 4 (4FE-4S) (BY SIMILARITY).
IRON-SULFUR 4 (4FE-4S) (BY SIMILARITY).

FT METAL 158 158 IRON-SULFUR 4 (4FE-4S) (BY SIMILARITY).
 FT METAL 162 162 IRON-SULFUR 4 (4FE-4S) (BY SIMILARITY).
 SQ SEQUENCE 205 AA; 22154 MW; C06EDBF80617B46B CRC64;
 Query Match 1.3%; Score 7; DB 1; Length 205;
 Best Local Similarity 100.0%; Pred. No. 38;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 258 CPNOALR 264
 Db 162 CPNOALR 168
 RESULT 12
 PCP_BACAM STANDARD; PRT; 215 AA.
 AC P46107;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Pyrolydione-carboxylate peptidase (EC 3.4.19.3) (5-oxoprolyl-
 peptidase) (Pyroglutamyl-peptidase I) (PGP-I) (Pyrase).
 GN PCP.
 OS Bacillus amyloliquefaciens.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 ON NCBI_TaxID=1390;
 RX MEDLINE=93203177; PubMed=8095933;
 RA Yoshimoto T., Shimoda T., Kitazono A., Kabashima T., Ito K.,
 Tezuru D.;
 RT "Pyroglutamyl peptidase gene from Bacillus amyloliquefaciens:
 cloning, sequencing, expression, and crystallization of the expressed
 enzyme";
 RL J. Biochem. 113:67-73(1993).
 RN [2]
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS).
 RA MEDLINE=99216536; PubMed=10196127;
 RA Odagaki Y., Hayaishi A., Okada K., Hirotsu K., Kabashima T., Ito K.,
 Yoshimoto T., Tezuru D., Sato M., Clardy J.;
 RT "The crystal structure of pyroglutamyl peptidase I from Bacillus
 amyloliquefaciens reveals a new structure for a cysteine protease";
 RL Structure 7:399-411(1999).
 CC -1- FUNCTION: REMOVES 5-OXOPROLINE FROM VARIOUS PENULTIMATE AMINO ACID
 CC RESIDUES EXCEPT L-PROLINE.
 CC -1- CATALYTIC ACTIVITY: 5-oxoprolyl-peptide + H(2)O = 5-oxoproline +
 CC peptide.
 CC -1- SUBUNIT: Homotetramer.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- MISCELLANEOUS: MOST ACTIVE AT PH 6.5 AND STABLE AT PH 7.0-9.0.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C15.
 CC
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 CC -----
 CC EMBL; D11035; BAA01791.1; -;
 DR PIR; JX0244; JX0244.
 DR PDB; 1AUG; 23-MAR-99.
 DR MEROPS; C15.001; -;
 DR HAVAP; MF_00417; -;
 DR InterPro; IPR000816; Peptidase_C15.
 DR Pfam; PF01470; Peptidase_C15; 1.
 DR ProDom; PD008480; Peptidase_C15; 1.
 DR TIGRFAMs; TIGR00504; Pyro_pdae; 1.
 DR PROSITE; PS01333; PYRASE_GLU; 1.
 DR PROSITE; PS01334; PYRASE_CYS; 1.
 KM Hydrolase; Thiol peptidase; 3D-structure.
 FT ACT_SITE 81 81

FT ACT_SITE 144 144
 FT ACT_SITE 168 168
 FT MUTAGEN 68 68 C->S: NO LOSS OF ACTIVITY.
 FT MUTAGEN 144 144 C->S: LOSS OF ACTIVITY.
 FT STRAND 3 10
 FT HELIX 20 26
 FT TURN 27 30
 FT STRAND 32 33
 FT TURN 34 35
 FT STRAND 36 43
 FT TURN 47 48
 FT HELIX 49 61
 FT STRAND 65 71
 FT TURN 73 74
 FT STRAND 78 81
 FT STRAND 83 85
 FT STRAND 88 88
 FT TURN 95 96
 FT STRAND 103 103
 FT TURN 107 108
 FT STRAND 112 114
 FT HELIX 119 128
 FT TURN 129 130
 FT STRAND 133 133
 FT STRAND 136 136
 FT HELIX 143 158
 FT TURN 160 161
 FT STRAND 163 169
 FT STRAND 173 175
 FT HELIX 177 202
 SQ SEQUENCE 215 AA; 23286 MW; 731A9F80733E807C CRC64;
 Query Match 1.3%; Score 7; DB 1; Length 215;
 Best Local Similarity 100.0%; Pred. No. 40;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 371 AAVSYTA 377
 Db 133 AAVSYTA 139
 RESULT 13
 PCP_BACSU STANDARD; PRT; 215 AA.
 AC P28618;
 DT 01-DEC-1992 (Rel. 24, Created)
 DT 01-DEC-1992 (Rel. 24, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Pyrolydione-carboxylate peptidase (EC 3.4.19.3) (5-oxoprolyl-
 peptidase) (Pyroglutamyl-peptidase I) (PGP-I) (Pyrase).
 GN PCP.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 ON NCBI_TaxID=1423;
 RX MEDLINE=92339527; PubMed=1353026;
 RA Awde A., Cleuziat P., Gonzales T., Robert-Baudouy J.;
 RT "Characterization of the pcg gene encoding the pyrolydione carboxyl
 RT peptidase of Bacillus subtilis";
 RL FEBS Lett. 305:67-73(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=95219079; PubMed=7704254;
 RA Ogawa K.-I., Akagawa E., Nakamura K., Yamane K.;
 RT "Determination of a 21548 bp nucleotide sequence around the 24 degrees
 RT region of the Bacillus subtilis chromosome";
 RL Microbiology 141:269-275(1995).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;

```

RX MEDLINE=98044033; PubMed=9384377;
RA Kunat F., Ogasawara N., Moscer I., Albertini A.M., Allion G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriss R., Bourcier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Broutlet S., Bruns C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Comercon I.F., Cummings N.J., Daniel R.A.,
RA Denicov F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emerson P.T.,
RA Entian K.D., Errington J., Fabre C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Golightly E.J., Grandi G.,
RA Guisepi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holstappel S., Hosono S., Hullo M.F., Ilaya M., Jones L.,
RA Jorja B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koester P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapides A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetle D., Porwollik S., Prescott A.M.,
RA Presecan E., Puig P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Roche E., Roche B., Rose M., Sadale Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scifone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B.,
RA Sorokin A., Taccanti E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpsira P., Tognoni A.,
RA Toesato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viati A., Wamut R., Wedler E., Wedler H., Weizenegger T.,
RA Wintere P., Wipat A., Yamamoto H., Yamane K., Yasunoto K., Yata K.,
RA Yoshida K., Yoshikawa H., Zumbstein E., Yoshikawa H., Danchin A.,
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis".
RT Nature 390:249-256(1997).
[4]
RP SEQUENCE OF 1-18, AND CHARACTERIZATION.
RX MEDLINE=93139164; PubMed=1362573;
RA Gonzales T., Awade A., Besson C., Robert-Baudouy J.,
RT "Purification and characterization of recombinant pyrrolidone carboxyl
RT peptidase of Bacillus subtilis".
RT J. Chromatogr. A 584:101-107(1992).
CC -1- FUNCTION: REMOVES 5-OXOPROLINE FROM VARIOUS PENULTIMATE AMINO ACID
CC RESIDUES EXCEPT L-PROLINE.
CC -1- CATALYTIC ACTIVITY: 5-oxopropyl-L-peptide + H(2)O = 5-oxoproline +
CC peptide.
CC -1- SUBUNIT: Homotetramer.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C15.
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CC -----
DR EMBL: X66034; CAA46833.1; -
DR EMBL: D30808; BAA06485.1; -
DR EMBL: A25847; CAA0177.1; -
DR EMBL: Z99105; CAB12059.1; -
DR PIR: S23432; S23432.
DR HSP: P46107; IAUO.
DR MEROPS: C15.001; -
DR Subtilisin; BG10873; pcp.
DR HAMAP: MF_00417; -; 1.
DR InterPro: IPR000816; Peptidase_C15.
DR Pfam: PF01470; Peptidase_C15; 1.
DR ProDom: PD008480; Peptidase_C15; 1.
DR TIGRfam: TIGR00504; pyro_pase; 1.
DR PROSITE: PS01333; PYRASE_GLU; 1.
DR PROSITE: PS01334; PYRASE_CYS; 1.
KW Hydrolase; Thiol protease; Complete proteome.
FT ACT_SITE 81 144
FT ACT_SITE 144 144 BY SIMILARITY.

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FT ACT_SITE 168 168 BY SIMILARITY.
SQ SEQUENCE 215 AA; 23774 MW; A8804117BCCFE24 CRC64;
Query Match
Best Local Similarity 1.3%; Score 7; DB 1; Length 215;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 371 AAVSYTA 377
DB 133 AAVSYTA 139
RESULT 14
CUD9 HUMAN STANDARD; PRT; 217 AA.
AC 095484;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Claudin-9.
GN CLDN9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Keen T.J., Ingleshear C.F.,
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ) STRANDS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to the claudin family.
CC -----
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CC -----
DR EMBL: AJ130941; CAA10254.1; -
DR Genew; HGNC:2051; CLDN9.
DR InterPro: IPR006187; Claudin.
DR InterPro: IPR006188; Claudin sup.
DR InterPro: IPR004031; PMP22_Claudin.
DR Pfam: PF00822; PMP22_Claudin; 1.
DR PRINTS: PR01077; CLAUDIN.
DR PROSITE: PS01346; CLAUDIN; 1.
KW Tight junction; Transmembrane.
FT TRANSMEM 8 28
FT TRANSMEM 82 102 POTENTIAL.
FT TRANSMEM 117 137 POTENTIAL.
FT TRANSMEM 160 180 POTENTIAL.
SQ SEQUENCE 217 AA; 22848 MW; 0E49C5B5CB3AAC9C CRC64;
Query Match
Best Local Similarity 1.3%; Score 7; DB 1; Length 217;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 467 LLLALGLG 473
DB 88 LLLALGLG 94
RESULT 15
CUD9 MOUSE STANDARD; PRT; 217 AA.
AC 092057;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Claudin-9.

```

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GN CLDN9.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RA SEQUENCE FROM N.A.
RA Morita K., Furuse M., Tsukita S.
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: COMPONENT OF TIGHT JUNCTION (TJ) STRANDS.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: Belongs to the claudin family.
CC -----
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CC -----
DR EMBL; AF124424; AAD17319.1; -
DR MGD; MGI:1913100; Cldn9.
DR InterPro; IPR006187; Claudin.
DR InterPro; IPR006188; Claudin sup.
DR Pfam; PF00822; PMP22_Claudin; 1.
DR PRINTS; PR01077; CLAUDIN.
DR PROSITE; PS01346; CLAUDIN; 1.
DR TIGHT junction; Transmembrane.
KM TRANSMEM 13 33
FT TRANSMEM 82 102 POTENTIAL.
FT TRANSMEM 117 130 POTENTIAL.
FT TRANSMEM 160 180 POTENTIAL.
SQ SEQUENCE 217 AA; 22984 MW; 2B46C7C43AE7BFDS CRC64;

Query Match 1.3%; Score 7; DB 1; Length 217;
Best Local Similarity 100.0%; Pred.No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 467 LLLALLG 473
Db 88 LLLALLG 94

RESULT 16
XG18 HAEN STANDARD; PRT; 217 AA.
ID YG18_HAEN
AC P45275;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical ABC transporter ATP-binding protein H11618.
GN H11618.
OS Haemophilus influenzae.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pasteurellales;
OC Pasteurellaceae; Haemophilus.
OX NCBI_TaxID=727;
RN [1]
RA SEQUENCE FROM N.A.
RA STRAIN=rd / KW20 / ATCC 51907;
RX MEDLINE=95350630; PubMed=7542800;
RA Fleischmann R.D., Adams M.D., White O., Clayton R.A., Kitzness E.F.,
RA Kerkvliet A.R., Bult C.J., Tomb J.-F., Dougherty B.A., Merrick J.M.,
RA McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D.,
RA Scott J.D., Shirley R., Liu L.-I., Glodek A., Kelley J.M.,
RA Weidman J.F., Phillips C.A., Spirigs T., Hedblom E., Cotton M.D.,
RA Uterback T.R., Hanna M.C., Nguyen D.T., Saudak D.M., Brandon R.C.,
RA Fine L.D., Fitchman J.L., Fuhrmann J.L., Geoghegan N.S.M.,
RA Gnehm C.L., McDonald L.A., Small K.V., Fraser C.M., Smith H.O.,
RA Venter J.C.;
RA "Whole-genome random sequencing and assembly of Haemophilus influenzae
RA Rd.";
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RL Science 269:496-512(1995).
CC -1- SIMILARITY: Belongs to the ABC transporter family.
CC -----
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CC -----
DR EMBL; U32835; AAC23266.1; -
DR PIR; A64133; A64133.
DR TIGR; H11618; -
DR InterPro; IPR003593; AAA_ATPase.
DR InterPro; IPR003439; ABC_transporter.
DR Pfam; PF00005; ABC_tran; 1.
DR ProDom; PD000006; ABC_transporter; 1.
DR SMART; SM00382; AAA; 1.
DR PROSITE; PS00211; ABC_TRANSPORTER_1; FALSE_NEG.
DR PROSITE; PS50893; ABC_TRANSPORTER_2; 1.
DR Hypothetical protein; ATP-binding; Transport; Complete proteome.
KM NP_BIND 46 53
FT NP_BIND 53 53 ATP (POTENTIAL).
SQ SEQUENCE 217 AA; 24079 MW; 8C0675189A65012B CRC64;

Query Match 1.3%; Score 7; DB 1; Length 217;
Best Local Similarity 100.0%; Pred.No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 467 LLLALLG 473
Db 55 LLLALLG 61

RESULT 17
RL1 BORBU STANDARD; PRT; 226 AA.
ID RL1_BORBU
AC O51353;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 50S ribosomal protein L1.
GN RPLA OR BB0392.
OS Borrelia burgdorferi (Lyme disease spirochete).
OC Bacteria; Spirochaetes; Spirochaetales; Spirochaetaceae; Borrelia.
OX NCBI_TaxID=139;
RN [1]
RA SEQUENCE FROM N.A.
RA STRAIN=ATCC 35210 / B31;
RX MEDLINE=98065943; PubMed=9403685;
RA Fraser C.M., Casjens S., Huang W.M., Sutton G.G., Clayton R.A.,
RA Lathigra R., White O., Ketchum K.A., Dodson R., Hickey E.K., Gwinn M.,
RA Dougherty B., Tomb J.-F., Fleischmann R.D., Richardson D.,
RA Peterson J., Kerkvliet A.R., Quackenbush J., Salzberg S., Hanson M.,
RA van Vugt R., Palmer N., Adams M.D., Gocayne J.D., Weidman J.,
RA Uterback T., Matthey L., McDonald L., Artlach P., Bowman C.,
RA Garland S., Fujii C., Cotton M.D., Horst K., Roberts K., Hatch B.,
RA Smith H.O., Venter J.C.;
RA "Genomic sequence of a Lyme disease spirochete, Borrelia
RA burgdorferi."
RL Nature 390:580-586(1997).
CC -1- FUNCTION: THIS PROTEIN BINDS DIRECTLY TO 23S RIBOSOMAL RNA AND IS
CC LOCATED IN THE NEIGHBORHOOD OF THE SITE WHERE ELONGATION FACTOR TU
CC IS BOUND TO THE RIBOSOME.
CC -1- SIMILARITY: BELONGS TO THE L1P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC -----
DR EMBL; AE001145; AAC66773.1; -.
DR PIR; G70148; G70148.
DR HSSP; P27150; 1AD2.
DR TIGR; BB0392; -.
DR InterPro; IPR005878; L1_bact_ch1.
DR InterPro; IPR002143; Ribosomal_L1.
DR Pfam; PF00687; Ribosomal_L1; 1.
DR PRODOM; PDD00134; Ribosomal_L1; 1.
DR TIGRFAMs; TIGR01169; rplA_bact; 1.
DR PROSITE; PS01199; RIBOSOMAL_L1; 1.
DR Ribosomal protein; rRNA-binding; Complete proteome.
SQ SEQUENCE 226 AA; 25668 MW; 980CC2BE949B802D CRC64;

Query Match 1.3%; Score 7; DB 1; Length 226;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 505 KKRPDDL 511
Db 195 KKRPDDL 201

RESULT 18
G45 RAT STANDARD; PRT; 234 AA.
AC P35898;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Possible gustatory receptor clone PTE45 (Fragment).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Piecher; TISSUE=Lingual epithelium;
RX MEDLINE=93138133; Pubmed=8380780;
RA Abe K., Kusakabe Y., Yamemura K., Emori Y., Arai S.;
RT "Multiple genes for G protein-coupled receptors and their expression
in lingual epithelia."
RL FEBS Lett. 316:253-256(1993).
CC -1- FUNCTION: POSSIBLE TASTE RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- TISSUE SPECIFICITY: TONGUE-SPECIFIC.
CC -1- SIMILARITY: BELONGS TO FAMILY 1 OF G-PROTEIN COUPLED RECEPTORS.
DR PIR; S29000; S29000.
DR InterPro; IPR000276; GPCR_Rhodopsin.
DR Pfam; PR00001; 7tm_1; 1.
DR PROSITE; PS00237; G-PROTEIN RECP_F1_1; 1.
DR PROSITE; PS00262; G-PROTEIN RECP_F1_2; 1.
KW G-protein coupled receptor; Transmembrane; Glycoprotein.
FT TRANSMEM 1 11
FT DOMAIN <1 11
FT TRANSMEM 12 42
FT TRANSMEM 43 62
FT DOMAIN 63 84
FT TRANSMEM 85 105
FT TRANSMEM 106 138
FT TRANSMEM 139 160
FT DOMAIN 161 182
FT TRANSMEM 183 202
FT TRANSMEM 203 212
FT TRANSMEM 213 234
FT DISULFID 39 121
FT NON TER 234 234
SQ SEQUENCE 234 AA; 25993 MW; BDA186448F257D9 CRC64;

Query Match 1.3%; Score 7; DB 1; Length 234;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy 470 ALLGGGC 476
Db 146 ALLGGGC 152

RESULT 19
FCEA HUMAN STANDARD; PRT; 257 AA.
AC P12319;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE High affinity immunoglobulin epsilon receptor alpha-subunit precursor
DE (FCER1) (IGE Fc receptor, alpha-subunit) (Fc-epsilon RI-alpha).
CN FCER1A OR FCER1A.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=88233953; Pubmed=2967464;
RA Kochan J., Petline L.F., Hakimi J., Kiehl K., Kinet J.-P.;
RT "Isolation of the gene coding for the alpha subunit of the human high
affinity IGE receptor."
RL Nucleic Acids Res. 16:3584-3584(1988).
RN [2]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RX TISSUE=Maat cells;
RX MEDLINE=8815102; Pubmed=2964640;
RA Shinitzu A., Tepler I., Bentley P.N., Berenstein E.H., Siraganian R.P.,
RA Leder P.;
RT "Human and rat mast cell high-affinity immunoglobulin E receptors:
RT characterization of putative alpha-chain gene products."
RL Proc. Natl. Acad. Sci. U.S.A. 85:1907-1911(1988).
RN [3]
RP 3D-STRUCTURE MODELING OF 26-197.
RX MEDLINE=93113350; Pubmed=1472946;
RA Padlan E.A., Helm B.A.;
RT "A modeling study of the alpha-subunit of human high-affinity
RT receptor for immunoglobulin-E."
RL Receptor 2:129-144(1992).
CC -1- FUNCTION: BINDS TO THE FC REGION OF IMMUNOGLOBULIN EPSILON. HIGH
CC AFFINITY RECEPTOR. RESPONSIBLE FOR INITIATING THE ALLERGIC
CC RESPONSE. BINDING OF ALLERGEN TO RECEPTOR-BOUND IGE LEADS TO CELL
CC ACTIVATION AND THE RELEASE OF MEDIATORS (SUCH AS HISTAMINE)
CC RESPONSIBLE FOR THE MANIFESTATIONS OF ALLERGY. THE SAME RECEPTOR
CC ALSO INDUCES THE SECRETION OF IMPORTANT Lymphokines.
CC -1- SUBUNIT: Tetramer of an alpha chain, a beta chain, and two
CC DISULFIDE LINKED gamma chains.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: Contains 2 immunoglobulin-like domains.
CC -----
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CC -----
DR EMBL; X06948; CAA30025.1; -.
DR EMBL; J03605; AAA36204.1; -.
DR EMBL; A21606; CAA01564.1; -.
DR PIR; S00682; S00682.
DR PDB; 1ALS; 27-FEB-95.
DR PDB; 1FZQ; 08-JUN-00.
DR PDB; 1I86; 29-AUG-01.
DR PDB; 1U87; 29-AUG-01.
DR PDB; 1U88; 29-AUG-01.
DR PDB; 1U89; 05-SEP-01.
DR Genew; HGNC:3609; FCER1A.

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DR MM; 147140;
DR GO; GO:0005887; C: integral to plasma membrane; TAS.
DR InterPro; IPR003598; IG_C2.
DR InterPro; IPR003006; IG_MHC.
DR Pfam; PF00047; Ig; 2.
DR SMART; SM00408; IGC2; 1.
DR PROSITE; PS00835; IG_LIKE; 2.
KW Ig-binding protein; Receptor; Transmembrane; Glycoprotein; Signal;
KW Immunoglobulin domain; Repeat; 3D-structure.
FT SIGNAL 1 25
FT CHAIN 26 257 HIGH AFFINITY IMMUNOGLOBULIN EPSILON
FT DOMAIN 26 205 RECEPTOR ALPHA-SUBUNIT.
FT TRANSSEM 206 224 EXTRACELLULAR (POTENTIAL).
FT DOMAIN 225 257 POTENTIAL.
FT DOMAIN 30 110 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 111 193 IG-LIKE 1.
FT DISULFID 51 93 IG-LIKE 2.
FT DISULFID 132 176 BY SIMILARITY.
FT CARBOHYD 46 46 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 67 67 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 99 99 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 160 160 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 165 165 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 191 191 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT STRAND 31 35
FT HELIX 39 42
FT TURN 43 43
FT STRAND 48 54
FT STRAND 61 66
FT TURN 67 68
FT STRAND 71 71
FT STRAND 74 74
FT TURN 75 76
FT STRAND 77 79
FT HELIX 82 87
FT STRAND 91 96
FT HELIX 98 100
FT TURN 101 101
FT STRAND 104 107
FT STRAND 114 116
FT HELIX 120 124
FT STRAND 128 133
FT STRAND 143 145
FT STRAND 146 148
FT HELIX 149 149
FT STRAND 150 150
FT TURN 152 153
FT STRAND 154 155
FT TURN 156 159
FT STRAND 160 163
FT HELIX 165 170
FT STRAND 175 178
FT STRAND 181 182
FT TURN 183 185
FT STRAND 186 187
FT STRAND 190 193
SQ SEQUENCE 257 AA; 29596 MW; F183BB2357DDAD58 CRC64;

Query Match 1.3%; Score 7; DB 1; Length 257;
Best Local Similarity 100.0%; Pred. No. 47;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DT 01-NOV-1997 (Rel. 35, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Hypothetical protein C32D5.1 in chromosome II.
GN C32D5.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Pelodermidae; Caenorhabditis.
OX NCBI_Taxid=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Miller N.;
RN Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RP REVISIONS.
RA Waterston R.;
RL Submitted (SEP-2001) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
DR EMBL; U23511; AAC46789.2; -
DR Wormpep; C32D5.1; CB29207.
RW Hypothetical protein.
SQ SEQUENCE 263 AA; 30461 MW; 374D139E822304BB CRC64;

Query Match 1.3%; Score 7; DB 1; Length 263;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 20
YOD1 CAEEL STANDARD; PRT; 263 AA.
AC 009262;

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DT 01-NOV-1997 (Rel. 35, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Phosphatidate cytidyltransferase (EC 2.7.7.41) (CDP-diglyceride
DE synthetase) (CDP-diglyceride pyrophosphorylase) (CDP-diacylglycerol
DE synthase) (CDP-phosphatidate cytidyltransferase) (CDP-DAG
DE synthase) (CDP-DG synthetase).
GN CDSR OR CDS OR PA3651.
OS Pseudomonas aeruginosa.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Pseudomonadales;
OC Pseudomonadaceae; Pseudomonas.
OX NCBI_Taxid=287;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PAO1;
RX MEDLINE=96257274; PubMed=8654980;
RA Taguchi K., Fukutomi H., Kuroda A., Kato J., Ohtake H.;
RT "Cloning of the Pseudomonas aeruginosa gene encoding CDP-diglyceride
RT synthetase."
RL Gene 172:165-166 (1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 15692 / PAO1;
RX MEDLINE=20437337; PubMed=10984043;
RA Stover C.K., Pham X.-O.T., Erwin A.L., Mizoguchi S.D., Warren P.,
RA Hickey M.J., Brinkman F.S.L., Hutnagle W.O., Kowalik D.J., Lagrou M.,
RA Garber R.L., Golty L., Tolentino E., Westbrook-Wadman S., Yuan Y.,
RA Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,

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RA Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,
RA Reiter J., Sater M.H., Hancock R.E.W., Lory S., Olson M.V.,
RA "Complete genome sequence of Pseudomonas aeruginosa PAO1, an
RT opportunistic pathogen."
RL Nature 406:959-964(2000).
CC -1- CATALYTIC ACTIVITY: CTP + phosphatidate = diphosphate + CDP-
CC dicyclicglycerol.
CC -1- PATHWAY: Phospholipid biosynthesis.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane.
CC -1- SIMILARITY: BELONGS TO THE CDS FAMILY.
CC -----
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CC -----
DR EMBL, D50811; BAA09437.1; -
DR EMBL, AE004785; AAC07039.1; -
DR PIR, F83188; F83188.
DR PIR, JC4832; JC4832.
DR InterPro: IPR000374; PCTRansf.
DR Pfam: PF01148; CTP_transf_1; 1.
DR PROSITE, PS01315; CDS_1_1; 1.
DR TRANSFERASE; Nucleotidyltransferase; Phospholipid biosynthesis;
KW Transmembrane; Inner membrane; Complete proteome.
FT TRANSFEMEM 12 32 POTENTIAL.
FT TRANSFEMEM 53 73 POTENTIAL.
FT TRANSFEMEM 75 95 POTENTIAL.
FT TRANSFEMEM 111 131 POTENTIAL.
FT TRANSFEMEM 136 156 POTENTIAL.
FT TRANSFEMEM 174 194 POTENTIAL.
FT TRANSFEMEM 199 219 POTENTIAL.
FT TRANSFEMEM 251 271 POTENTIAL.
FT TRANSFEMEM 131 133 WPL -> VAA (IN REF. 1).
FT TRANSFEMEM 131 133 WPL -> VAA (IN REF. 1).
SQ SEQUENCE 271 AA; 28856 MW; 5025059C3F1A64C7 CRC64;

Query Match 1.3%; Score 7; DB 1; Length 271;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 467 LLLALLG 473
DB 202 LLLALLG 208

RESULT 22
UPK_YERPE STANDARD; PRT; 272 AA.
AC Q82165;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Putative undecaprenol kinase (EC 2.7.1.66) (Bactitracin resistance
DE protein).
GN UPK OR BACA OR YPO0649 OR Y3530.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360;
RA Parhill J., Wren B.W., Thomson N.R., Tibball R.W., Holden M.T.G.,
RA Prentice M.B., Sebatina M., James K.D., Churcher C., Mangall K.L.,
RA Baker S., Basham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Fellwell T., Hamlin N., Holtroyd S., Jagsels K., Karlyshev A.V.,
RA Leather S., Moule S., Oyatton P.C.F., Quail M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrett B.G.;

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RT "Genome sequence of Yersinia pestis, the causative agent of plague."
RL Nature 413:523-527(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=22137863; PubMed=12142430;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Liss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Straley S.C., McMonough K.A., Nilles M.L., Matson J.S., Blattner F.R.,
RA Perry R.D.;
RL "Genome sequence of Yersinia pestis KIM."
RT J. Bacteriol. 184:4601-4611(2002).
CC -1- FUNCTION: Probably phosphorylates undecaprenol to undecaprenyl
CC phosphate. Confers resistance to bacitracin (by similarity).
CC -1- CATALYTIC ACTIVITY: ATP + undecaprenol = ADP + undecaprenyl
CC phosphate.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
CC -1- MISCELLANEOUS: Bacitracin is thought to be involved in inhibition
CC of peptidoglycan synthesis by sequestering undecaprenyl
CC diphosphate reducing the pool of lipid carrier available.
CC -1- SIMILARITY: BELONGS TO THE UPK FAMILY.
CC -----
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CC -----
DR EMBL, AJ414144; CAC89503.1; -
DR EMBL, AE013956; AAM87078.1; -
DR PIR, AD0080; AD0080.
DR PIR, AD0080; AD0080.
DR HAMAP, MF_01006; -; 1.
DR InterPro: IPR003824; BACA.
DR Pfam: PF02673; BACA_1.
DR TIGRFAMs: TIGR00753; undec_kin_baca_1.
KW Transferase; Kinase; Antibiotic resistance; Transmembrane;
KW Complete proteome.
FT TRANSFEMEM 4 26 POTENTIAL.
FT TRANSFEMEM 47 69 POTENTIAL.
FT TRANSFEMEM 89 108 POTENTIAL.
FT TRANSFEMEM 121 138 POTENTIAL.
FT TRANSFEMEM 153 172 POTENTIAL.
FT TRANSFEMEM 184 206 POTENTIAL.
FT TRANSFEMEM 226 248 POTENTIAL.
FT TRANSFEMEM 253 271 POTENTIAL.
SQ SEQUENCE 272 AA; 29483 MW; 164FC644788F2189 CRC64;

Query Match 1.3%; Score 7; DB 1; Length 272;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 464 GGVLLLA 470
DB 128 GGVLLLA 134

RESULT 23
GLPG_ECOLI STANDARD; PRT; 276 AA.
AC P09351; P76691;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Protein GLPG.
GN GLPG OR B3424.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxID=562;
RN (1)

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RP SEQUENCE FROM N.A., AND SEQUENCE OF 1-8.
RC STRAIN=K12;
RX MEDLINE=97113527; PubMed=8955387;
RA Zeng G., Ye S., Larson T.J.;
RT "Repressor for the sn-glycerol 3-phosphate regulon of Escherichia
RT coli K-12: primary structure and identification of the DNA-binding
RT domain."
RL J. Bacteriol. 178:7080-7089(1996).
RN
RP SEQUENCE FROM N.A.
RC STRAIN=K12;
RX MEDLINE=88319970; PubMed=3045764;
RA Choi Y.-L., Kawase S., Nishida T., Sakai H., Romano T., Kawamukai M.,
RA Uetsumi R., Kohara Y., Akiyama K.;
RT "Nucleotide sequence of the glpR gene encoding the repressor for the
RT glycerol-3-phosphate regulon of Escherichia coli K12."
RL Nucleic Acids Res. 16:7732-7732(1988).
RN
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
RA Riley M., Collado-VIDES J., Glasner J.D., Rode C.K., Mayhew G.F.,
RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
RA Mau B., Shao Y.;
RT "The complete genome sequence of Escherichia coli K-12."
RL Science 277:1453-1474(1997).
RN
RP SEQUENCE FROM N.A.
CC -1- FUNCTION: NOT YET KNOWN.
CC -----
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CC -----
DR EMBL; M54940; AAA23890.1; -.
DR EMBL; M96795; AAC28166.1; -.
DR EMBL; X07520; CAA30398.1; -.
DR EMBL; U18997; AAB58222.1; ALT. INTT.
DR EMBL; AE000418; AAC76449.1; -.
DR PIR; G65138; BVECGG.
DR EcoGene; EG10397; glpG.
DR InterPro; IPR002610; Rhomboid.
DR Pfam; PF01694; Rhomboid.1.
KM Glycerol metabolism; DNA-binding; Complete proteome.
FT DNAS_BIND 190 209 H-T-H MOTIF (BY SIMILARITY).
FT CONFLICT 47 47 R -> H (IN REF. 1).
FT CONFLICT 178 179 RS -> TL (IN REF. 3).
FT CONFLICT 193 193 S -> T (IN REF. 2).
SQ SEQUENCE 276 AA; 31307 MW; B55AFB3454B07A7E CRC64;

Query Match 1.3%; Score 7; DB 1; Length 276;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 458 IAGIANG 464
DB 255 IAGIANGV 261

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OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=98794;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=22084549; PubMed=12089438;
RA Tamai I., Klassen L., Canbaeck B., Naeslund A.K., Eriksson A.-S.,
RA Wernegreen J.J., Sandstrom J.P., Moran N.A., Anderson S.G.E.;
RT "50 million years of genomic stasis in endosymbiotic bacteria."
RL Science 296:2376-2379(2002)
RN
CC -1- CATALYTIC ACTIVITY: L1-2,6-diaminohexanedioate = meso-
CC diaminohexanedioate.
CC -1- PATHWAY: Biosynthesis of lysine from aspartate semialdehyde; sixth
CC step.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -1- SIMILARITY: Belongs to the diaminopimelate epimerase family.
CC -----
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CC -----
DR EMBL; AE014130; AAM68104.1; -.
DR HAMAP; MF_00197; -.
DR InterPro; IPR001653; DAP-epimerase.
DR Pfam; PF01678; DAP-epimerase; 2.
DR TIGRFAMs; TIGR00652; DapF; 1.
DR PROSITE; PS01326; DAP-EPIMERASE; FALSE NEG.
KM Isomerase; lysine biosynthesis; Complete proteome.
FT ACT_SITE 83 83 BY SIMILARITY.
FT ACT_SITE 227 227 BY SIMILARITY.
SQ SEQUENCE 284 AA; 32024 MW; EB37B370320A0089 CRC64;

Query Match 1.3%; Score 7; DB 1; Length 284;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 149 ELLEKXS 155
DB 187 ELLEKXS 193

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RESULT 25.
AROK METTH STANDARD; PRT; 289 AA.
AC 026896;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Shikimate kinase (EC 2.7.1.71) (SK).
GN AROK OR MTH805.
OS Methanobacterium thermoautotrophicum.
CC Archaea; Euryarchaeota; Methanobacteria; Methanobacteriales;
CC Methanobacteriaceae; Methanobacter.
OX NCBI_TaxID=187420;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Delta H;
RX MEDLINE=98037514; PubMed=9371463;
RA Smith D.R., Doucette-Stamm L.A., Delonghery C., Lee H.-M., Dubois J.,
RA Aldredge T., Bashirzaeh R., Blakey D., Cook R., Gilbert K.,
RA Harrison D., Hoang L., Keagle P., Lumm W., Pochter B., Qiu D.,
RA Spadafora R., Vicare R., Wang Y., Wierzbowski J., Gibson R.,
RA Jiwani N., Caruso A., Bush D., Safer H., Patwell D., Prabhakar S.,
RA McDougall S., Shimer G., Goyal A., Pietrowski S., Church G.M.,
RA Daniels C.J., Mao J.-I., Rice P., Noelling J., Reeve J.N.;
RT "Complete genome sequence of Methanobacterium thermoautotrophicum
RT deltaH: functional analysis and comparative genomics."
RL J. Bacteriol. 179:7135-7155(1997).
CC -1- CATALYTIC ACTIVITY: ATP + shikimate = ADP + shikimate 3-phosphate.
CC -1- PATHWAY: Aromatic amino acids biosynthesis; shikimate pathway;

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```

CC      fifth step.
CC      -1- SUBCELLULAR LOCATION: Cytoplasmic (Probable).
CC      -1- SIMILARITY: BELONGS TO THE GHMP KINASE FAMILY. ARCHAEL
CC      SHIKIMATE KINASE SUBFAMILY.
CC      -----
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CC      -----
DR      EMBL; AB000858; AAB85305.1; -.
DR      PIR; E69207; E69207.
DR      HAMAP; MF_00370; -.
DR      InterPro; IPR006204; GHMP_kinase.
DR      InterPro; IPR006203; GHMP_kinase_ATP.
DR      InterPro; IPR000670; Homoser_Kin.
DR      Pfam; PF00288; GHMP_kinase_1.
DR      PRINTS; PR00958; HOMSERKINASE.
DR      PROSITE; PS00627; GHMP_KINASES_ATP_1.
KW      Aromatic amino acid biosynthesis; Transferase; Kinase; ATP-binding;
KW      Complete proteome.
FT      NP_BIND 84 94 ATP (POTENTIAL).
SQ      SEQUENCE 289 AA; 30474 MW; 8BE9CC2042AED3FD8 CRC64;

Query Match      1.3%; Score 7; DB 1; Length 289;
Best Local Similarity 100.0%; Pred. No. 52;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      20 ASGLSSS 26
DB      86 ASGLSSS 92

RESULT 26
Y727_METJA      STANDARD; PRT; 298 AA.
ID      Y727_METJA
AC      Q58137;
DT      01-NOV-1997 (Rel. 35, Created)
DT      01-NOV-1997 (Rel. 35, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      Hypothetical protein MJ0727.
GN      MJ0727.
OS      Methanococcus jannaschii.
OC      Archaea; Euryarchaeota; Methanococci; Methanococcales;
OC      Methanocaldococcaceae; Methanocaldococcus.
OX      NCBI_TaxID=2190;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=JAL-1 / DSM 2661 / ATCC 43067;
RX      MEDLINE=96337999; PubMed=8688087;
RA      Bult C.J., White O., Olsen G.J., Zhou L., Fleischmann R.D.,
RA      Kutter J.L., Geoghegan N.S.M., Weidman J.F., Adams M.D., Reich C.I.,
RA      Overbeek R., Kirkness E.F., Weinstock K.G., Merrick J.M., Glodek A.,
RA      Scott J.L., Geoghegan N.S.M., Weidman J.F., Fuhmann J.L., Nguyen D.,
RA      Uitterback T.R., Kelley J.M., Peterson J.D., Sadow P.W., Hanna M.C.,
RA      Cotton M.D., Roberts K.M., Hurst M.A., Kaine B.P., Borodovsky M.,
RA      Klenk H.-P., Fraser C.M., Smith H.O., Woese C.R., Venter J.C.;
RT      "Complete genome sequence of the methanogenic archaeon, Methanococcus
RT      jannaschii."
RL      Science 273:1058-1073 (1996).
CC      -1- SIMILARITY: SOME, TO COENZYME F420 HYDROGENASE ALPHA SUBUNIT.
CC      -----
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CC      -----
DR      EMBL; U67519; AAB98723.1; -.
DR      PIR; G64390; G64390.
DR      TIGR; MJ0727; -.
DR      InterPro; IPR001501; Ni_hdl.
DR      Pfam; PF00374; NiFeSe_Hases; 1.
KW      Hypothetical protein; Complete proteome.
SQ      SEQUENCE 298 AA; 33519 MW; 4DAD534096A680D CRC64;

Query Match      1.3%; Score 7; DB 1; Length 298;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      461 LAVGVL 467
DB      100 LAVGVL 106

RESULT 27
YSCQ_YERPE      STANDARD; PRT; 307 AA.
ID      YSCQ_YERPE
AC      P42113;
DT      01-NOV-1995 (Rel. 32, Created)
DT      01-NOV-1995 (Rel. 32, Last sequence update)
DT      15-SEP-2003 (Rel. 42, Last annotation update)
DE      Yop proteins translocation protein O.
DE      YSCQ OR YPCD1.43 OR Y5035 OR Y0038.
GN      Yersinia pestis.
OS      Yersinia pestis.
OC      Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC      Enterobacteriaceae; Yersinia.
OX      NCBI_TaxID=632;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=KIM5 / Biovar Mediaevalis;
RX      MEDLINE=94131934; PubMed=8300512;
RA      Fields K.A., Plano G.V., Straley S.C.;
RT      "A low-Ca2+ response (LCR) secretion (ysc) locus lies within the lcrB
RT      region of the LCR plasmid in Yersinia pestis."
RL      J. Bacteriol. 176:569-579 (1994).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      STRAIN=KIM5 / Biovar Mediaevalis;
RX      MEDLINE=98427122; PubMed=9746557;
RA      Perry R.D., Straley S.C., Fetherston J.D., Rose D.J., Gregor J.,
RA      Blatner F.R.;
RT      "DNA sequencing and analysis of the low-Ca2+-response plasmid pCD1 of
RT      Yersinia pestis KIM5."
RL      Infect. Immun. 66:4611-4623 (1998).
RN      [3]
RP      SEQUENCE FROM N.A.
RC      STRAIN=KIM5 / Biovar Mediaevalis;
RX      MEDLINE=99422474; PubMed=9746454;
RA      Hu P., Elliott J., McCreedy P., Skowronski E., Garnea J.,
RA      Kobayashi A., Brubaker R.R., Garcia E.;
RT      "Structural organization of virulence-associated plasmids of Yersinia
RT      pestis."
RL      J. Bacteriol. 180:5192-5202 (1998).
RN      [4]
RP      SEQUENCE FROM N.A.
RC      STRAIN=CO-92 / Biovar Orientalis;
RX      MEDLINE=21470413; PubMed=11586360;
RA      Parkhill J., Wren B.W., Thomson N.R.,
RA      Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,
RA      Baker S., Baeham D., Bentley S.D., Brooks K., Cerdeno-Tarraga A.M.,
RA      Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA      Felwell T., Hamlin N., Holtroyd S., Jagsis K., Karlyshev A.V.,
RA      Leather S., Mule S., Oyston P.C.F., Quail M., Rutherford K.,
RA      Simmonds M., Skellon J., Stevens K., Whitehead S., Barrett B.G.;
RT      "Genome sequence of Yersinia pestis, the causative agent of plague."
RL      Nature 413:523-527 (2001).
CC      -1- FUNCTION: COMPONENT OF THE YOP SECRETION MACHINERY.
CC      -1- SIMILARITY: BELONGS TO THE FLIN/MOPA/SPAO FAMILY.

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CC -----
DR EMBL; AF020214; AAB72200.1; -
DR EMBL; AF074612; AAC69788.1; -
DR EMBL; AF053946; AAC62561.1; -
DR EMBL; AL117189; CAB54920.1; -
DR PIR; A36955; A36955.
DR InterPro; IPR001172; Flagellar Flin.
DR InterPro; IPR003283; SecYIOMPO.
DR InterPro; IPR001543; Spoa.
DR Pfam; PF01052; Spoa_1.
DR PRINTS; PR00956; FLGMOTORFLIN.
DR PRINTS; PR01339; TYPE3OMOPROT.
DR ProDom; PD001777; Spoa; 1.
DR Transport; Protein transport; Plasmid; Virulence; Complete proteome.
SQ SEQUENCE 307 AA; 34418 MW; A936083FAE1CC6C4 CRC64;

Query Match 1.3%; Score 7; DB 1; Length 307;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 AYGGENP 251
Db 196 AYGGENP 202

RESULT 28
YSCO YERPS STANDARD; PRT; 307 AA.
AC P40296;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE YOP proteins translocation protein Q.
GN YSCO.
OS Yersinia pseudotuberculosis.
OG Plasmid pIB1.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=633;
RN NM
RP SEQUENCE FROM N.A.
RC STRAIN=YPIII;
RX MEDLINE=94222840; PubMed=8169210;
RA Bergman T., Erickson K., Galyov E., Persson C., Wolf-Matz H.;
RT "The Yop (Yersinia Outer Protein) gene cluster of Yersinia pseudotuberculosis is
RT involved in top secretion and shows high homology to the spa gene
RT clusters of Shigella flexneri and Salmonella typhimurium.";
RL J. Bacteriol. 176:2619-2626 (1994).
CC -1- FUNCTION: COMPONENT OF THE YOP SECRETION MACHINERY.
CC -1- SIMILARITY: BELONGS TO THE FLIN/MOPA/SPOA FAMILY.
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CC -----
DR EMBL; L25667; AAA27677.1; -
DR InterPro; IPR001172; Flagellar Flin.
DR InterPro; IPR003283; SecYIOMPO.
DR InterPro; IPR001543; Spoa.
DR Pfam; PF01052; Spoa_1.
DR PRINTS; PR00956; FLGMOTORFLIN.

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DR PRINTS; PR01339; TYPE3OMOPROT.
DR ProDom; PD001777; Spoa; 1.
DR Transport; Protein transport; Plasmid; Virulence.
SQ SEQUENCE 307 AA; 34419 MW; AC360E39C397941F CRC64;

Query Match 1.3%; Score 7; DB 1; Length 307;
Best Local Similarity 100.0%; Pred. No. 54;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 245 AYGGENP 251
Db 196 AYGGENP 202

RESULT 29
NIOH BUCAI STANDARD; PRT; 322 AA.
AC P57258;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE NADH-quinone oxidoreductase chain H (EC 1.6.99.5) (NADH dehydrogenase
DE I, chain H) (NDH-1, chain H).
GN NIOH OR BUI60.
OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
OS symbiotic bacterium).
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Buchnera.
OX NCBI_TaxID=118099;
RN NM
RP SEQUENCE FROM N.A.
RC STRAIN=Tokyo 1998;
RX MEDLINE=20445173; PubMed=10993077;
RA Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT "Genome sequence of the endocellular bacterial symbiont of aphids
RT Buchnera sp. Aps.";
RL Nature 407:81-86 (2000).
CC -1- FUNCTION: NDH-1 shuttles electrons from NADH, via FMN and iron-
CC sulfur (Fe-S) centers, to quinones in the respiratory chain.
CC Couples the redox reaction to proton translocation (for every two
CC electrons transferred, four hydrogen ions are translocated across
CC the cytoplasmic membrane), and thus conserves the redox energy in
CC a proton gradient (By similarity).
CC -1- CATALYTIC ACTIVITY: NADH + quinone = NAD(+) + quinol.
CC -1- SUBUNIT: COMPOSED OF 13 DIFFERENT SUBUNITS. SUBUNITS NIOA, H, J,
CC K, L, M, N CONSTITUTE THE MEMBRANE SECTOR OF THE COMPLEX (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein.
CC -1- SIMILARITY: BELONGS TO THE COMPLEX I SUBUNIT 1 FAMILY.
CC -----
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CC -----
DR EMBL; AP001118; BAB12878.1; -
DR InterPro; IPR001694; Resp_NADH_dhl.
DR Pfam; PF00146; NADHdh; 1.
DR PROSITE; PS00667; COMPLEX1_NDI_1; FALSE NEG.
DR PROSITE; PS00668; COMPLEX1_NDI_2; FALSE NEG.
KM Oxidoreductase; NAD; Quinone; Transmembrane; Complete proteome.
FT TRANSMEM 15
FT TRANSMEM 81
FT TRANSMEM 101
FT TRANSMEM 114
FT TRANSMEM 134
FT TRANSMEM 149
FT TRANSMEM 169
FT TRANSMEM 186
FT TRANSMEM 206
FT TRANSMEM 237
FT TRANSMEM 257
FT TRANSMEM 265
FT TRANSMEM 285
FT TRANSMEM 302
FT TRANSMEM 322
SQ SEQUENCE 322 AA; 36972 MW; P251144E9A6A6B52 CRC64;

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Query Match      1.3%; Score 7; DB 1; Length 322;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      457 LINGLAV 463
      |||||
      200 LINGLAV 206

RESULT 30
FHR4 HUMAN      STANDARD;      PRT;      331 AA.
ID FHR4_HUMAN
AC 092456; O9UJY6;
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Complement factor H-related protein 4 precursor (FHR-4).
GN FHR4.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
(1)
SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=97190290; PubMed=9038172; Tilkom A., Buck F., Marti T.,
RX Skerka C., Hellwege J., Weber W., Zipfel P.F.;
RX Kampen E., Beisiegel U., Zipfel P.F.;
RT "The human factor H-related protein 4 (FHR-4). A novel short consensus
RT repeat-containing protein is associated with human triglyceride-rich
RT lipoproteins."
RT J Biol. Chem. 272:5627-5634(1997).
RL (2)
SEQUENCE OF 1-19 FROM N.A.
RA Male D.A., Ormsby R.J., Giannakis E., Gordon D.L.;
RA "Promoter region of complement factor H-related 4 (FHR-4) gene."
RA Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
RN (3)
CHARACTERIZATION.
RX MEDLINE=98136603; PubMed=9476126;
RX Hellwege J., Skerka C., Zipfel P.F.;
RX "Biochemical and functional characterization of the factor-H-related
RX protein 4 (FHR-4)."
RL Immunopharmacology 38:149-157(1997).
CC -1- FUNCTION: INVOLVED IN COMPLEMENT REGULATION. CAN ASSOCIATE WITH
CC LIPOPROTEINS AND MAY PLAY A ROLE IN LIPID METABOLISM.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- TISSUE SPECIFICITY: Synthesized by liver and secreted in plasma.
CC -1- PTM: GLYCOSYLATED.
CC -1- SIMILARITY: Contains 5 Sushi (SCR) domains.
CC -1- SIMILARITY: STRONG, TO FACTOR H.
CC -----
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CC -----
DR EMBL, X88337; CAA66980.1;
DR EMBL, AF190816; AAF05951.1;
DR HSSP, P10998; IVD.
DR MIM, 605337;
DR GO; GO:0005320; F:apolipoprotein; TAS.
DR GO; GO:0005209; F:plasma protein; TAS.
DR InterPro; IPR000436; Sushi_SCR_CCP.
DR Pfam; PF00084; sushi; 5.
DR SMART; SM00032; CCP; 4.
DR Repeat; Glycoprotein; Sushi; Signal.
KW SIGNAL.
FT 1 19 POTENTIAL.

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FT CHAIN 20 331 COMPLEMENT FACTOR H-RELATED PROTEIN 4.
FT DOMAIN 23 85 SUSHI 1.
FT DOMAIN 87 146 SUSHI 2.
FT DOMAIN 148 205 SUSHI 3.
FT DOMAIN 210 266 SUSHI 4.
FT DOMAIN 268 331 SUSHI 5.
FT DISULFID 24 73 BY SIMILARITY.
FT DISULFID 56 84 BY SIMILARITY.
FT DISULFID 88 134 BY SIMILARITY.
FT DISULFID 117 145 BY SIMILARITY.
FT DISULFID 149 193 BY SIMILARITY.
FT DISULFID 176 204 BY SIMILARITY.
FT DISULFID 211 254 BY SIMILARITY.
FT DISULFID 240 265 BY SIMILARITY.
FT DISULFID 269 320 BY SIMILARITY.
FT DISULFID 303 330 BY SIMILARITY.
FT CARBOHYD 127 127 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 186 186 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 206 206 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 310 310 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 331 AA; 37325 MW; 5A0D04AB4B841424 CRC64;

Query Match      1.3%; Score 7; DB 1; Length 331;
Best Local Similarity 100.0%; Pred. No. 58;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      134 NPVTSPG 140
      |||||
      59 NPVTSPG 65

RESULT 31
CAP1 DICDI      STANDARD;      PRT;      333 AA.
ID CAP1_DICDI
AC P19198;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE CAMP binding protein CABP1A/CABP1B (CABP1 protein).
GN CAPA OR CABP1.
OS Dictyostelium discoideum (Slime mold).
OC Eukaryota; Mycetozoa; Dictyostelida; Dictyostelium.
OX NCBI_TaxID=44689;
(1)
SEQUENCE FROM N.A.
RC STRAIN=AX2;
RX MEDLINE=91016829; PubMed=2216719;
RX Grant C.E., Bain G., Tsang A.;
RT "The molecular basis for alternative splicing of the CABP1
RT transcripts in Dictyostelium discoideum."
RT Nucleic Acids Res. 18:5457-5463(1990).
RN (2)
SEQUENCE FROM N.A.
RP STRAIN=AX3;
RC STRAIN=AX3;
RX MEDLINE=9109678; PubMed=2176639;
RX Grant C., Tsang A.;
RT "Cloning and characterization of cDNAs encoding a novel cyclic AMP-
RT binding protein in Dictyostelium discoideum."
RL Gene 96:213-218(1990).
RN (3)
SEQUENCE FROM N.A.
RC STRAIN=V12M2;
RX MEDLINE=91113722; PubMed=1989693;
RX Bonfils C., Hebert J., Tsang A.;
RT "A 27-bp deletion is responsible for the expression of a variant
RT CABP1, a cyclic AMP-binding protein of Dictyostelium discoideum."
RL Biochim. Biophys. Acta 1088:145-146(1991).
CC -1- SUBUNIT: HETERO-DIMER OF CABP1A AND CABP1B. CABP1A/CABP1B COULD
CC ALSO ASSOCIATE WITH P31/P34 TO FORM AN ACTIVE COMPLEX.
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative splicing; Named isoforms=2;
CC Name=1; Synonyms=CABP1A;
CC IsoId=P19198-1; Sequence=Displayed;

```

CC Name=2; Synonyms=CABPIB;
CC IsoId=P19198-2; Sequence=VSP 000758;
CC -1 SIMILARITY: BELONGS TO THE CAPAB / TERDEX2 FAMILY.
CC -----
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DR EMBL; X52688; CAB36913.1; -;
DR EMBL; X52688; CAB36913.1; -;
DR EMBL; M36176; AAA3173.1; -;
DR EMBL; X55975; CAB39445.1; -;
DR PIR; S11484; S11484;
DR PIR; S13497; S13497;
DR Dictydb; DD02019; capa.
DR InterPro; IPR003325; TERD.
DR InterPro; IPR006031; XYPPX.
DR Pfam; PF02342; Terd; 1.
DR Pfam; PF02162; XYPPX; 4.
KM CAMP-binding; Repeat; Alternative splicing.
FT DOMAIN 48 83 3 X 5 AA REPEATS OF MOTIF A.
FT REPEAT 48 52 A-1.
FT REPEAT 67 71 A-2.
FT REPEAT 79 83 A-3.
FT DOMAIN 84 107 2 X 12 AA REPEATS OF MOTIF B.
FT REPEAT 84 95 B-1.
FT REPEAT 96 107 B-2.
FT DOMAIN 87 134 5 X 9 AA REPEATS OF MOTIF C.
FT REPEAT 87 95 C-1.
FT REPEAT 99 107 C-2.
FT REPEAT 108 116 C-3.
FT REPEAT 117 125 C-4.
FT REPEAT 126 134 C-5.
FT DOMAIN 52 138 GLN/PRO-RICH.
FT VARSPLIC 13 49 Missing (in isoform 2).
FT VARIANT 99 107 MISSING (IN VARIANT V12M2).
FT VARIANT 312 316 LLLLV -> EVAAG (IN VARIANT V12M2).
FT VARIANT 318 322 VCKAF -> GMOGA (IN VARIANT V12M2).
SQ SEQUENCE 333 AA; 35521 MW; 9A274606139E0EC1 CRC64;

Query Match 1.3%; Score 7; DB 1; Length 333;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 454 NTALIAG 460
|||
Db 292 NTALIAG 298

RESULT 32
BTUC YERPE STANDARD; PRT; 335 AA.
AC OeDkA;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Vitamin B12 transport system permease protein btuc.
GN BTUC OR YPO2425 OR Y1914.
OS Yersinia pestis.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Yersinia.
OX NCBI_TaxID=632;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CO-92 / Biovar Orientalis;
RX MEDLINE=21470413; PubMed=11586360;
RA Parkhill J., Wren B.W., Thomson N.R., Tittball R.W., Holden M.T.G.,
RA Prentice M.B., Sebahia M., James K.D., Churcher C., Mungall K.L.,

RA Baker S., Baaham D., Bentley S.D., Brooks K., Cerdano-Tarraga A.M.,
RA Chillingworth T., Cronin A., Davies R.M., Davis P., Dougan G.,
RA Fellwell T., Hamlin N., Holroyd S., Jagsels K., Kariyeh A.V.,
RA Jørgensen S., Mouton S., Oyston P.C.F., Oatli M., Rutherford K.,
RA Simmonds M., Skelton J., Stevens K., Whitehead S., Barrett B.G.,
RA "Genome sequence of Yersinia pestis, the causative agent of plague.",
RA Nature 413:523-527(2001).
[2]
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=KIM5 / Biovar Mediaevalis;
RX MEDLINE=22137863; PubMed=12142430;
RA Deng W., Burland V., Plunkett G. III, Boutin A., Mayhew G.F., Jiss P.,
RA Perna N.T., Rose D.J., Mau B., Zhou S., Schwartz D.C.,
RA Fetherston J.D., Lindler L.E., Brubaker R.R., Plano G.V.,
RA Straley S.C., McDonough K.A., Niles M.L., Matson J.S., Blattner F.R.,
RA Perry R.D.,
RT "Genome sequence of Yersinia pestis KIM.",
RL J. Bacteriol. 184:4601-4611(2002).
CC -1 FUNCTION: Part of the binding-protein-dependent transport system
CC for vitamin B12. Involved in the translocation of the substrate
CC across the membrane (by similarity).
CC -1 SUBCELLULAR LOCATION: Integral membrane protein. Inner membrane
CC (Probable).
CC -1 SIMILARITY: BELONGS TO THE BINDING-PROTEIN-DEPENDENT TRANSPORT
CC SYSTEM PERMEASE FAMILY. FECD SUBFAMILY.
CC -----
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DR EMBL; AJ414152; CAB91229.1; -;
DR EMBL; AE013794; AAM85481.1; ALT_INIT.
DR PIR; A10295; A10295.
DR HAMAP; MF_01004; -; 1.
DR InterPro; IPR000515; BPD transp.
DR InterPro; IPR000522; FECD.
DR Pfam; PF01032; FECD; 1.
DR ProDom; PD001557; FECD; 1.
DR PROSITE; PS00402; BPD TRANSP. INN MEMBER; FALSE NEG.
KM Transport; Cobalt transport; Transmembrane; Inner membrane;
KW Complete proteome.
FT TRANSMEM 21 43 POTENTIAL.
FT TRANSMEM 65 87 POTENTIAL.
FT TRANSMEM 94 113 POTENTIAL.
FT TRANSMEM 117 139 POTENTIAL.
FT TRANSMEM 153 173 POTENTIAL.
FT TRANSMEM 200 220 POTENTIAL.
FT TRANSMEM 243 263 POTENTIAL.
FT TRANSMEM 282 302 POTENTIAL.
FT TRANSMEM 309 329 POTENTIAL.
SQ SEQUENCE 335 AA; 36331 MW; 839381BADF5E5A74 CRC64;

Query Match 1.3%; Score 7; DB 1; Length 335;
Best Local Similarity 100.0%; Pred. No. 59;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 464 GGVLLLA 470
|||
Db 291 GGVLLLA 297

RESULT 33
Z185 MOUSE STANDARD; PRT; 352 AA.
ID Z185 MOUSE
AC Oe235A;
DT 15-JUL-1999 (Rel. 38, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE Zinc finger protein 185 (ZIM-domain protein ZFP185) (P1-A).

```

CN ZNF185 OR ZFP185.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96425694; PubMed=8828036;
RA Levin M.L., Chatterjee A., Pragliola A., Worley K.C., Wehnert M.,
RA Zhuchenko O., Smith R.F., Lee C.C., Herman G.E.;
RT "A comparative transcription map of the murine bare patches (Bpa) and
RT striated (Str) critical regions and human Xq28.";
RL Genome Res. 6:465-477(1996).
CC -1- FUNCTION: MAY BE INVOLVED IN THE REGULATION OF CELLULAR
CC PROLIFERATION AND/OR DIFFERENTIATION (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: Nuclear (Potential).
CC -1- TISSUE SPECIFICITY: EXPRESSED IN SKIN, KIDNEY, OVARY, TESTIS. ALSO
CC EXPRESSED IN BRAIN, CARTILAGE, HEART, LUNG, SPLEEN AND THYMUS.
CC -1- DEVELOPMENTAL STAGE: AT E14.5 ONLY EXPRESSED IN MESENCHYMAL
CC CELLS. AT E16.5 EXPRESSED ALSO IN CELLS LINING THE VERTEBRAE AND
CC TENDONS OF THE PROXIMAL TAIL. IN LATE EMBRYOGENESIS, EXPRESSED IN
CC MESENCHYMAL CELLS ADJACENT TO THE DISTAL LIMB BONES (TIBIA AND
CC CALCANEUM), IN TENDONS AND IN THE CONNECTIVE TISSUE SHEATH
CC (EPIMYSIUM) SURROUNDING THE SKELETAL MUSCLE. ALSO EXPRESSED IN THE
CC EPITHELIA OF THE EPIDIDYMIS OF THE TESTIS.
CC -1- SIMILARITY: contains 1 LIM zinc-binding domain.
-----
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-----
DR EMBL: U46687; AAC52628.1; -
DR MGD: MGI:108095; Zfp185.
DR InterPro: IPR001781; LIM.
DR ProDom: PD000094; LIM; 1.
DR SMART: SM00132; LIM; 1.
DR PROSITE: PS00478; LIM DOMAIN 1; FALSE_NEG.
DR PROSITE: PS00023; LIM DOMAIN 2; 1.
DR LIM domain; Metal-binding; Zinc.
FT DOMAIN 23 26 POLY-GLU.
FT DOMAIN 292 347 LIM.
SQ SEQUENCE 352 AA; 38322 MW; 2AB1F833D7AF1A5C CRC64;

Query Match
Best Local Similarity 1.3%; Score 7; DB 1; Length 352;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 21 SGLSSST 27
DB 103 SGLSSST 109

RESULT 34
YOCB_EBWCA STANDARD; PRT; 376 AA.
ID YOCB_EBWCA
AC 047417;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Exoenzyme regulation regulon ORF1.
OS Erwinia carotovora.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Pectobacterium.
OX NCBI_TaxID=554;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SCRI193;
RA Golby P., Jones S.E., Stephens S., Reeves P.J., Bycroft B.,
RA Stewart G., Williams P., Salmond G.P.C.;

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RT "Global regulation of Erwinia carotovora exoenzyme virulence
RT factors: multicopy suppression of rex mutants and evidence for a
RT global repression region.";
RL Submitted (MAY-1994) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE RLJ FAMILY OF PSEUDOURIDINE SYNTHASES.
CC STRONG, TO E.COLI YOCB.
CC -1- SIMILARITY: IN THE N-TERMINAL, STRONG, TO E.COLI YOCB; IN THE C-
CC TERMINAL, STRONG, TO E.COLI YOCB.
-----
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-----
DR EMBL: X79474; CAA55982.1; -
DR PIR: S45107; S45107.
DR InterPro: IPR006145; Pseudou synth.
DR InterPro: IPR006224; PSI_RLU.
DR Pfam: PF04287; DUF446; 1.
DR Pfam: PF00849; Pseudou synth. 2; 1.
DR ProDom: PD001819; PSI_RLU; 1.
DR PROSITE: PS01129; PSI_RLU; 1.
DR PROSITE: PS01129; PSI_RLU; 1.
SQ SEQUENCE 376 AA; 43605 MW; F35992CAAAD22E30 CRC64;

Query Match
Best Local Similarity 1.3%; Score 7; DB 1; Length 376;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 465 GVLLAL 471
DB 173 GVLLAL 179

RESULT 35
GALL_LACLA STANDARD; PRT; 399 AA.
ID GALL_LACLA
AC 0947D7; 087521;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Galactokinase (EC 2.7.1.6) (Galactose kinase).
DE GALK OR LI1983.
CN Lactococcus lactis (subsp. lactis) (Streptococcus lactis).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1360;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 7962;
RA Lee J.M., Chung D.K., Park J.H., Lee W.K., Chang H.C., Kim J.H.,
RA Lee H.J.;
RT "The organization of genes involved in metabolism of gal/lac of
RT Lactococcus lactis.";
RL Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=IL1403;
RX MEDLINE=21235186; PubMed=11337471;
RA Bocolin A., Wincker P., Manger S., Jallion O., Malarme K.,
RA Weisenbach J., Ehrlich S.D., Sorokin A.;
RT "The complete genome sequence of the lactic acid bacterium Lactococcus
RT lactis bsp. lactis IL1403.";
RL Genome Res. 11:731-753(2001).
RN [3]
RP SEQUENCE OF 276-399. FROM N.A.
RC STRAIN=NCDO 2054;
RX MEDLINE=98406043; PubMed=9733593;
RA Vaughan E.E., Pridmore R.D., Moller B.;
RT "Transcriptional regulation and evolution of lactose genes in the
RT galactose-lactose operon of Lactococcus lactis NCDO2054.";
RL J. Bacteriol. 180:4893-4902(1998).

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CC -1- CATALYTIC ACTIVITY: ATP + D-galactose = ADP + D-galactose 1-
CC phosphate.
CC -1- PATHWAY: Galactose metabolism; first step.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- SIMILARITY: BELONGS TO THE GHMP KINASE FAMILY. GALK SUBFAMILY.
CC -----
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CC -----
CC EMBL; U60828; AAD11510.1; -.
CC EMBL; AB006428; AAK06081.1; -.
CC EMBL; AF062008; AAC63017.1; -.
CC PIR; G68672; G68672.
CC HAMAP; MF_00246; -.
CC DR InterPro; IPR000705; Galactokinase.
CC DR InterPro; IPR001174; Galkinase.
CC DR InterPro; IPR006204; GHMP Kinase.
CC DR InterPro; IPR006203; GHMPkinase ATP.
CC DR InterPro; IPR006206; Mew_galkinase.
CC DR Pfam; PF00288; GHMP_kinases; 1.
CC DR PRINTS; PR00473; GALTOKINASE.
CC DR PRINTS; PR00960; LMPPROTEIN.
CC DR TIGRFBMS; TIGR00131; gal_kin; 1.
CC DR PROSITE; PS00106; GALACTOKINASE; 1.
CC DR PROSITE; PS00627; GHMP_KINASES_ATP; 1.
CC DR Transferase; Kinase; Galactose metabolism; ATP-binding;
CC Complete proteome.
CC NP BIND 131 141 ATP (POTENTIAL).
CC FT CONFLICT 290 290 T -> A (IN REF. 3).
CC SQ SEQUENCE 399 AA; 43824 MW; D013EA01C4CE2EAB CRC64;

Query Match 1.3%; Score 7; DB 1; Length 399;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 20 ASGLSSS 26
Db 133 ASGLSSS 139

RESULT 36
GALI LACTC STANDARD; PRT; 399 AA.
AC Q95652;
DT 16-OCT-2001 (Rel. 40; Created)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DT 28-FEB-2003 (Rel. 41; Last annotation update)
DE Galactokinase (EC 2.7.1.6) (Galactose Kinase).
GN GALK.
OS Lactococcus lactis (subsp. cremoris) (Streptococcus cremoris).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; Lactococcus.
OX NCBI_TaxID=1359;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=MG1363;
RA Grossclord B.P., Luesink E.J., Vaughan E.E., Kuipers O.P., De Vos W.M.;
RT "Characterization, expressions, and mutations of the Lactococcus lactis
RT galK gene involved in galactose utilization via the leloir
RT pathway."
RL Submitted (SEP-1998) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: ATP + D-galactose = ADP + D-galactose 1-
CC phosphate.
CC -1- PATHWAY: Galactose metabolism; first step.
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- SIMILARITY: BELONGS TO THE GHMP KINASE FAMILY. GALK SUBFAMILY.
CC -----
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CC -----
CC EMBL; AJ011653; CAB44216.1; -.
CC HAMAP; MF_00246; -.
CC DR InterPro; IPR000705; Galactokinase.
CC DR InterPro; IPR001174; Galkinase.
CC DR InterPro; IPR006204; GHMP Kinase.
CC DR InterPro; IPR006203; GHMPkinase ATP.
CC DR InterPro; IPR006206; Mew_galkinase.
CC DR Pfam; PF00288; GHMP_kinases; 1.
CC DR PRINTS; PR00473; GALTOKINASE.
CC DR PRINTS; PR00960; LMPPROTEIN.
CC DR TIGRFBMS; TIGR00131; gal_kin; 1.
CC DR PROSITE; PS00106; GALACTOKINASE; 1.
CC DR PROSITE; PS00627; GHMP_KINASES_ATP; 1.
CC DR Transferase; Kinase; Galactose metabolism; ATP-binding.
CC NP BIND 131 141 ATP (POTENTIAL).
CC FT SEQUENCE 399 AA; 43741 MW; 31EB38FE3AE2277 CRC64;

Query Match 1.3%; Score 7; DB 1; Length 399;
Best Local Similarity 100.0%; Pred. No. 69;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 20 ASGLSSS 26
Db 133 ASGLSSS 139

RESULT 37
PEK-THKAC STANDARD; PRT; 408 AA.
AC Q9HJ95;
DT 16-OCT-2001 (Rel. 40; Created)
DT 16-OCT-2001 (Rel. 40; Last sequence update)
DT 28-FEB-2003 (Rel. 41; Last annotation update)
DE Phosphoglycerate kinase (EC 2.7.2.3).
GN PGK OR TAI075.
OS Thermoplasma acidophilum.
OC Archaea; Euryarchaeota; Thermoplasmata; Thermoplasmatales;
OC Thermoplasmataceae; Thermoplasma.
OX NCBI_TaxID=2303;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=DSM 1728;
RA MERLIN=20479972; PubMed=11029001;
RA Ruepp A., Gremel W., Santos-Martinez M.-L., Koretke K.K., Volker C.,
RA Mewes H.-W., Frishman D., Stocker S., Lupas A.N., Baumeister W.;
RT "The genome sequence of the thermophilic scavenger Thermoplasma
RT acidophilum."
RL Nature 407:508-513(2000).
CC -1- CATALYTIC ACTIVITY: ATP + 3-phospho-D-glycerate = ADP + 3-
CC phospho-D-glyceroyl phosphate.
CC -1- SUBUNIT: Monomer (By similarity).
CC -1- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
CC -1- SIMILARITY: Belongs to the phosphoglycerate kinase family.
CC -----
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CC -----
CC EMBL; AL445066; CAC12203.1; -.
CC HSBP; P07378; 16PK.

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DR HAMAP: MF_00145: -. 1.
DR InterPro: IPR001576; PCK.
DR Pfam: PF00162; PCK; 1.
DR PRINTS: PR00477; PHGLYCKINASE.
DR PROSITE: PS00111; POLYMERASE KINASE; FALSE NEG.
DR TRANSFERASE: Kinase; GLYCOLYSIS; Complete proteome.
SQ SEQUENCE 408 AA; 45372 MW; 6F3C62357F5849 CRC64;

Query Match
Best Local Similarity 1.3%; Score 7; DB 1; Length 408;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 138 PSCGRIS 144
DB 284 PSCGRIS 290

RESULT 38
VG46_BPP1 STANDARD; PRT; 424 AA.
AC P25131;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-MAY-1992 (Rel. 22, Last annotation update)
DE 46.5 kDa protein (ORF 424).
OS Bacteriophage Pfl.
OC Viruses; ssDNA viruses; Inoviridae; Inovirus.
OX NCBI_TaxID=10871;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 25102-B1;
RX MEDLINE=91186399; PubMed=2010913;
RA Hill D.F., Short N.D., Pernam R.N., Petersen G.B.;
RT "DNA sequence of the filamentous bacteriophage Pfl.";
RJ J. Mol. Biol. 218:349-364(1991).
CC -----
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CC -----
CC EMBL: X52107; CAA36334.1; -.
CC PIR: S15146; S15146.
CC SEQUENCE 424 AA; 46539 MW; 108EA88EA407BEC7 CRC64;

Query Match
Best Local Similarity 1.3%; Score 7; DB 1; Length 424;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 466 VILLALL 472
DB 230 VILLALL 236

RESULT 39
YKJ5_STRCO STANDARD; PRT; 430 AA.
ID YKJ5_STRCO
AC 09KYSO;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-FEB-2003 (Rel. 42, Last annotation update)
DE Hypothetical zinc metalloprotease SCOS695 (EC 3.4.24.-).
GN SCOS695 OR SC5H4.19.
OS Streptomyces coelicolor.
OC Bacteria; Actinobacteria; Actinobacteridae; Actinomycetales;
OC Streptomyces; Streptomyces; Streptomyces; Streptomyces.
OX NCBI_TaxID=1902;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=A3(2) / M145;

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RX MEDLINE=21996410; PubMed=12000953;
RA Bentley S.D., Chater K.F., Cardeno-Tarraga A.-M., Challis G.L.,
RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
RA Huang C.-H., Kleser T., Larke L., Murphy L., Oliver K., O'Neill S.,
RA Rabinowitz E., Rajandream M.A., Rutherford K., Rutter S.,
RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
RA Warren T., Wierhorrek A., Woodward J., Barrell B.G., Parkhill J.,
RA Hopwood D.A.;
RT "Complete genome sequence of the model actinomycete Streptomyces
RT coelicolor A3(2).";
RL Nature 417:141-147(2002).
CC -1- COFACTOR: zinc (Probable).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY M50B.
CC -1- SIMILARITY: Contains 1 PDZ/DRH domain.
CC -----
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CC -----
CC EMBL: AL393124; CAB9131.1; -.
CC InterPro: IPR001478; PDZ.
CC InterPro: IPR006025; Zn_MTPetase.
CC Pfam: PF00595; PDZ; 1.
CC Pfam: PF02163; Peptidase_M50; 1.
CC SMART: SMO0228; PDZ; 1.
CC PROSITE: PS0106; PDZ; FALSE NEG.
CC PROSITE: PS00142; ZINC_PROTEASE; 1.
CC Hypothetical protein; Hydrolase; Metalloprotease; Zinc; Transmembrane;
CC Complete proteome.
CC -----
CC METAL 20 ZINC (CATALYTIC) (POTENTIAL).
CC ACT SITE 21 ZINC (CATALYTIC) (POTENTIAL).
CC METAL 24 ZINC (CATALYTIC) (POTENTIAL).
CC TRANSMEM 122 144 POTENTIAL.
CC TRANSMEM 341 363 POTENTIAL.
CC TRANSMEM 402 424 POTENTIAL.
CC DOMAIN 146 227 PDZ.
CC SEQUENCE 430 AA; 46239 MW; 3586ABD3FD1F44F CRC64;

Query Match
Best Local Similarity 1.3%; Score 7; DB 1; Length 430;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 LVLVAD 15
DB 416 LVLVAD 422

RESULT 40
NMTH_CIOAB STANDARD; PRT; 431 AA.
ID NMTH_CIOAB
AC 097TN5;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Probable manganese transport protein nmth.
GN NMTH OR CAP0063.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Clostridia; Clostridiales; Clostridiaceae;
OC Clostridium.
OX NCBI_TaxID=1488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,

```

RA Gibson R., Lee H.M., Dubois J., Qiu D., Hlti J., Wolf Y.I.,
 RA Tatusov R.L., Sabathe F., Doucette-Stamm L., Soucaille P., Daly M.J.,
 RA Bennett G.N., Koonin E.V., Smith D.R.,
 RT "Genome sequence and comparative analysis of the solvent-producing
 RT bacterium Clostridium acetobutylicum."
 RL J. Bacteriol. 183:4823-4838(2001).
 CC -1- FUNCTION: H(+)-stimulated, highly selective, manganese uptake
 CC system (by similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Probable).
 CC -1- SIMILARITY: BELONGS TO THE NRAMP FAMILY.
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 CC -----

DR EMBL; AE001438; AK76809.1; -
 DR HAMAP; MF_00221; -; 1.
 DR InterPro; IPR001046; Nramp.
 DR Pfam; PF01566; Nramp; 1.
 DR PRINTS; PR00447; NATRESASCOMP.
 DR PRODOM; PD001861; Nramp; 1.
 DR TIGRFAMs; TIGR01197; nramp; 1.
 KW Transport; Symport; Manganese; Transmembrane; Plasmid;
 KW Complete proteome.
 FT TRANSMEM 33 53 POTENTIAL.
 FT TRANSMEM 61 81 POTENTIAL.
 FT TRANSMEM 110 130 POTENTIAL.
 FT TRANSMEM 141 161 POTENTIAL.
 FT TRANSMEM 170 190 POTENTIAL.
 FT TRANSMEM 211 231 POTENTIAL.
 FT TRANSMEM 258 278 POTENTIAL.
 FT TRANSMEM 307 327 POTENTIAL.
 FT TRANSMEM 347 367 POTENTIAL.
 FT TRANSMEM 368 388 POTENTIAL.
 FT TRANSMEM 406 426 POTENTIAL.
 SQ SEQUENCE 431 AA; 47025 MW; C44D77DDPDS028E9 CRC64;

Query Match 1.3%; Score 7; DB 1; Length 431;
 Best Local Similarity 100.0%; Pred. No. 73;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 20 ASGLSSS 26
 |||||
 Db 315 ASGLSSS 321

Search completed: October 2, 2003, 16:03:48
 Job time : 45 secs

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GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 2, 2003, 15:51:44 ; Search time 67 Seconds

(without alignments)
1277.511 Million cell updates/sec

Title: US-10-039-770a-1

Perfect score: 2822
Sequence: 1 MGLVGVQLVLVADCTIFA.....EAEENIDQDETHVWEGDY 541

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 587654 seqs, 158212981 residues

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

1: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep:.*
2: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.pep:.*
3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep:.*
4: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB.pep:.*
5: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.pep:.*
6: /cgn2_6/ptodata/2/pubppaa/PCTUS_PUBCOMB.pep:.*
7: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB.pep:.*
8: /cgn2_6/ptodata/2/pubppaa/US08_PUBCOMB.pep:.*
9: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep:.*
10: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep:.*
11: /cgn2_6/ptodata/2/pubppaa/US09C_PUBCOMB.pep:.*
12: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.pep:.*
13: /cgn2_6/ptodata/2/pubppaa/US10A_PUBCOMB.pep:.*
14: /cgn2_6/ptodata/2/pubppaa/US10B_PUBCOMB.pep:.*
15: /cgn2_6/ptodata/2/pubppaa/US10C_PUBCOMB.pep:.*
16: /cgn2_6/ptodata/2/pubppaa/US10C_NEW_PUB.pep:.*
17: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep:.*
18: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
1	404	13.8	478	12	US-10-271-145-2	Sequence 2, Appl
2	404	13.8	478	12	US-10-271-145-2	Sequence 2, Appl
3	114	3.9	549	15	US-10-156-761-8993	Sequence 8993, Ap
4	105.5	3.6	782	15	US-10-124-436-1	Sequence 1, Appl
5	105	3.6	758	12	US-09-949-039-66	Sequence 66, Appl
6	104	3.6	1253	15	US-10-146-473-72	Sequence 72, Appl
7	104	3.6	1253	10	US-09-769-508-2	Sequence 2, Appl
8	104	3.6	1255	10	US-09-854-356-1	Sequence 1, Appl
9	104	3.6	1255	11	US-09-125-2	Sequence 6, Appl
10	104	3.6	1255	11	US-09-441-411-6	Sequence 2, Appl
11	104	3.6	1255	12	US-10-313-644-2	Sequence 2, Appl
12	104	3.6	1255	15	US-10-207-655-45	Sequence 45, Appl
13	103.5	3.5	365	9	US-09-925-299-847	Sequence 847, App
14	103.5	3.5	365	11	US-09-925-299-847	Sequence 847, App
15	103.5	3.5	365	15	US-10-106-698-6387	Sequence 6387, Ap

16	103	3.5	1255	9	US-09-811-123-9	Sequence 9, Appl
17	103	3.5	1255	9	US-09-811-115-3	Sequence 3, Appl
18	103	3.5	1255	12	US-10-207-498-6	Sequence 6, Appl
19	103	3.5	1255	12	US-10-338-730-2	Sequence 2, Appl
20	103	3.5	1255	12	US-10-322-892-4	Sequence 4, Appl
21	103	3.5	1255	15	US-10-177-293-126	Sequence 126, App
22	102	3.5	470	10	US-09-859-053-36	Sequence 36, Appl
23	101.5	3.5	418	10	US-09-887-879-14	Sequence 14, Appl
24	101.5	3.5	418	12	US-09-992-964-14	Sequence 14, Appl
25	101.5	3.5	418	10	US-10-242-383-14	Sequence 14, Appl
26	101.5	3.5	467	12	US-10-280-407-6	Sequence 6, Appl
27	101.5	3.5	468	12	US-10-322-673-1	Sequence 1, Appl
28	101.5	3.5	468	13	US-10-039-785-1	Sequence 1, Appl
29	101.5	3.5	468	15	US-10-226-296-2	Sequence 2, Appl
30	101.5	3.5	468	15	US-10-226-318-2	Sequence 2, Appl
31	101.5	3.5	468	15	US-10-175-902-2	Sequence 2, Appl
32	100.5	3.4	1702	10	US-09-738-973-434	Sequence 434, App
33	100.5	3.4	1702	10	US-09-854-133-434	Sequence 434, App
34	100.5	3.4	1702	15	US-10-144-649A-434	Sequence 434, App
35	99	3.4	470	10	US-09-859-053-32	Sequence 32, Appl
36	98.5	3.4	327	9	US-09-820-893-60	Sequence 60, Appl
37	98.5	3.4	327	12	US-10-216-163-236	Sequence 236, App
38	98.5	3.4	327	15	US-10-227-884-236	Sequence 236, App
39	98.5	3.4	327	15	US-10-230-163-236	Sequence 236, App
40	98.5	3.4	327	15	US-10-230-338-236	Sequence 236, App
41	98.5	3.4	327	15	US-10-218-631-236	Sequence 236, App
42	98.5	3.4	327	15	US-10-230-414-236	Sequence 236, App
43	98.5	3.4	327	15	US-10-216-159A-236	Sequence 236, App
44	98.5	3.4	327	15	US-10-218-849-236	Sequence 236, App
45	98.5	3.4	327	15	US-10-227-873-236	Sequence 236, App

ALIGNMENTS

RESULT 1
US-10-271-145-2
Sequence 2, Application US/10271145
Publication No. US20030138450A1
GENERAL INFORMATION:
/4
APPLICANT: Lanar, David E.
APPLICANT: Dutta, Sheetfj
APPLICANT: Ware, Lisa A.
APPLICANT: Nair, Lalitha P. V.
TITLE OR INVENTION: Plasmodium falciparum AMA-1 Protein and Uses Thereof
FILE REFERENCE: 003/255/SAP
CURRENT APPLICATION NUMBER: US/10/271,145
PRIOR FILING DATE: 2002-10-15
PRIOR APPLICATION NUMBER: 10/105,717
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Apple Macintosh Microsoft Word 6.0
SEQ ID NO 2
LENGTH: 478
TYPE: PRT
ORGANISM: Artificial sequence
FEATURE:
OTHER INFORMATION: Expressed partial sequence of Plasmodium falciparum AMA-1
US-10-271-145-2

Query Match 13.8%; Score 404; DB 12; Length 478;

Best Local Similarity 27.0%; Pred. No. 6.3e-30;

Matches 123; Conservative 71; Mismatches 163; Indels 98; Gaps 18;

QY 41 GNPQANVEKTEMERENLTHHOSGIYVDLGGQKEVDGLYRBPAGLCPIWGHIELOQ 100

Db 43 GNPQANVEKTEMERENLTHHOSGIYVDLGGQKEVDGLYRBPAGLCPIWGHIELOQ 96

QY 101 PDRIPYNNLLEDDVPTKEKYGKSGNPLPGGFNNLFTVPSQGRISPFME---LLEKSN 156

Db 97 SN-----TTLVLPVATNGOYLKD---GGFAF---PTEPLMSPTLDEMRHFYKUNKY 143

157 IKASTDLCRCBAEPKTVAMDKNNKATKYRPVYDSKKRLCHILYVSMQMEGKYSV 216
144 VKNIDELTLCRHHGNNMI--PDNDKNSNYKTPAVYDDKDKCHILYIAQENNGRYCN- 200
217 KGEPPDLTWYCFKPKRSYVTENHLLYGSAYGEN--PDAFISKCPNOALRGYFGWKKGR 275
201 KDESBNNSMFCFRPAKDISFQNY-----TYSKNVVDNMKEKVCPRKNLONAKFGLMVDGN 255
276 CLDYTELTD-TVIERVESKAQCWVTFENDGVASQPHYTP--LTSQASMNDDMP----- 327
256 CEDIPHVEFPALDIFE-----CNKLVEFELS--ASDQPKQYEQHLLDYERKIKGFKNNKAS 309
328 -----LHSDQPHSGGVGRNYGFYVDTTGEGKCALSDQVPCDCLVSDSAVSYTA 377
310 MIKSAFKPTGAFKADRYSHGKGNWGNVNTETO--KCEIFNVKPTCLINNSSIATTA 366
378 AGSLSEETPNFIIPSN-----PSVTPPTPETAL 405
367 LSHPIEVENN--PCSLYKDEIMKEIERESKRIKLNDDNDEGNKKIAPRIFISDDKSL 424
406 OCTADKFPDSFGACDVQACKROKTSVGGQIQSTS 440
425 KCPDPEWVNSSTCRFFVCK-----CVERRAEVTS 454

RESULT 2
US-10-105-717-2
; Sequence 2, Application US/10105717
; Publication No. US20030032787A1
; GENERAL INFORMATION:
/4
; APPLICANT: Lanar, David E.
; APPLICANT: Dutta, Sheelaj
; APPLICANT: Ware, Lisa A.
; APPLICANT: Nair, Lalitha P. V.
; TITLE OF INVENTION: Plasmodium falciparum AMA-1 Protein and Uses Thereof
; FILE REFERENCE: 003/246/SAP
; CURRENT APPLICATION NUMBER: US/10/105,717
; CURRENT FILING DATE: 2002-07-24
; PRIOR APPLICATION NUMBER: US 60/278,616
; PRIOR FILING DATE: 2001-03-26
; NUMBER OF SEQ ID NOS: 5
; SOFTWARE: Apple Macintosh Microsoft Word 6.0
; SEQ ID NO 2
; LENGTH: 478
; TYPE: PRT
; ORGANISM: Artificial sequence
; FEATURE:
; OTHER INFORMATION: Expressed partial sequence of Plasmodium falciparum AMA-1
US-10-105-717-2

Query Match 13.8%; Score 404; DB 15; Length 478;
Best Local Similarity 27.0%; Pred. No. 6,3e-30;
Matches 123; Conservative 71; Mismatches 163; Indels 98; Gaps 18;

41 GNPFOANVMKTFMERFNLTHHOSGIYVDLQDKEVDGTLVREBAGLCPIWGKHIELQ 100
43 GNPW-----TEYMAKYDIEBVHSGIRVLDGDAVAGTQYRLPSGKCPVFGKGIITEN 96
101 PRLRYRNNFLLEDVPEKEKYKSGNPLPGGFNLNFVTPSGORISPPRME-----LLEKNSN 156
97 SN-----TTFLLTPVATGNQYLD-----GGFAF--PTEPLMSPTLDEMHHFYDNKY 143
157 IKASTDLGRCAEPKTVAMDKNNKATKYRPVYDSKKRLCHILYVSMQMEGKYSV 216
144 VKNIDELTLCRHHGNNMI--PDNDKNSNYKTPAVYDDKDKCHILYIAQENNGRYCN- 200
217 KGEPPDLTWYCFKPKRSYVTENHLLYGSAYGEN--PDAFISKCPNOALRGYFGWKKGR 275
201 KDESBNNSMFCFRPAKDISFQNY-----TYSKNVVDNMKEKVCPRKNLONAKFGLMVDGN 255
276 CLDYTELTD-TVIERVESKAQCWVTFENDGVASQPHYTP--LTSQASMNDDMP----- 327

256 CEDIPHVEFPALDIFE-----CNKLVEFELS--ASDQPKQYEQHLLDYERKIKGFKNNKAS 309
328 -----LHSDQPHSGGVGRNYGFYVDTTGEGKCALSDQVPCDCLVSDSAVSYTA 377
310 MIKSAFKPTGAFKADRYSHGKGNWGNVNTETO--KCEIFNVKPTCLINNSSIATTA 366
378 AGSLSEETPNFIIPSN-----PSVTPPTPETAL 405
367 LSHPIEVENN--PCSLYKDEIMKEIERESKRIKLNDDNDEGNKKIAPRIFISDDKSL 424
406 OCTADKFPDSFGACDVQACKROKTSVGGQIQSTS 440
425 KCPDPEWVNSSTCRFFVCK-----CVERRAEVTS 454

RESULT 3
US-10-156-761-8993
; Sequence 8993, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; CURRENT FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 8993
; LENGTH: 549
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-8993

Query Match 3.9%; Score 114; DB 15; Length 549;
Best Local Similarity 20.7%; Pred. No. 0.066;
Matches 76; Conservative 57; Mismatches 107; Indels 128; Gaps 20;

44 FOANYEMKTFMERFNLTHHOSGIYVDLQDKEVDGTLVREBAGLCPIWGKHIELQFDR 103
151 FRAKVE-----KWLGEGLDLSIRQADGNYYLP-----GLHEKVSQVS 189
104 LPRNNFLE-----DVPE-----KEYKQS-----GNPLPGGFNLNFVTPSG 140
190 LSFRLDVLLKKGGLDLPYTWDOYVYLKALKAAYPRVYFPFSDRWGQPTFGALINLYGRA- 248
141 QRISFPMBELLEKNSNIRASTDLGRCAEPKTVAMDKNNKATKYRPVYDSKKRLCHI 200
249 -----FGTKAGMSYANTAMD--TKARKVVFQATDEYQOMLEY 284
201 L--VYSQMEGKYSVSKYKGEPPDLTWYCFKPKRSYVTENHLLYGSAYGENPDAFISGC 258
285 LRKLVAELKMDPESTQDD-----AVRK-----LTSKSPF-----ISAN 321
259 PNOALRGYRFGVWK--KGRCLDYTEL-----TDVTI--BRVESKAQCWVTFENDGVASQ 310
322 PDELQNNRYNNGKQVKATTEMTFVPIGPGEVIVGSRLEGNLAVAGRAABGDS----- 376
311 PHTYPLTQASWMDM--WPLHOSDQPHSGGVGRNYGFYVD-----TTGEGKCALSDQV 364
377 -----FVAMMGVVDLW-----YSDG--GGEFAKYGVGTYYTSSGAGRYKVDGI-S 421
365 CLVSDSAA 372
422 YMGSDPSA 429


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? LOCATION: (676)..(1255)
? OTHER INFORMATION: intracellular domain (ICD)
? NAME/KEY: DOMAIN
? LOCATION: (990)..(1255)
? OTHER INFORMATION: phosphorylation domain (PD)
? NAME/KEY: DOMAIN
? LOCATION: (990)..(1048)
? OTHER INFORMATION: fragment of the phosphorylation domain, preferred
? OTHER INFORMATION: portion (delta PD)
? OS-09-854-356-1

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Query Match	3.6%	Score 104	DB 10	Length 1255
Best Local Similarity	22.5%	Pred. No. 2.2		
Matches 108	Conservative 43	Mismatches 174	Indels 156	Gaps 27

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QY      81  LYREBAGLCPIWGKHIELQDPRLRPYRNNFLEVPREKEYKQSGNLPGS---FNINFWT 137
Db      256 LHFNHSGIC-----ELHCPALVTYNTDTFBSMPN-----PEGRYTFGASCVT 297
QY      138 PSGQRISPPFMELLEKNISNIKASTDLGRCAEFA---FKTVAMDKNKKATKYVPPFYDS 193
Db      298 AC-----PNYVL-----STDVGSCTLYCPLHNGEYTAEDGTQRECKSKPCA--- 339
QY      194 KKRILCH-----ILVYSMQLMEGKKYC-----SVKGEPPDLTWYCFEPRK 232
Db      340 --RVCYGGMEHLREVBATVSANIQFACKCKIKFSLAFLPESFDODPASNTAPLQPEQL 397
QY      233 SVTENHHLIYGSAVYGENPDAF--ISKCPN-QALRG-----YRFGV-WKKGRC 276
Db      398 QVFETLEBITGYLYIASWEDSPDLDSVFONLQVIRGIILHNGAYSLTLQGLIGISMLGLRS 457
QY      277 LDYETELDTVIERVSKAQCWKTFENDVADAQO---PHTYLTYSQASNMDMWPLHOSD 332
Db      458 L-RELSSGGLALIHNTHTLCFVHT---VPMQLFRNPH-----QAL-----LHTAN 498
QY      333 QPHSGGVGRNRYGYVYDTLGE-----GKCALSDQ-----VPDCLVSDSAVSYTAAG 379
Db      499 RPEDCSVEGLACHQLCARGHCMGPRPTQVNCISQPLRGOECYBEGRVLOGLPREYVNAAR 558
QY      380 SLSEETENFIIPSNDSVTPPTETALQCTAD-----KF 412
Db      559 HCLPCHPE-CGQONGSVTCFGBE-ADQVACAHAHYKDPFCVACSPSGVKRDLSSYMPIWK 616
QY      413 PDSFACDVQACKRQKTSVGGQIQISTVDCITRADENEGSGNTALLAGLAVGVALLALL 472
Db      617 PDEBAC--QPC---PINCTHSCVLDLDDKXCPABQR--ASPLTSIIS-AVWGILLVVVL 667
QY      473 G 473
Db      668 G 668

```

```

1  RESULT 9
2  US-09-930-125-2
3  : Sequence 2, Application US/09930125
4  : Publication No. US20020193329A1
5  : GENERAL INFORMATION:
6  : APPLICANT: Hand-Zimmerman, Susan
7  : APPLICANT: Cheever, Martin A.
8  : APPLICANT: Foy, Teresa M.
9  : APPLICANT: Lodes, Michael J.
10 : APPLICANT: Kalos, Michael D.
11 : APPLICANT: McNeill, Patricia D.
12 : APPLICANT: Vedevick, Thomas S.
13 : TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY AND DIAGNOSIS
14 : OF HER-2/NEU-ASSOCIATED MALIGNANCIES
15 : FILE REFERENCE: 210121.544
16 : CURRENT APPLICATION NUMBER: US/09/930.125
17 : CURRENT FILING DATE: 2001-08-14
18 : NUMBER OF SEQ ID NOS: 25
19 : SOFTWARE: PatSeq for Windows Version 3.0
20 : SEQ ID NO 2
21 : LENGTH: 1255

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-930-125-2

```

Query Match	3.6%;	Score 104;	DB 10;	Length 1255;
Best Local Similarity	22.5%;	Pred. No. 2.2;		
Matches 108;	Conservative 43;	Mismatches 174;	Indels 156;	Gaps 27

```

QY      81  LVYEPGLCPIMKGIHEILOQPRLEPYRNPLFEDVTEKEYQSGNPLPGG---FNLUFVT 137
Db      256 LHMNSHGIC-----ELHCPLALVTYNDTDESMFN-----PEGRYTFGASCVT 297
QY      138 PSGQRISPPMELKEKNSNIKASTDLGRCAEFA---FKTVAMDKNKKATKYRYPFYDS 193
Db      298 AC-----PYNVL-----STDVGSCTLVCPILHQEVTAEDGTQRCEKSKPCA--- 339
QY      194 KRLCH-----ILVSNQJMEGKKYC-----SVKEPPDLTYCFKPRK 222
Db      340 --RVCTGLMEHLREVRAVTSANTIOEFAGCKIKIGSLAFLPESFDGPASNTAPLOEOL 397
QY      233 SVYENHLLYGSAYVGENDDAF--ISKCPN-QALRG-----YRFQV-WKKGRG 276
Db      398 QVFETLEEITGLYLSAMPDLSPLDLSVFQNLQVIRGRIHLNGAVSLTQGLGSLWGLRS 457
QY      277 LDVETLTDIVIBREVSKAQCMWKTPEENDGVA SDQ---PHTYPLTISOASWNMDMPLHQSD 332
Db      458 L-RELGSGLALIHNTHLCPVHT-----VEMDQLFRNPH-----QAL-----LHTAN 498
QY      333 QPHSGGVGNRYFYVDTTGE-----GKCALSDQ-----YBCLVSDSAAVSYTAAG 379
Db      499 RPDEDCVSGGLAQHQLCARHGCMWGPFGPQVCNCSQFLRGQECVBECCVLLQGLPREVYNAR 558
QY      380 SLSEETPNFIIIDNSVTPPTPETALQCTAD-----KF 412
Db      559 HCLPCHPE-CQPNQNSVTCFGBE-ADQCVAACAHYKDPFCVARCPSGVKCDLSYMPIWKF 616
QY      413 PDSFGACDVQACKRQKTCVSGQIGOSTSVQCTAQBQNECGSNTALLIAGLVGVTLLALL 472
Db      617 PDEEGAC-QPE--PINCTHSQVDLDKDGCPAEOR--ASPLTISIS--AVGILLVVL 667
QY      473 G 473
Db      668 G 668

```

```

RESULT 10
US-09-441-11-6
; Sequence 6, Application US/09441411
; Publication No. US2003008342A1
; GENERAL INFORMATION:
; APPLICANT: Scholler, Nathalie B.
; APPLICANT: Diels, Mary L.
; APPLICANT: Hellstrom, Ingegerd
; APPLICANT: Hellstrom, Karl Erik
; TITLE OF INVENTION: SURFACE RECEPTOR ANTIGEN VACCINES
; FILE REFERENCE: 730033.409
; CURRENT APPLICATION NUMBER: US/09/441,411
; CURRENT FILING DATE: 1999-11-16
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-441-11-6

Query Match      3.6%; Score 104; DB 11; Length 1255;
Best Local Similarity 22.5%; Pred. No. 2.2;
Matches 108; Conservative 43; Mismatches 174; Indels 156; Gaps 27;

Oy      81  L Y R P A L C P I W G H I L L Q Q D R L P Y N N F L E D V P T E R E Y K Q S G N P L P G C --- P Y L N F V T 137
Db      256 L H F H N S G I C ----- S L H C A L V T Y N T D F F E S M P N ----- P E G R Y T G A S C V T 297

```

Qy 138 PSGQRISPPMELLEKNSTIKASTDLGRCAEFA-----FKTVAMDGNKATKRYPFVYDS 193
 Db 298 AC-----PYNVL-----STDVGSCTLVCPPLHNOEVTAEDETOCEKSKPCA--- 339
 Qy 194 KKRLLCH-----ILVYSQMLEGKKYC-----SYGGEPPDLTWYCFKPRK 232
 Db 340 --RVCYGLGMEHLREVRAVTSANIOEPAGCKKIFGSLAFLPESFGDDPASNTAPLQPEOL 397
 Qy 233 SVTEHHLLIYGSAYVGENPDAF--ISKCPN-QALRG-----YRFGV-WKKGRG 276
 Db 398 QVFETLEITGYLYISAMPDSL.PDLISVFQNLQVIRGRILHNGAYSLTLQGLISWLGKRS 457
 Qy 277 LDYTELDTVIERVESKACQWKTFFENDGVASDQ---PHTYPLTSQASWMDWMLHOSD 332
 Db 458 L--RELGSGLALIHNNHLCFVHT-----VPMDQLFRNPH-----QAL-----LHTAN 498
 Qy 333 QPHSGGVGRNYGFYVDTTGE-----GKCALSDQ-----VPDCLVSDSAVSYTAAG 379
 Db 499 RPEDECVGEGLAGHQLCARGHCWGPGPTQCVNCSQPLRGQECVEBCRYLQGLPREVYVAR 558
 Qy 380 SLSEETPNFIIPNSPVTPTPTETALQCTAD-----KF 412
 Db 559 HCLPCHPE-CQPNQSVTCFGE-ADQCVACAHYKDPFCVARGPSGVKPDLSYMPWKF 616
 Qy 413 PDSFGACDVQACKRKQKTSVCGGQIOSTVDCITADEQNECGSNTALIGLAVGYLLALL 472
 Db 617 PDEEGAC--QPC---PINCTHSCVLDLDDKGCPRABOR--ASPLTSIIS--AVVGILLVVL 667
 Qy 473 G 473
 Db 668 G 668

RESULT 11

US-10-313-644-2
 ; Sequence 2, Application US/10313644
 ; Publication No. US20030157119A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gaiger, Alexander
 ; APPLICANT: Cheever, Martin A.
 ; APPLICANT: Hand-Zimmerman, Susan
 ; TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND THERAPY OF HEMATOLOGICAL
 ; FILE REFERENCE: 210121.483C3
 ; CURRENT APPLICATION NUMBER: US/10/313,644
 ; CURRENT FILING DATE: 2002-12-04
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: PatSeq for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 1255
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 ; US-10-313-644-2

Query Match 3.6%; Score 104; DB 12; Length 1255;
 Best Local Similarity 22.5%; Pred. No. 2.2; 174; Indels 156; Gaps 27;
 Matches 108; Conservative 43; Mismatches 174;
 Qy 81 LYREPAGLCPWKGKHEIQPDRLPYRNNFLEDVTEKEYKQSGNPLPGG---FNLNFTY 137
 Db 256 LHFNSHGIC-----ELHCPALVTYNTDTFESMPN-----PEGRTYFGASCVT 297
 Qy 138 PSGQRISPPMELLEKNSTIKASTDLGRCAEFA-----FKTVAMDGNKATKRYPFVYDS 193
 Db 298 AC-----PYNVL-----STDVGSCTLVCPPLHNOEVTAEDETOCEKSKPCA--- 339
 Qy 194 KKRLLCH-----ILVYSQMLEGKKYC-----SYGGEPPDLTWYCFKPRK 232
 Db 340 --RVCYGLGMEHLREVRAVTSANIOEPAGCKKIFGSLAFLPESFGDDPASNTAPLQPEOL 397
 Qy 233 SVTEHHLLIYGSAYVGENPDAF--ISKCPN-QALRG-----YRFGV-WKKGRG 276

Db 398 QVFETLEITGYLYISAMPDSL.PDLISVFQNLQVIRGRILHNGAYSLTLQGLISWLGKRS 457
 Qy 277 LDYTELDTVIERVESKACQWKTFFENDGVASDQ---PHTYPLTSQASWMDWMLHOSD 332
 Db 458 L--RELGSGLALIHNNHLCFVHT-----VPMDQLFRNPH-----QAL-----LHTAN 498
 Qy 333 QPHSGGVGRNYGFYVDTTGE-----GKCALSDQ-----VPDCLVSDSAVSYTAAG 379
 Db 499 RPEDECVGEGLAGHQLCARGHCWGPGPTQCVNCSQPLRGQECVEBCRYLQGLPREVYVAR 558
 Qy 380 SLSEETPNFIIPNSPVTPTPTETALQCTAD-----KF 412
 Db 559 HCLPCHPE-CQPNQSVTCFGE-ADQCVACAHYKDPFCVARGPSGVKPDLSYMPWKF 616
 Qy 413 PDSFGACDVQACKRKQKTSVCGGQIOSTVDCITADEQNECGSNTALIGLAVGYLLALL 472
 Db 617 PDEEGAC--QPC---PINCTHSCVLDLDDKGCPRABOR--ASPLTSIIS--AVVGILLVVL 667
 Qy 473 G 473
 Db 668 G 668

RESULT 12

US-10-207-655-45
 ; Sequence 45, Application US/10207655
 ; Publication No. US20030118592A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Ledbetter, Jeffrey A.
 ; APPLICANT: Hayden-Ledbetter, Martha S.
 ; TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
 ; FILE REFERENCE: 390069.401C1
 ; CURRENT APPLICATION NUMBER: US/10/207,655
 ; CURRENT FILING DATE: 2002-07-25
 ; NUMBER OF SEQ ID NOS: 426
 ; SOFTWARE: PatentIn version 3.0
 ; SEQ ID NO 45
 ; LENGTH: 1255
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-207-655-45

Query Match 3.6%; Score 104; DB 15; Length 1255;
 Best Local Similarity 22.5%; Pred. No. 2.2;
 Matches 108; Conservative 43; Mismatches 174; Indels 156; Gaps 27;
 Qy 81 LYREPAGLCPWKGKHEIQPDRLPYRNNFLEDVTEKEYKQSGNPLPGG---FNLNFTY 137
 Db 256 LHFNSHGIC-----ELHCPALVTYNTDTFESMPN-----PEGRTYFGASCVT 297
 Qy 138 PSGQRISPPMELLEKNSTIKASTDLGRCAEFA-----FKTVAMDGNKATKRYPFVYDS 193
 Db 298 AC-----PYNVL-----STDVGSCTLVCPPLHNOEVTAEDETOCEKSKPCA--- 339
 Qy 194 KKRLLCH-----ILVYSQMLEGKKYC-----SYGGEPPDLTWYCFKPRK 232
 Db 340 --RVCYGLGMEHLREVRAVTSANIOEPAGCKKIFGSLAFLPESFGDDPASNTAPLQPEOL 397
 Qy 233 SVTEHHLLIYGSAYVGENPDAF--ISKCPN-QALRG-----YRFGV-WKKGRG 276
 Db 398 QVFETLEITGYLYISAMPDSL.PDLISVFQNLQVIRGRILHNGAYSLTLQGLISWLGKRS 457
 Qy 277 LDYTELDTVIERVESKACQWKTFFENDGVASDQ---PHTYPLTSQASWMDWMLHOSD 332
 Db 458 L--RELGSGLALIHNNHLCFVHT-----VPMDQLFRNPH-----QAL-----LHTAN 498
 Qy 333 QPHSGGVGRNYGFYVDTTGE-----GKCALSDQ-----VPDCLVSDSAVSYTAAG 379
 Db 499 RPEDECVGEGLAGHQLCARGHCWGPGPTQCVNCSQPLRGQECVEBCRYLQGLPREVYVAR 558
 Qy 380 SLSEETPNFIIPNSPVTPTPTETALQCTAD-----KF 412
 Db 559 HCLPCHPE-CQPNQSVTCFGE-ADQCVACAHYKDPFCVARGPSGVKPDLSYMPWKF 616

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QY 413 PDSTGACDVQACKQKTSVGGQIQSTSVDTADEQNECGSNALIAAGLVALL 472
Db 617 PDEEGAC--QC---PINCSTCVLDLDDKGPAPQR--ASPLTSIIS--AVGILLVVL 667
QY 473 G 473
Db 668 G 668

RESULT 13
US-09-925-299-847
; Sequence 847, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 847
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-299-847

Query Match 3.5%; Score 103.5; DB 9; Length 365;
Best Local Similarity 19.7%; Pred. No. 0.36;
Matches 93; Conservative 48; Mismatches 121; Indels 211; Gaps 22;

QY 101 PDRLPYNNFLEDPVTEKE---YKQGNP-----LPG-----GFNLFVTPSGQRIS-P 145
Db 6 PGCGPWVLPSPLPDQTDLDPRPGSRRTGRPDMAAELPGFLCGALLGFLCLSGLAWEVK 65
QY 146 FPMELLEKNINIKASTDLGRCAEFAPKTVAMDKNKATKYRYPVYDSKKRLCHILVYSM 205
Db 66 VPTPEPL-----STPLGKTAEILT-----C----- 83
QY 206 QLMGKKYCSVKGEPPDLTWYCFKPKRSVTENHLLIYSAVYGENPDATISKCPNOLRG 265
Db 84 -----TYSTVSGSFALWSPVOPGKRISHSHILYFT-----NG 118
QY 266 YRFGVWKKGRCCLDYTELTDVIERVESKACQWKTFFENDVYASDQPHTYPLTQSASNDW 325
Db 119 HLYPTGSKSRVSLQNPPTV-----GVA-----TLKLTID----- 148
QY 326 WPLHQSOPHSGGVGRNYGYVDTTGEKCALSDQVPCLVSAVSYTAAGSLSEET 385
Db 149 --VHPSD-----TGTYLQVANNP-PDFTYNGLGILNLTIV----- 179
QY 386 PNFIFPSNP-----SVTPPTETALQCTADK-----FPDSFGACDVQACKR 426
Db 180 --LVPPSNPLCSQSGQTSVGGSTALRCSSSGAKRPVYNNVRLGTFTPPSGSNVQ----- 233
QY 427 QKTSVGGQIQSTSVDTAD-----EQNECGS-----NTALIAGLAVG---G 465
Db 234 ---DEVSGQLITLNLSTLSTSGTYRCVATNQMGASCELTLSTVTPSGGRVAGALIGVLG 290
QY 466 VLLALLGGCGYFAKRLDRNKGVQAHHHEHFQSDRGARKRP---SDLMQEA 515
Db 291 VLLLSV-----AAFLVAFQERKKRPETYGGSDLREDA 325

RESULT 14
US-09-925-299-847
; Sequence 847, Application US/09925299
; Publication No. US20030040617A9
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; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 847
; LENGTH: 365
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-299-847

Query Match 3.5%; Score 103.5; DB 11; Length 365;
Best Local Similarity 19.7%; Pred. No. 0.36;
Matches 93; Conservative 48; Mismatches 121; Indels 211; Gaps 22;

QY 101 PDRLPYNNFLEDPVTEKE---YKQGNP-----LPG-----GFNLFVTPSGQRIS-P 145
Db 6 PGCGPWVLPSPLPDQTDLDPRPGSRRTGRPDMAAELPGFLCGALLGFLCLSGLAWEVK 65
QY 146 FPMELLEKNINIKASTDLGRCAEFAPKTVAMDKNKATKYRYPVYDSKKRLCHILVYSM 205
Db 66 VPTPEPL-----STPLGKTAEILT-----C----- 83
QY 206 QLMGKKYCSVKGEPPDLTWYCFKPKRSVTENHLLIYSAVYGENPDATISKCPNOLRG 265
Db 84 -----TYSTVSGSFALWSPVOPGKRISHSHILYFT-----NG 118
QY 266 YRFGVWKKGRCCLDYTELTDVIERVESKACQWKTFFENDVYASDQPHTYPLTQSASNDW 325
Db 119 HLYPTGSKSRVSLQNPPTV-----GVA-----TLKLTID----- 148
QY 326 WPLHQSOPHSGGVGRNYGYVDTTGEKCALSDQVPCLVSAVSYTAAGSLSEET 385
Db 149 --VHPSD-----TGTYLQVANNP-PDFTYNGLGILNLTIV----- 179
QY 386 PNFIFPSNP-----SVTPPTETALQCTADK-----FPDSFGACDVQACKR 426
Db 180 --LVPPSNPLCSQSGQTSVGGSTALRCSSSGAKRPVYNNVRLGTFTPPSGSNVQ----- 233
QY 427 QKTSVGGQIQSTSVDTAD-----EQNECGS-----NTALIAGLAVG---G 465
Db 234 ---DEVSGQLITLNLSTLSTSGTYRCVATNQMGASCELTLSTVTPSGGRVAGALIGVLG 290
QY 466 VLLALLGGCGYFAKRLDRNKGVQAHHHEHFQSDRGARKRP---SDLMQEA 515
Db 291 VLLLSV-----AAFLVAFQERKKRPETYGGSDLREDA 325

RESULT 15
US-10-106-698-6387
; Sequence 6387, Application US/10106698
; Publication No. US20030109690A1
; GENERAL INFORMATION:
; APPLICANT: Ruben et al.
; TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
; FILE REFERENCE: PA0056P1
; CURRENT APPLICATION NUMBER: US/10/106,698
; CURRENT FILING DATE: 2002-03-27
; PRIOR APPLICATION NUMBER: PCT/US00/26524
; PRIOR FILING DATE: 2000-09-28
; PRIOR APPLICATION NUMBER: US 60/157,137
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: US 60/163,280
; PRIOR FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 8564
; SOFTWARE: Patentin Ver. 3.0
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SEQ ID NO 6387
 LENGTH: 365
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-698-6387

Query Match 3.5%; Score 103.5; DB 15; Length 365;
 Best Local Similarity 19.7%; Pred. No. 0.36; Indels 211; Gaps 22;
 Matches 93; Conservative 48; Mismatches 121

101 PDLRYNNFLDVPTEKE---YKSGNP-----LPG---GNLNFVTPSGORIS-P 145
 6 PGCGWVLPSPDPTQDLDPRPGRSRTGRDPAAMALPGLCGALGLGSLAVEYK 65
 146 PFMELLEKNKNIKASTDLGRCAEFAPKTYAMDKNKATKYRPFYVYDSKKLCHLYSM 205
 66 VTEPL-----STPLGKTAELE-----C----- 83
 206 QLMEEKYCSVKGPEPDLTWYCFKPKSVTENHLLIYGSAYVGENPDAFISKCPQALRG 265
 84 -----TSTSVGDSFPALEMSFVQPKPTSESHPLVFT-----NG 118
 266 YRFGWKGRCLDYELDTVIERVESKAQCWKTFFENDVASDQPHYPLTSQASNDW 325
 119 HLYPTGSKSKRYSLQNPPTV-----GVA-----TLKLTID----- 148
 326 WPLHSDOPHSGGVGRNNGFYVDVTGEGKALSDQVDPCLVSDAANSYTAGSLSEET 385
 149 --VHESD-----TGTYLCQVNNP-PDFTNGGLMLTV----- 179
 386 PNFIIIPSNP-----SVTPPTPETAQCTADK-----FPDSFGACDYOACKR 426
 180 --LVPSNPFLCSGSGCTSVGSTALLKCSSEGAPEKVVWVWALGTFPTSPSSMQV---- 233
 427 QKTSVCGQIOSTSVYDCTAD-----EQNEGCS-----NTALIAGLVAG--G 465
 234 ---DEVSGQLITLNTSLTSSGTYRCVATNQMSASCELFTSTPEQGRVAGALIGVLG 290
 466 VLLALLGGCCYFAKRLDNKGYOAAHHEHFERQSDRGAKRP---SDLMQEA 515
 291 VLLLSV-----AAFCLVRFQKERGKKPKETGYGSDLREDA 325

RESULT 16
 US-09-811-123-9
 Sequence 9, Application US/09811123
 Patent No. US20020001587A1
 GENERAL INFORMATION:
 APPLICANT: Sharon Erickson
 APPLICANT: Ralph Schwall
 APPLICANT: Mark Sliwowski
 TITLE OF INVENTION: METHODS OF TREATMENT USING ANTI-EBB
 FILE REFERENCE: GENENT. 073A2
 CURRENT APPLICATION NUMBER: US/09/811,123
 CURRENT FILING DATE: 2001-03-16
 PRIOR APPLICATION NUMBER: 60/238,327
 PRIOR FILING DATE: 2000-10-05
 PRIOR APPLICATION NUMBER: 09/602,530
 PRIOR FILING DATE: 2000-06-23
 NUMBER OF SEQ ID NOS: 11
 SOFTWARE: FaastSeq for Windows Version 4.0
 SEQ ID NO 9
 LENGTH: 1255
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-811-123-9

Query Match 3.5%; Score 103; DB 9; Length 1255;
 Best Local Similarity 22.2%; Pred. No. 2.7;
 Matches 107; Conservative 44; Mismatches 174; Indels 156; Gaps 27;
 81 LVREPAGLCPWIKHIELOQPDRLPRNNFLDVPTEKEVKSGNPPLPGS---FNLNFTV 137

DB 256 LHFHNSGIC-----ELHCPALVTYNTDFESMN-----PEGRYTGASCVT 297
 QY 138 PEGGRISPEFMELLEKNKNIKASTDLGRCAEFA-----FKTYAMDKNKATKYRPFYVDS 193
 DB 298 AC-----PYNVL-----STDVSGCTLVCPHLNHOEVTAEQTCERCKSKPCA-- 339
 QY 194 KKRLLCH-----ILVSNQLMGKKYC-----SVKGEPPDLTWYCFKPKR 232
 DB 340 --RVCYGLGMHLREAVRATVSANIQEFAGCKKIGSLAFLPESDGDPASTALQPEQL 397
 QY 233 SVTENHLLIYGSAYVGENPDAF--ISKCPN-QALRG-----YRFGV-WKKGRC 276
 DB 398 QVFETLEETGYLVISAMPDLPDLSTVFOQLVIRGRILHNGAYSLTLQIGIGISLGRS 457
 QY 277 LDYBELDVTVIERVESKAQCWKTFFENDVASDQ-----PHYPLTSQASNDWVPLHOSD 332
 DB 458 L--RELGSGLALHNNHLCFVHT-----VWMDLFRNPH-----QAL-----LHTAN 498
 QY 333 QPHSGVGRNNGFYVDVTGE-----GKCALSDQ-----VPCLVSDAANSYTAG 379
 DB 499 RPEDECGEGGLACHOLCARGHCMGPGPTQCVNCSQFLRGQECVECRVLOGLPREYNAR 558
 QY 380 SLSEETPNFIIPSNPSVTPPTPETAQCTAD-----KF 412
 DB 559 HCLPCHPE-CQPKNGSVTCFGE-ADQVCAHYKDPFCVARGPSGVKPLSYMPIKF 616
 QY 413 PDSFACVQACKQKTSVCGQIOSTSVYDCTABQNEGCSNTALIAGLVAGVLLALL 472
 DB 617 PDEBAGC--QPC---PINCHSCVDLDKGCAPABOR--ASPLTIVS--AAVGLILVVL 667
 QY 473 G 473
 DB 668 G 668

RESULT 17
 US-09-811-115-3
 Sequence 3, Application US/09811115
 Patent No. US20020005736A1
 GENERAL INFORMATION:
 APPLICANT: Erickson, Sharon
 APPLICANT: Schwall, Ralph
 APPLICANT: King, Kathleen
 TITLE OF INVENTION: HER-2 TRANSGENIC NON-HUMAN TUMOR MODEL
 FILE REFERENCE: GENENT. 034A
 CURRENT APPLICATION NUMBER: US/09/811,115
 CURRENT FILING DATE: 2001-03-16
 PRIOR APPLICATION NUMBER: 60/189,844
 PRIOR FILING DATE: 2000-03-16
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: FaastSeq for Windows Version 4.0
 SEQ ID NO 3
 LENGTH: 1255
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-09-811-115-3

Query Match 3.5%; Score 103; DB 9; Length 1255;
 Best Local Similarity 22.2%; Pred. No. 2.7;
 Matches 107; Conservative 44; Mismatches 174; Indels 156; Gaps 27;
 81 LVREPAGLCPWIKHIELOQPDRLPRNNFLDVPTEKEVKSGNPPLPGS---FNLNFTV 137
 DB 256 LHFHNSGIC-----ELHCPALVTYNTDFESMN-----PEGRYTGASCVT 297
 QY 138 PEGGRISPEFMELLEKNKNIKASTDLGRCAEFA-----FKTYAMDKNKATKYRPFYVDS 193
 DB 298 AC-----PYNVL-----STDVSGCTLVCPHLNHOEVTAEQTCERCKSKPCA-- 339
 QY 194 KKRLLCH-----ILVSNQLMGKKYC-----SVKGEPPDLTWYCFKPKR 232
 DB 340 --RVCYGLGMHLREAVRATVSANIQEFAGCKKIFGSLAFLPESDGDPASTALQPEQL 397

QY 223 SYTENHHLIYGSAYVGENPDAF--ISKCPN-QALRG-----YRFGV-WKKGRC 276
DB 398 QVFETLEETITGLYISAMPDSL.PDLISVFQNLQVIRGLHNGAYSLTLQGLISWLGARS 457
QY 277 LDYELTDTVIERVESKQAQCKWKTENDGVASDQ---PHITYPLTSQASNDWMLHOSD 332
DB 458 L--RELGSGLALIHNNHLCFVHT---VPMDOLEFRNPH-----QAL-----LHTAN 498
QY 333 QPHSGGVGRNRYFYVDTTGE-----GKCALSDQ-----VPCULVSDSAVSYTAAG 379
DB 499 RPEDECVEGLACHQLCARHGWGPGPTQCVNCSQFLRGQCEVBCRYLQGLPREYVNR 558
QY 380 SLSEETPNFIIPSNPSVTPPTETALQCTAD-----KF 412
DB 559 HCLPCHPE-COPONGSVTCFGE-ADQVCAHYKDPFCVARGSPGVKPDLSYMPWK 616
QY 413 PDSFGACDVQACKRQKTSVCGGQIOSTSVDTADEQNECGSNTALLAGLAVGVLLALL 472
DB 617 PDEEGAC--QPC---PINCTHSCVDLDDKCPAQR--ASPLTSIVS--AVGILLVVL 667
QY 473 G 473
DB 668 G 668

RESULT 18

US-10-207-498-6
; Sequence 6, Application US/10207498
; Publication No. US20030143568A1
; GENERAL INFORMATION:
; APPLICANT: Elizebeth Singer
; APPLICANT: Ralf Landgraf
; APPLICANT: Dennis J. Slamon
; APPLICANT: David Eisenberg
; TITLE OF INVENTION: METHODS AND MATERIALS FOR CHARACTERIZING
; TITLE OF INVENTION: AND MODULATING INTERACTIONS BETWEEN HERGULIN AND HER3
; FILE REFERENCE: 30448.103-US-01
; CURRENT APPLICATION NUMBER: US/10/207,498
; PRIOR FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 60/308,431
; PRIOR FILING DATE: 2001-07-27
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 6
; LENGTH: 1255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-207-498-6

Query Match 3.5%; Score 103; DB 12; Length 1255;
Best Local Similarity 22.2%; Pred. No. 2.7; Indels 156; Gaps 27;
Matches 107; Conservative 44; Mismatches 174;

QY 81 LYREPAGLCPIWGHIELOQDRLPYRNNFLEDVTEKEYKQSGNPLPGG---FNLANFVT 137
DB 256 LHFHNSGIC-----ELHCPALVTYNTDTFESMEN-----DEGRYTFGASCVT 297
QY 138 PSGQRISFPFMELEKSNINIKASTDLGRCAEFA---FKTVAMDKNKATKRYRPFYVDS 193
DB 298 AC-----PYNVL-----STDVGSCTLVCPHLHNOEVTAEADGTQCEKSKPCA--- 339
QY 194 KKRLLCH-----ILVSMQLMGKKYC-----SYKGEPDLTWYCFKPRK 232
DB 340 --RVCYGLGMEHLREVRATVSANIQEPAGCKKIPGSLAFLEPSFDGDPASNTAPLQPEQL 397
QY 233 SVTENHHLIYGSAYVGENPDAF--ISKCPN-QALRG-----YRFGV-WKKGRC 276
DB 398 QVFETLEETITGLYISAMPDSL.PDLISVFQNLQVIRGLHNGAYSLTLQGLISWLGARS 457
QY 277 LDYELTDTVIERVESKQAQCKWKTENDGVASDQ---PHITYPLTSQASNDWMLHOSD 332
DB 458 L--RELGSGLALIHNNHLCFVHT---VPMDOLEFRNPH-----QAL-----LHTAN 498

QY 333 QPHSGGVGRNRYFYVDTTGE-----GKCALSDQ-----VPCULVSDSAVSYTAAG 379
DB 499 RPEDECVEGLACHQLCARHGWGPGPTQCVNCSQFLRGQCEVBCRYLQGLPREYVNR 558
QY 380 SLSEETPNFIIPSNPSVTPPTETALQCTAD-----KF 412
DB 559 HCLPCHPE-COPONGSVTCFGE-ADQVCAHYKDPFCVARGSPGVKPDLSYMPWK 616
QY 413 PDSFGACDVQACKRQKTSVCGGQIOSTSVDTADEQNECGSNTALLAGLAVGVLLALL 472
DB 617 PDEEGAC--QPC---PINCTHSCVDLDDKCPAQR--ASPLTSIVS--AVGILLVVL 667
QY 473 G 473
DB 668 G 668

RESULT 19

US-10-338-730-2
; Sequence 2, Application US/10338730
; Publication No. US20030147905A1
; GENERAL INFORMATION:
; APPLICANT: Genzyme Corporation
; APPLICANT: Nicolette, Charles A.
; TITLE OF INVENTION: THERAPEUTIC COMPOUNDS
; FILE REFERENCE: 5017C
; CURRENT APPLICATION NUMBER: US/10/338,730
; PRIOR FILING DATE: 2003-01-08
; PRIOR APPLICATION NUMBER: US 09/527,487
; PRIOR FILING DATE: 2002-03-16
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 2
; LENGTH: 1255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-338-730-2

Query Match 3.5%; Score 103; DB 12; Length 1255;
Best Local Similarity 22.2%; Pred. No. 2.7; Indels 156; Gaps 27;
Matches 107; Conservative 44; Mismatches 174;

QY 81 LYREPAGLCPIWGHIELOQDRLPYRNNFLEDVTEKEYKQSGNPLPGG---FNLANFVT 137
DB 256 LHFHNSGIC-----ELHCPALVTYNTDTFESMEN-----DEGRYTFGASCVT 297
QY 138 PSGQRISFPFMELEKSNINIKASTDLGRCAEFA---FKTVAMDKNKATKRYRPFYVDS 193
DB 298 AC-----PYNVL-----STDVGSCTLVCPHLHNOEVTAEADGTQCEKSKPCA--- 339
QY 194 KKRLLCH-----ILVSMQLMGKKYC-----SYKGEPDLTWYCFKPRK 232
DB 340 --RVCYGLGMEHLREVRATVSANIQEPAGCKKIPGSLAFLEPSFDGDPASNTAPLQPEQL 397
QY 233 SVTENHHLIYGSAYVGENPDAF--ISKCPN-QALRG-----YRFGV-WKKGRC 276
DB 398 QVFETLEETITGLYISAMPDSL.PDLISVFQNLQVIRGLHNGAYSLTLQGLISWLGARS 457
QY 277 LDYELTDTVIERVESKQAQCKWKTENDGVASDQ---PHITYPLTSQASNDWMLHOSD 332
DB 458 L--RELGSGLALIHNNHLCFVHT---VPMDOLEFRNPH-----QAL-----LHTAN 498
QY 333 QPHSGGVGRNRYFYVDTTGE-----GKCALSDQ-----VPCULVSDSAVSYTAAG 379
DB 499 RPEDECVEGLACHQLCARHGWGPGPTQCVNCSQFLRGQCEVBCRYLQGLPREYVNR 558
QY 380 SLSEETPNFIIPSNPSVTPPTETALQCTAD-----KF 412
DB 559 HCLPCHPE-COPONGSVTCFGE-ADQVCAHYKDPFCVARGSPGVKPDLSYMPWK 616
QY 413 PDSFGACDVQACKRQKTSVCGGQIOSTSVDTADEQNECGSNTALLAGLAVGVLLALL 472

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Db      617 PDEBAGAC--QPC---PINCTHSCVDLDDKGCBAEQR--ASPLTSIVS--AVVIGILLVVVL 667
QY      473 G 473
Db      668 G 668

RESULT 20
US-10-322-892-4
; Sequence 4, Application US/10322892
; Publication No. US20030171257A1
; GENERAL INFORMATION:
; APPLICANT: STIRBL, ROBERT C.
; APPLICANT: SNEAD, MALCOLM L.
; APPLICANT: XU, JIMMY
; APPLICANT: VITETTA, ELLEN S.
; APPLICANT: WILK, PETER J.
; TITLE OF INVENTION: METHOD AND RELATED COMPOSITION EMPLOYING NANOSTRUCTURES
; FILE REFERENCE: W07-505
; CURRENT APPLICATION NUMBER: US/10/322,892
; CURRENT FILING DATE: 2002-12-18
; PRIOR APPLICATION NUMBER: 60/342,894
; PRIOR FILING DATE: 2001-12-19
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 1255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-322-892-4

Query Match      3.5%; Score 103; DB 12; Length 1255;
Best Local Similarity 22.2%; Pred. No. 2.7; Indels 156; Gaps 27;
Matches 107; Conservative 44; Mismatches 174; Indels 156; Gaps 27;

QY      81 LYREPAAGCPIMGKHIELQOPDRLPYRNNFLEDVPTKEKYKSGNPLPGG---FNLNFT 137
      256 LHPNHSIC-----ELHCPALVTYNTDTFESMPN-----PEGRTFGASCVT 297
      138 PEGQRISPPMELLENKSNIKASTDLCRCABFA---FTVAMDKNKATKRYPFVYDS 193
      298 AC-----PYNVL-----STDVGSCTLVCPHNGEVTAEEDGTQREKSKPCA--- 339
      194 KKRLLCH-----ILVYSQMLMEGKKYC-----SVKGEPDRLTWYCFKPRK 232
      340 --RVCGGLGMEHLREVRAVTSANIQEPAGCKIFGSLAFLPESFDGDPASNTAPLOPEOL 397
      233 SVTENHHLIYGSAYGENPDAF--ISKCPN-QALRG-----YRFGV-WKKGR 276
      398 QVFETLEETITGYLISAWPDSLPDLSVPQNLQVIRGRILHNGAVSLTLQGLISWGLRS 457
      277 LDYTELDTVIERVESKAQCWVKTFFENDGVASDQ---PHTYPLTQASWMDMPLHOSD 332
      458 L--RELGSGLALIHNTLHCFVHT-----VPMQDLFRNPH-----QAL-----LHTAN 498
      333 QHSGGVGNRYGYVDTTGE-----GKCALSDQ-----VPDCLVSDSAVSYTAAG 379
      499 RPEDECVGGLACHQICARHCGCPGPTQCVCNCSQFLRGOECVEEGRVLOGLPREYVNR 558
      380 SLSEETPNFLIPSPNPTPTETALQCTAD-----XK 412
      559 HCLPCHPE-CQPNNGSVTCGPRE-ADQCVACAHYKDPFCVANCSPGSKVDPDLSYMWKWF 616
      413 PDSFGACDVQACKRQKTSVCGGQIGSTSVDTCTADEONEGCSNTALAGLAVGVLLALL 472
      617 PDEBAGAC--QPC---PINCTHSCVDLDDKGCBAEQR--ASPLTSIVS--AVVIGILLVVVL 667

QY      473 G 473
Db      668 G 668

RESULT 21

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US-10-177-293-126
; Sequence 126, Application US/10177293
; Publication No. US20030124126A1
; GENERAL INFORMATION:
; APPLICANT: Lillie, James
; APPLICANT: Glatc, Karen
; APPLICANT: Zhao, Xumei
; APPLICANT: Gannavarpu, Manjula
; APPLICANT: Kamatkar, Shubhangi
; APPLICANT: Mertens, Maureen
; APPLICANT: Myer, Vic
; APPLICANT: Wang, Youzhen
; APPLICANT: Xu, Yongyao
; APPLICANT: Hoersch, Sebastian
; APPLICANT: Monahan, John
; APPLICANT: Meyers, Rachel E.
; APPLICANT: Baet Jr., Robert C.
; APPLICANT: Hortobagyi, Gabriel N.
; APPLICANT: Puzatzi, Lajos
; APPLICANT: Meric, Funda
; APPLICANT: Sabin, Aysegul
; APPLICANT: Mills, Gordon B.
; TITLE OF INVENTION: COMPOSITIONS, KITS, AND METHODS FOR IDENTIFICATION, ASSESSMENT,
; TITLE OF INVENTION: PREVENTION, AND THERAPY OF BREAST CANCER
; FILE REFERENCE: MRI-038
; CURRENT APPLICATION NUMBER: US/10/177,293
; CURRENT FILING DATE: 2002-06-21
; PRIOR APPLICATION NUMBER: US 60/299,887
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: US 60/301,572
; PRIOR FILING DATE: 2001-06-27
; PRIOR APPLICATION NUMBER: US 60/306,501
; PRIOR FILING DATE: 2001-07-18
; PRIOR APPLICATION NUMBER: US 60/325,002
; PRIOR FILING DATE: 2001-09-25
; PRIOR APPLICATION NUMBER: US 60/362,585
; PRIOR FILING DATE: 2002-03-05
; PRIOR APPLICATION NUMBER: US 60/xxx,xxx
; PRIOR FILING DATE: 2002-05-14
; NUMBER OF SEQ ID NOS: 506
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 126
; LENGTH: 1255
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-177-293-126

Query Match      3.5%; Score 103; DB 15; Length 1255;
Best Local Similarity 22.2%; Pred. No. 2.7;
Matches 107; Conservative 44; Mismatches 174; Indels 156; Gaps 27;

QY      81 LYREPAAGCPIMGKHIELQOPDRLPYRNNFLEDVPTKEKYKSGNPLPGG---FNLNFT 137
      256 LHPNHSIC-----ELHCPALVTYNTDTFESMPN-----PEGRTFGASCVT 297
      138 PEGQRISPPMELLENKSNIKASTDLCRCABFA---FTVAMDKNKATKRYPFVYDS 193
      298 AC-----PYNVL-----STDVGSCTLVCPHNGEVTAEEDGTQREKSKPCA--- 339
      194 KKRLLCH-----ILVYSQMLMEGKKYC-----SVKGEPDRLTWYCFKPRK 232
      340 --RVCGGLGMEHLREVRAVTSANIQEPAGCKIFGSLAFLPESFDGDPASNTAPLOPEOL 397
      233 SVTENHHLIYGSAYGENPDAF--ISKCPN-QALRG-----YRFGV-WKKGR 276
      398 QVFETLEETITGYLISAWPDSLPDLSVPQNLQVIRGRILHNGAVSLTLQGLISWGLRS 457
      277 LDYTELDTVIERVESKAQCWVKTFFENDGVASDQ---PHTYPLTQASWMDMPLHOSD 332
      458 L--RELGSGLALIHNTLHCFVHT-----VPMQDLFRNPH-----QAL-----LHTAN 498
      333 QHSGGVGNRYGYVDTTGE-----GKCALSDQ-----VPDCLVSDSAVSYTAAG 379

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Db 499 RPEDECBGSLACIHCQLCARGHCWGFPGPCVANCQSLRGQECVEECVLLQGLPREYVNA 558
Qy 380 SLSEETPNFIIPNSPVTPTPTALQCTAD-----KF 412
Db 559 HCLPCHPE-CQPNQSVTCFGE-ADQVACHMYKDPFCVACRCSGVKPDLSYPIKPF 616
Qy 413 PDSFACVQACROKTCSCVGOISTVDCTADEQNEGNTALIALAGVGLLALL 472
Db 617 PDEBAC--QPC---PINCTHSCVDLBDKGCFAQR--ASPLTISV--AVVGILLVVVL 667
Qy 473 G 473
Db 668 G 668

RESULT 22
US-09-859-053-36
; Sequence 36, Application US/09859053
; Patent No. US20020102658A1
; GENERAL INFORMATION:
; APPLICANT: Tezuka, Takeshi
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, No. US20020102658A1uaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE ALLIM AND
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859, 053
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 36
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-859-053-36

Query Match 3.5%; Score 102; DB 10; Length 470;
Best Local Similarity 22.2%; Pred. No. 0.74;
Matches 70; Conservative 34; Mismatches 140; Indels 72; Gaps 14;
Qy 111 LEDVTEKEXYQSGMPL--PCGFNLPFTPGQRISSPFMBLEKNSIKXSTDLGRCAE 168
Db 14 LEGVQCEVQLVESGGGLVQPGSLRLSCAASGFTFSYDMH-----VROATGKLEWV 67
Qy 169 FAFKTVAMDKNKATKYRPFYVDSKRLCHILVSMQMEGKKYCSVKGEPDLTWYCF 228
Db 68 SAIGAGTGYTTPGSKGRFT---SRENAKSLYQNMSLA-----GD--TAVYICV 115
Qy 229 KPRKSVTENHLIGSAYVGENPDAFISKPNQALRGYRFGVKKGRCLDYTELDTVIE 288
Db 116 RDKRTVTEHHYYGMDVWGCTVTVVSASTGP-----SVFLAPCSRSTS----- 163
Qy 289 RVESKAO--CWKTF-----ENDGVASDOPHTYPLTSQASNDMMPLIQ----- 330
Db 164 --ESTALGCLVKDFFPEPVTVSNMGSGLTGVHFFPVLQSS--GLYSLSSVTVPSN 219
Qy 331 -SDPHSGGVRNRYFYVDTTGEKCALSDVPDCLVSDSAVAVSYTAAGSLSEETPNFI 389
Db 220 FGTQVTCNVDHKKENTKVDKVERKCV--ECPPCAPPAAGPSV-----FL 265
Qy 390 IPSNPSVT--PTPE 402
Db 266 FPPKPKDTLMISRTPE 281

RESULT 23
US-09-887-879-14
; Sequence 14, Application US/09887879

; Patent No. US20020102706A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Gunthartapal, Anan
; APPLICANT: Gurney, Austin
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Apo-2DCR
; FILE REFERENCE: P1110P1
; CURRENT APPLICATION NUMBER: US/09/887, 879
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 09/096, 500
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: US 60/049, 911
; PRIOR FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 14
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-887-879-14

Query Match 3.5%; Score 101.5; DB 10; Length 418;
Best Local Similarity 24.2%; Pred. No. 0.69;
Matches 59; Conservative 27; Mismatches 83; Indels 75; Gaps 14;
Qy 313 TYPLTSQASNDMWN---PL-----HSDQPHSGGVRNRYFYVDTTGEKCALSDQ 361
Db 60 TIKHDSIGTQOQHESPLGELCPGSHRSERF--GACNR-----CTEVDGYTNASN 110
Qy 362 VPDCLVDSAAVSYTAAGSLSEETPNFIIPNSPVTPTPTALQCTADKPPDSFGACDV 421
Db 111 LFACL-----PCTACKSDEE-----RSPCTT--TRNTACQCRPGTFRNNSA--- 151
Qy 422 QACRROKTCSCVGOISTVDCTADEQNEC-----GSN-----TALIALAGVGL 467
Db 152 EMCRKSGTCGPRGMVKV--DCTPMSDIECVHKGESGHNIMVILVTVLVPLLVAVLI 209
Qy 468 LIALGGG-----CYFAKRLDRNKGVC-AAHHE-----HEFQSDGARKKR 507
Db 210 VCCIGSGCGGDPKCMRVCFWRIGLLRGPAEDNANEILSNADSLSTFVSEQMESQE 269
Qy 508 PSDL 511
Db 270 PADL 273

RESULT 24
US-09-992-964-14
; Sequence 14, Application US/09992964
; Patent No. US20020161202A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin
; APPLICANT: Gurney, Austin
; APPLICANT: Wood, William
; TITLE OF INVENTION: Apo-2DCR
; FILE REFERENCE: P1110
; CURRENT APPLICATION NUMBER: US/09/992, 964
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 08/878, 168
; PRIOR FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 14
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-992-964-14

Query Match 3.5%; Score 101.5; DB 10; Length 418;
Best Local Similarity 24.2%; Pred. No. 0.69;
Matches 59; Conservative 27; Mismatches 83; Indels 75; Gaps 14;

```
QY 313 TYPLTSQASWMDW---PL-----HOSDQPHSGVGRNYGFYVDITGEGKCALSDQ 361
DB 60 TKLHDQSIGTOQWHSPLGELCPGSHSRER--GACNR-----CTEGVGYMASNN 110
QY 362 VPDCLVSDAASVYTAAGSLSEETPNFIIPSNPVTPTPTALQCTADKFPDSFGACDV 421
DB 111 LFACL-----PCTACKSDEE-----RSPCTT--TRNTACQCKPGTFRNDNSA--- 151
QY 422 QACKRQKTSVGGQIOSTSVDTADEQNEC-----GSN-----TALINGLAVGVL 467
DB 152 EMCRCKSTGCPRGWVKV--DCTPMSDIECVHKEGNGHNIWILVTLVPLLVAVLI 209
QY 468 LIALIGGG-----CYFAKRLDRNKGVQ-AAHHE-----HEFOSDRGARKKR 507
DB 210 VCCIGSGGGGPKCMDRVCFWRLGLRGPAGADNANHILSNADSLSTFVSEQMESOE 269
QY 508 PSDL 511
DB 270 PADL 273

RESULT 25
US-10-242-383-14
; Sequence 14, Application US/10242383
; Publication No. US20030138915A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chuntcharapai, Anan
; APPLICANT: Gurney, Auestin
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: Apo-2DCR
; FILE REFERENCE: P110P1
; CURRENT APPLICATION NUMBER: US/10/242,383
; CURRENT FILING DATE: 2002-09-11
; PRIOR APPLICATION NUMBER: US/09/887,879
; PRIOR FILING DATE: 2001-06-21
; PRIOR APPLICATION NUMBER: 09/096,500
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: US 60/049,911
; PRIOR FILING DATE: 1997-06-18
; NUMBER OF SEQ ID NOS: 17
; SEQ ID NO 14
; LENGTH: 418
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-242-383-14

Query Match 3.5%; Score 101.5; DB 12; Length 418;
Best Local Similarity 24.2%; Pred. No. 0.69; Indels 75; Gaps 14;
Matches 59; Conservative 27; Mismatches 83;

QY 313 TYPLTSQASWMDW---PL-----HOSDQPHSGVGRNYGFYVDITGEGKCALSDQ 361
DB 60 TKLHDQSIGTOQWHSPLGELCPGSHSRER--GACNR-----CTEGVGYMASNN 110
QY 362 VPDCLVSDAASVYTAAGSLSEETPNFIIPSNPVTPTPTALQCTADKFPDSFGACDV 421
DB 111 LFACL-----PCTACKSDEE-----RSPCTT--TRNTACQCKPGTFRNDNSA--- 151
QY 422 QACKRQKTSVGGQIOSTSVDTADEQNEC-----GSN-----TALINGLAVGVL 467
DB 152 EMCRCKSTGCPRGWVKV--DCTPMSDIECVHKEGNGHNIWILVTLVPLLVAVLI 209
QY 468 LIALIGGG-----CYFAKRLDRNKGVQ-AAHHE-----HEFOSDRGARKKR 507
DB 210 VCCIGSGGGGPKCMDRVCFWRLGLRGPAGADNANHILSNADSLSTFVSEQMESOE 269
QY 508 PSDL 511
DB 270 PADL 273
```

```
RESULT 26
US-10-280-047-6
; Sequence 6, Application US/10280047
; Publication No. US20030180883A1
; GENERAL INFORMATION:
; APPLICANT: Ni, Jian
; APPLICANT: Roosen, Craig A
; TITLE OF INVENTION: Human Tumor Necrosis Factor Receptor 10
; FILE REFERENCE: P379P1D1
; CURRENT APPLICATION NUMBER: US/10/280,047
; CURRENT FILING DATE: 2002-10-25
; PRIOR APPLICATION NUMBER: 09/580,212
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: 09/086,483
; PRIOR FILING DATE: 1998-05-29
; PRIOR APPLICATION NUMBER: 60/069,112
; PRIOR FILING DATE: 1997-12-09
; PRIOR APPLICATION NUMBER: 60/050,936
; PRIOR FILING DATE: 1997-05-30
; PRIOR APPLICATION NUMBER: 60/144,023
; PRIOR FILING DATE: 1999-07-15
; PRIOR APPLICATION NUMBER: 60/142,563
; PRIOR FILING DATE: 1999-07-07
; PRIOR APPLICATION NUMBER: 60/136,786
; PRIOR FILING DATE: 1999-05-28
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 6
; LENGTH: 467
; TYPE: PRT
; ORGANISM: human
US-10-280-047-6

Query Match 3.5%; Score 101.5; DB 12; Length 467;
Best Local Similarity 24.2%; Pred. No. 0.82;
Matches 59; Conservative 27; Mismatches 83; Indels 75; Gaps 14;

QY 313 TYPLTSQASWMDW---PL-----HOSDQPHSGVGRNYGFYVDITGEGKCALSDQ 361
DB 110 TKLHDQSIGTOQWHSPLGELCPGSHSRER--GACNR-----CTEGVGYMASNN 160
QY 362 VPDCLVSDAASVYTAAGSLSEETPNFIIPSNPVTPTPTALQCTADKFPDSFGACDV 421
DB 161 LFACL-----PCTACKSDEE-----RSPCTT--TRNTACQCKPGTFRNDNSA--- 201
QY 422 QACKRQKTSVGGQIOSTSVDTADEQNEC-----GSN-----TALINGLAVGVL 467
DB 202 EMCRCKSTGCPRGWVKV--DCTPMSDIECVHKEGNGHNIWILVTLVPLLVAVLI 259
QY 468 LIALIGGG-----CYFAKRLDRNKGVQ-AAHHE-----HEFOSDRGARKKR 507
DB 260 VCCIGSGGGGPKCMDRVCFWRLGLRGPAGADNANHILSNADSLSTFVSEQMESOE 319
QY 508 PSDL 511
DB 320 PADL 323

RESULT 27
US-10-322-673-1
; Sequence 1, Application US/10322673
; Publication No. US20030180296A1
; GENERAL INFORMATION:
; APPLICANT: Salcedo et al.
; TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
; FILE REFERENCE: P585
; CURRENT APPLICATION NUMBER: US/10/322,673
; CURRENT FILING DATE: 2002-12-19
; PRIOR APPLICATION NUMBER: 60/341,237
; PRIOR FILING DATE: 2001-12-20
```

PRIOR APPLICATION NUMBER: 60/369,877
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 60/384,828
PRIOR FILING DATE: 2002-06-04
PRIOR APPLICATION NUMBER: 60/396,591
PRIOR FILING DATE: 2002-07-18
PRIOR APPLICATION NUMBER: 60/403,370
PRIOR FILING DATE: 2002-08-15
PRIOR APPLICATION NUMBER: 60/425,737
PRIOR FILING DATE: 2002-11-13
NUMBER OF SEQ ID NOS: 72
SEQ ID NO 1
LENGTH: 468
TYPE: PRT
ORGANISM: Homo sapiens
US-10-322-673-1

Query Match 3.5%; Score 101.5; DB 12; Length 468;
Best Local Similarity 24.2%; Pred. No. 0.82;
Matches 59; Conservative 27; Mismatches 83; Indels 75; Gaps 14;

QY 313 TYPLTSQASNDW---PL-----HSDQPHSGVGRNYGYVDTTGEKCALSDQ 361
DB 110 TIKLHDQSIGTQWHEHPLGELCPGSHRSERP--GACNR-----CTEGVGTNMSNN 160
QY 362 VPDLVSDSAVSYTAAGSLSEETPNFLIPSNPVTPTPTALQCTADKFPDSFGACDV 421
DB 161 LFACL-----PCTACKSDEE-----RSPCTT--TRNTACCKRGTRNDNSA--- 201
QY 422 QACKROKTSYVGGQIGSTVSDCTADEQNEC-----GSN-----TALAGLAVGVL 467
DB 202 EMCRKSTGCPRGWVKV--DCTPWSIDECVHKESGNHNIWLVTLVPLLVAVLI 259
QY 468 LIALIGG-----CYFAKRLDRNKGVQ-AAHHE-----HEFQSDRGARKR 507
DB 260 VCCIGSGCGGDPKCMRVCFWRGLRGPAEDNHNELISNADSLSTFVSEQMESOE 319
QY 508 PSDL 511
DB 320 PADL 323

RESULT 28
US-10-039-785-1
Sequence 1, Application US/10039785
Publication No. US20020067646A1
GENERAL INFORMATION:
APPLICANT: Salcedo et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind to TRAIL
FILE REFERENCE: PF550
CURRENT APPLICATION NUMBER: US/10/039,785
CURRENT FILING DATE: 2002-05-07
PRIOR APPLICATION NUMBER: 60/369,860
PRIOR FILING DATE: 2002-04-05
PRIOR APPLICATION NUMBER: 60/341,237
PRIOR FILING DATE: 2001-12-20
PRIOR APPLICATION NUMBER: 60/331,310
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/331,044
PRIOR FILING DATE: 2001-11-07
PRIOR APPLICATION NUMBER: 60/327,364
PRIOR FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 60/323,807
PRIOR FILING DATE: 2001-09-21
PRIOR APPLICATION NUMBER: 60/309,176
PRIOR FILING DATE: 2001-08-02
PRIOR APPLICATION NUMBER: 60/294,981
PRIOR FILING DATE: 2001-06-04
PRIOR APPLICATION NUMBER: 60/293,473
PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 66
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 1
LENGTH: 468
TYPE: PRT
ORGANISM: Homo sapiens
US-10-039-785-1

Query Match 3.5%; Score 101.5; DB 13; Length 468;
Best Local Similarity 24.2%; Pred. No. 0.82;
Matches 59; Conservative 27; Mismatches 83; Indels 75; Gaps 14;

QY 313 TYPLTSQASNDW---PL-----HSDQPHSGVGRNYGYVDTTGEKCALSDQ 361
DB 110 TIKLHDQSIGTQWHEHPLGELCPGSHRSERP--GACNR-----CTEGVGTNMSNN 160
QY 362 VPDLVSDSAVSYTAAGSLSEETPNFLIPSNPVTPTPTALQCTADKFPDSFGACDV 421
DB 161 LFACL-----PCTACKSDEE-----RSPCTT--TRNTACCKRGTRNDNSA--- 201
QY 422 QACKROKTSYVGGQIGSTVSDCTADEQNEC-----GSN-----TALAGLAVGVL 467
DB 202 EMCRKSTGCPRGWVKV--DCTPWSIDECVHKESGNHNIWLVTLVPLLVAVLI 259
QY 468 LIALIGG-----CYFAKRLDRNKGVQ-AAHHE-----HEFQSDRGARKR 507
DB 260 VCCIGSGCGGDPKCMRVCFWRGLRGPAEDNHNELISNADSLSTFVSEQMESOE 319
QY 508 PSDL 511
DB 320 PADL 323

RESULT 29
US-10-226-296-2
Sequence 2, Application US/10226296
Publication No. US20030036168A1
GENERAL INFORMATION:
APPLICANT: Ni, Jian
Rosen, Craig A.
Pan, James G.
Gentz, Reiner L.
Dixite, Vishva M.
TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4: Death Receptor 4), Member of the TNF-Receptor Superfamily and Binding to Trail (AP02-L)
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESSES:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.
STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD
COUNTRY: US
ZIP: 20850
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/226,296
FILING DATE: 23-Aug-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/448,868
FILING DATE: <Unknown>
APPLICATION NUMBER: 09/013,895
FILING DATE: 27-JAN-1998
ATTORNEY/AGENT INFORMATION:
NAME: STEEFE, ERIC K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1488.1300004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (202) 371-2540

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 468 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-226-296-2

Query Match 3.5%; Score 101.5; DB 15; Length 468;
Best Local Similarity 24.2%; Pred. No. 0.82;
Matches 59; Conservative 27; Mismatches 83; Indels 75; Gaps 14;

QY 313 TYPPLTSQASNDWM---PL-----HOSDQPHSGGVGRNGFYVDTTGGKCALSDQ 361
DB 110 TIKLHDQSIGTQWEHSPGLGELCPGSHRSERP--GACNR-----CTEGVGTNNSNN 160
QY 362 VPDCLVSDSAVSYTAAGSLSEETPNFIIPNSVTPPTPETALQCTADKFPDSFGACDV 421
DB 161 LFACL-----PCTACKSDEEB-----RSPCTT--TRNTACQCKGTFRNDNSA---- 201
QY 422 QACKRKQKTSVCGGQIOSTSVDTCTADEQNEC-----GSN-----TALAGLAVGCVL 467
DB 202 EMCRCRQKSTGCPRGWVKV--DCTPMSDIECVHKSNGNHNIMVILVTVLVLVAVLI 259
QY 468 LIALIGGG-----CYFAKRLDRNKGVQ-AAHHE-----HEFQSDRGARKKR 507
DB 260 VCCIGSGCGGDPKCMDRVCFWRGLLRGPAEDNAHNEILSNADSLSTFVSEQMESOE 319
QY 508 PSDL 511
DB 320 PADL 323

RESULT 30

US-10-226-318-2
Sequence 2, Application US/10226318
Publication No. US20030073187A1
GENERAL INFORMATION:
APPLICANT: NI, Jian

Rosen, Craig A.
Pan, James G.
Gentz, Reiner L.
Dixit, Vishva M.

TITLE OF INVENTION: Death Domain Containing Receptor 4 (DR4): Death
Receptor 4), Member of the TNF-Receptor
Superfamily and Binding to Trail (Ap02-L)

NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: HUMAN GENOME SCIENCES, INC.

STREET: 9410 KEY WEST AVENUE
CITY: ROCKVILLE
STATE: MD

COUNTRY: US

ZIP: 20850

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30

CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/226,318

FILING DATE: 23-Aug-2002

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/448,868

FILING DATE: <Unknown>

APPLICATION NUMBER: 09/013,895

FILING DATE: 27-JAN-1998

ATTORNEY/AGENT INFORMATION:
NAME: STEFFE, ERIC K.

REGISTRATION NUMBER: 36,688

REFERENCE/DOCKET NUMBER: 1488,1300004

TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
TELEFAX: (802) 371-2540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 468 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-226-318-2

Query Match 3.5%; Score 101.5; DB 15; Length 468;
Best Local Similarity 24.2%; Pred. No. 0.82;
Matches 59; Conservative 27; Mismatches 83; Indels 75; Gaps 14;

QY 313 TYPPLTSQASNDWM---PL-----HOSDQPHSGGVGRNGFYVDTTGGKCALSDQ 361
DB 110 TIKLHDQSIGTQWEHSPGLGELCPGSHRSERP--GACNR-----CTEGVGTNNSNN 160
QY 362 VPDCLVSDSAVSYTAAGSLSEETPNFIIPNSVTPPTPETALQCTADKFPDSFGACDV 421
DB 161 LFACL-----PCTACKSDEEB-----RSPCTT--TRNTACQCKGTFRNDNSA---- 201
QY 422 QACKRKQKTSVCGGQIOSTSVDTCTADEQNEC-----GSN-----TALAGLAVGCVL 467
DB 202 EMCRCRQKSTGCPRGWVKV--DCTPMSDIECVHKSNGNHNIMVILVTVLVLVAVLI 259
QY 468 LIALIGGG-----CYFAKRLDRNKGVQ-AAHHE-----HEFQSDRGARKKR 507
DB 260 VCCIGSGCGGDPKCMDRVCFWRGLLRGPAEDNAHNEILSNADSLSTFVSEQMESOE 319
QY 508 PSDL 511
DB 320 PADL 323

RESULT 31

US-10-175-902-2
Sequence 2, Application US/10175902
Publication No. US20030108516A1
GENERAL INFORMATION:
APPLICANT: NI, Jian

Rosen, Craig A.
Pan, James G.
Gentz, Reiner L.
Dixit, Vishva M.

TITLE OF INVENTION: Death Domain Containing Receptor 4
CURRENT APPLICATION NUMBER: US/10/175,902

FILE REFERENCE: 1488,1300005

CURRENT FILING DATE: 2002-06-21

PRIOR APPLICATION NUMBER: 09/565,918

PRIOR FILING DATE: 2000-05-05

PRIOR APPLICATION NUMBER: US 60/132,922

PRIOR FILING DATE: 1999-05-06

PRIOR APPLICATION NUMBER: US 09/013,895

PRIOR FILING DATE: 1998-01-27

PRIOR APPLICATION NUMBER: US 60/037,829

PRIOR FILING DATE: 1997-02-05

PRIOR APPLICATION NUMBER: US 60/035,722

PRIOR FILING DATE: 1997-01-28

NUMBER OF SEQ ID NOS: 13

SOFTWARE: Patent in Ver. 2.1

SEQ ID NO 2

LENGTH: 468

TYPE: PRT

ORGANISM: Homo sapiens

US-10-175-902-2

Query Match 3.5%; Score 101.5; DB 15; Length 468;
Best Local Similarity 24.2%; Pred. No. 0.82;
Matches 59; Conservative 27; Mismatches 83; Indels 75; Gaps 14;

Qy 313 TYPILTSQASWMDW---PL-----HOSDPHSGGVGRNYGYVVDITGCKCALSDQ 361
Db 110 TIKHJDOSIGTQOMHESPLGELCPGSHSRERP--GACNR-----CTEGVGTNANNN 160
Qy 352 VDDCLVSSAASVYPAAGLSSEETNFIIIPSNPSVTPPTPTALQCTADKFPDSCGADV 421
Db 161 LFACL-----PCTACKSDEEB-----RSPCTT--TRNTACOCKPCTFNDSA-- 201
Qy 422 QACKROKITSVCGOIGTSTSVDTADEQNEC-----GSN-----TALIALGAVGVYL 467
Db 202 EMCRCSTGCPRGWVK--DCTPMSDIECHKESGNGNIVILVTLVPLLVAVILI 259
Qy 468 LIALIGG-----CYPAKLDRNKVQ-AAHE-----HEFOSDRGARKKR 507
Db 260 VCCGSGGGGDKPKCMRVCFWRLGLRGPAEDNAHNEILSNADSLSTFVSEQMESQE 319
Qy 508 PSDL 511
Db 320 PADL 323

RESULT 32

US-09-738-973-434
; Sequence 434, Application US/09738973
; Patient No. US20020110563A1
; GENERAL INFORMATION:
; APPLICANT: Reed, Steven G.
; APPLICANT: Henderson, Robert A.
; APPLICANT: Lodes, Michael J.
; APPLICANT: Fling, Steven P.
; APPLICANT: Mohamath, Raedoh
; APPLICANT: Algate, Paul A.
; APPLICANT: Secrist, Heather
; APPLICANT: Indrias, Carol Yoseph
; APPLICANT: Benson, Darin R.
; APPLICANT: Eliot, Mark
; APPLICANT: Mannion, Jane
; APPLICANT: Kalos, Michael D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 210121.475C9
; CURRENT APPLICATION NUMBER: US/09/738,973
; CURRENT FILING DATE: 2000-12-14
; NUMBER OF SEQ ID NOS: 587
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 434
; LENGTH: 1702
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-738-973-434

Query Match 3.4%; Score 100.5; DB 10; Length 1702;

Best Local Similarity 20.1%; Pred. No. 7.5; Mismatches 183; Indels 245; Gaps 30;

Matches 122; Conservative 57; Mismatches 183; Indels 245; Gaps 30;
Qy 20 ASGLSSSTRRESQT-----LSASTG-----NPFQANVE 49
Db 312 AEGTLRAKSEBSLTLAAVGDGSKLRRPRRSSDLSASFNGEMGNRCNSYD--- 367
Qy 50 MKTFRERFNLTHHOSGIYVDLQDKEVDGTLYREPAGLCPITWGHIELQDP----- 102
Db 368 -----NLPHDNE-----EEGGLHLIPALMSPHSAVDVLSPPDIGVASLD 409
Qy 103 -----RLPYRNNLEADVPTKEKYKQGN-----PLPGFNLNF 135
Db 410 FDPMSFOCSPPKAESCELESASFL-DSFGYSKDPSPANKKDAETGSSQCOTPGS----- 463
Qy 136 VTPSGORISPPMELERKSNIKASTDLGRCAEFAFTVAM-----DKNNKATKYRPFVY 191
Db 464 -TASSEPVSP---LQEKLS-----PFTLDSLPTEDKSKSPSTTEKVVY 504
Qy 192 DSKRLCHILIVSNQLMGKKYCSYKGEPPDLTWYCFPRKSVTENHHLIYGSAYGENP 251

Db 505 AFSPKIGRKLKSSPSM-----SI-SEPISTV---LPPRVS----- 535
Qy 252 DAFISKCPNQLRGVRFQWKKGRCLDYTELTDVIERVESKACQWTFENDGVASD-- 309
Db 536 -EVGTYSNTTAQNAASSTWDK--CVERDXTN-----RSPQT--VMKTNETVAQEA 585
Qy 310 QPHTYPLTSQASWMDWMLHOSDPHSGGVGRNYGYVVDITGCKCALSDQVDDCLVSD 369
Db 586 ESEVQPLDQVAA-----BEVELP-----GK---EQSVSSS9SK 616
Qy 370 SAASVYPAAGLSSEETNFIIIPSNPSV--TPPTPTALQCTADKFPDSCGADVQACKR 426
Db 617 AVASGQOTGTGAVTHDPPQDSVPSVSLIPPPPKVYARMIALALAESAOASTQSLKR 676
Qy 427 QKTCGVG---GQIGTSTSVDTADEQNECSNTALIALGAVGVLALLGCGCFARL 482
Db 677 PGTQAGTYNYGDI---AVATTEBNLS-----SSYSAAAL 708
Qy 483 DRNKGVOAAHHEHFOSDRGARKKRPSDLMQEAEP-----SFWDEAENIEODG 531
Db 709 DK-----AYFQTDRAPEQFH-----LONNAPGNDHLPETTTAGDPTHNTTESG 754

RESULT 33

US-09-854-133-434
; Sequence 434, Application US/09854133
; Publication No. US20020183499A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Mohamath, Raedoh
; APPLICANT: Henderson, Robert A.
; APPLICANT: Benson, Darin R.
; APPLICANT: Secrist, Heather
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; FILE REFERENCE: 210121.475C10
; CURRENT APPLICATION NUMBER: US/09/854,133
; CURRENT FILING DATE: 2001-05-11
; NUMBER OF SEQ ID NOS: 735
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 434
; LENGTH: 1702
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-854-133-434

Query Match 3.4%; Score 100.5; DB 10; Length 1702;

Best Local Similarity 20.1%; Pred. No. 7.5; Mismatches 183; Indels 245; Gaps 30;

Matches 122; Conservative 57; Mismatches 183; Indels 245; Gaps 30;
Qy 20 ASGLSSSTRRESQT-----LSASTG-----NPFQANVE 49
Db 312 AEGTLRAKSEBSLTLAAVGDGSKLRRPRRSSDLSASFNGEMGNRCNSYD--- 367
Qy 50 MKTFRERFNLTHHOSGIYVDLQDKEVDGTLYREPAGLCPITWGHIELQDP----- 102
Db 368 -----NLPHDNE-----EEGGLHLIPALMSPHSAVDVLSPPDIGVASLD 409
Qy 103 -----RLPYRNNLEADVPTKEKYKQGN-----PLPGFNLNF 135
Db 410 FDPMSFOCSPPKAESCELESASFL-DSFGYSKDPSPANKKDAETGSSQCOTPGS----- 463
Qy 136 VTPSGORISPPMELERKSNIKASTDLGRCAEFAFTVAM-----DKNNKATKYRPFVY 191
Db 464 -TASSEPVSP---LQEKLS-----PFTLDSLPTEDKSKSPSTTEKVVY 504
Qy 192 DSKRLCHILIVSNQLMGKKYCSYKGEPPDLTWYCFPRKSVTENHHLIYGSAYGENP 251
Db 505 AFSPKIGRKLKSSPSM-----SI-SEPISTV---LPPRVS----- 535

QY 252 DAFISKCPNOLRGYRFGVWKKGRCLDYTELDTVIERVESKAQOCWKTFFENDGVASD-- 309
DB 536 -EVIGTSTNTTAQNASSSTWDX--CVERDATN-----RSPTQI-VKMKTNETVAQEA 585
QY 310 QPHTYPLTSQASWMDMWPPLHOSDOPHSGGVRNGYFYVDTTGEKCALSDQVPCLVSD 369
DB 586 ESEVQPLDQVAA-----EEVELP-----GK---EDQSVSSSQSK 616
QY 370 SAAVSYTAAGSLSEETPNFIIP-SNPSV--TPPTETALQCTADKFPDSFGACDVQACKR 426
DB 617 AVASGQTGTGAVTHDPQDSVPVSSVSLIPPPPKVVARMLALALAESAOQASTQSLKR 676
QY 427 QKTSVCG---GQIOSTSVDCITADEONEGCSNTALIALAGVGVLLALLGGGCYFAPARL 482
DB 677 PGTSGAGYTNVGD---AVATTEDNLS-----SSYSAAVL 708
QY 483 DRNKGVQAAHHEHFOSDRGARKRPSDLMQEAEP-----SFWDAEENIEODG 531
DB 709 DK-----AYFQTRPAEQFH-----LQNNAPGNCDBLPETATGDPHSTTSESG 754
QY 532 ETHVWVE 538
DB 755 EQHHQVD 761

RESULT 34

US-10-144-649A-434
; Sequence 434, Application US/10144649A
; Publication No. US20030118599A1
; GENERAL INFORMATION:
; APPLICANT: Lodes, Michael J.
; APPLICANT: Wang, Tongrong
; APPLICANT: Pan, Liqun
; APPLICANT: Algate, Paul A.
; APPLICANT: McNeill, Patricia D.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
; FILE OF INVENTION: THE THERAPY AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.475C11
; CURRENT APPLICATION NUMBER: US/10/144,649A
; NUMBER OF SEQ ID NOS: 749
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 434
; LENGTH: 1702
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-144-649A-434

Query Match 3.4%; Score 100.5; DB 15; Length 1702;

Best Local Similarity 20.1%; Pred. No. 7.5; Indels 245; Gaps 30;

Matches 122; Conservative 57; Mismatches 183; Indels 245; Gaps 30;

QY 20 ASGLSSTRRESQOT-----LASTSG-----NPFQANVE 49
DB 312 AGCTLRASASBSLSLHAVDGSKLFRPRRSSDALSAFNGMLNRCNSVD----- 367
QY 50 MKTFRERFLTHHOSGIYVDLGQDKEVDGTLYPEAGLCPTWGKHIELQDP----- 102
DB 368 -----NLPHDNES-----EEEGGLHIFALMSPHSAEDVDLSPPDIGVASLD 409
QY 103 -----RLPYRNNFLEADVTEKEYKOSGN-----PLPGCGFNLMF 135
DB 410 FDPMSFQCSPPRAESECLESASFL-DSFGYSKDKPSAKKKADEGTSSQCTPFGS----- 463
QY 136 VTPSGQRISPPFMELEKSNIKASTDLGRCAEFAKTYAM-----DKNNKATKYRYPFY 191
DB 464 -TASSEPVSP-----LQEKLS-----PFTIDLSPTEDKSKSPSFTKXYV 504
QY 192 DSKRKLCHILYVSMQMEGKCYCSVKGEPPDLTWYCFKPKSVTENHLLIYSAIVGENP 251
DB 505 AFSPIKGRKLSKSPSM-----SI-SEPISVT-----LPPRVS----- 535

QY 252 DAFISKCPNOLRGYRFGVWKKGRCLDYTELDTVIERVESKAQOCWKTFFENDGVASD-- 309
DB 536 -EVIGTSTNTTAQNASSSTWDX--CVERDATN-----RSPTQI-VKMKTNETVAQEA 585
QY 310 QPHTYPLTSQASWMDMWPPLHOSDOPHSGGVRNGYFYVDTTGEKCALSDQVPCLVSD 369
DB 586 ESEVQPLDQVAA-----EEVELP-----GK---EDQSVSSSQSK 616
QY 370 SAAVSYTAAGSLSEETPNFIIP-SNPSV--TPPTETALQCTADKFPDSFGACDVQACKR 426
DB 617 AVASGQTGTGAVTHDPQDSVPVSSVSLIPPPPKVVARMLALALAESAOQASTQSLKR 676
QY 427 QKTSVCG---GQIOSTSVDCITADEONEGCSNTALIALAGVGVLLALLGGGCYFAPARL 482
DB 677 PGTSGAGYTNVGD---AVATTEDNLS-----SSYSAAVL 708
QY 483 DRNKGVQAAHHEHFOSDRGARKRPSDLMQEAEP-----SFWDAEENIEODG 531
DB 709 DK-----AYFQTRPAEQFH-----LQNNAPGNCDBLPETATGDPHSTTSESG 754
QY 532 ETHVWVE 538
DB 755 EQHHQVD 761

RESULT 35

US-09-859-053-32
; Sequence 32, Application US/09859053
; Patent No. US20020102658A1
; GENERAL INFORMATION:
; APPLICANT: Tezuka, Takashi
; APPLICANT: Tezuka, Katsunari
; APPLICANT: Hori, No. US20020102658A1uaki
; TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODY AGAINST A
; TITLE OF INVENTION: COSTIMULATORY SIGNAL TRANSDUCTION MOLECULE AILM AND
; FILE OF INVENTION: PHARMACEUTICAL USE THEREOF
; FILE REFERENCE: 06501-079001
; CURRENT APPLICATION NUMBER: US/09/859,053
; PRIOR FILING DATE: 2001-05-16
; PRIOR APPLICATION NUMBER: JP 2001-99508
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: JP 2000-147116
; PRIOR FILING DATE: 2000-05-18
; NUMBER OF SEQ ID NOS: 43
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 32
; LENGTH: 470
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-859-053-32

Query Match 3.4%; Score 99; DB 10; Length 470;

Best Local Similarity 22.2%; Pred. No. 1.4; Indels 72; Gaps 14;

Matches 70; Conservative 32; Mismatches 142; Indels 72; Gaps 14;

QY 111 LEDVTEKEYKOSGNPL--PGGFNLNFTVTPSGQRISPPFMELEKSNIKASTDLGRCAE 168
DB 14 LEVQCEVQVLYESGGGLVQPGSLRLSCAAGFTTSSIDTM-----VRQATGGLBHV 67
QY 169 FAFKTVANDKNNKATKYRYPFYVDSKRLCHILYVSMQMEGKCYCSVKGEPPDLTWYCF 228
DB 68 SAIGTAGDTYYPGVSKGFTI--SRENAKSLYLQNNSLRA-----GD--TAVYVCV 115
QY 229 KPRKSVTENHLLIYSAIVGENPDAFISKCPNOLRGYRFGVWKKGRCLDYTELDTVIE 288
DB 116 RDNRYVTEHHYVYGMVGGQTTVTYSSASTGP-----SVFLAPCSRSSTIS----- 163
QY 289 RVESKAQ--CWYKTF-----ENDGVAADQPHYPLTSQASWMDMWPPLHQ----- 330
DB 164 --ESTALGCLVQVDFPEPVVSNMNGALVSGHTFFRAVLOSS--GLYSLSSVTVPPSSN 219
QY 331 -SDQPHSGGVGRNGYFYVDTTGEKCALSDQVPCLVDSAAVSYTAAGSLSEETPNFI 389

Db 220 FCTOTYTCNVHKBKSNKVDKTEKCCV--ECPPCAPVAVGPGSV-----FL 265
Qy 390 IPSNPSVT--PPTPE 402
Db 266 PPPKPKOTLMISRTP 281

RESULT 36
US-09-820-893-60
; Sequence 60, Application US/09820893
; Patent No. US20020076705A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 31 Human Secreted Proteins
; FILE REFERENCE: P2033p1
; CURRENT APPLICATION NUMBER: US/09/820,893
; PRIOR FILING DATE: 2001-03-30
; PRIOR APPLICATION NUMBER: 09/531,119
; PRIOR FILING DATE: 2000-03-20
; PRIOR APPLICATION NUMBER: 60/102,895
; PRIOR FILING DATE: 1998-10-02
; NUMBER OF SEQ ID NOS: 140
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO: 60
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-820-893-60

Query Match 3.4%; Score 98.5; DB 9; Length 327;
Beet Local Similarity 19.2%; Pred. No. 0.92;
Matches 84; Conservative 43; Mismatches 109; Indels 201; Gaps 19;

Qy 127 LPG-----GFNINFTVPSGORIS--PPMELLEKNINIKASTDLCRCACFAFTVAMDKNK 181
Db 4 LPGPFLCALGLFLCLSLGLAVEVVKPTPEPL-----STPLGKTABLT----- 44
Qy 182 ATKRYRPFVYDSKRLCHILVYSQMLEGKKYCSVKGEPPDLTWYCFPRKSVTEHHLI 241
Db 45 -----C-----TYSTVSDSPALFVSGFVQPGKPRISHPIL 75
Qy 242 YGSAYGENPDPAFISKCPNQLRGYRFGVKKGRCLDTYELTDYIERVESKAQCWVKT 301
Db 76 YFT-----NGHLYPTGSKSKRVSLQNPPTV----- 101
Qy 302 ENDGVASDQPHTYPLTQASWMDWMLHQSOPHSGVGRNYGFYVDTTGEKCALSDQ 361
Db 102 ---GVA---TLKLTID-----VHPSD-----TGYLCOVNNP 126
Qy 362 VPDCLVSDSAVSYTAAGLSLEETPNFIIPSNP-----SVTPPTETALQCTADK----- 411
Db 127 -PDPYTNGLGLINLTV-----LVPSNPFLCSGSGQTSVGSSTALRCSSSGAKRP 175
Qy 412 -----PDPSPGACDVQACKROKTSVGGQIQSTSVDTCTADBEONEGCSNTAL----- 457
Db 176 VYNNWRLGTFTPTSPGSMVQ-----DEVSGQLITLNLSTSGTYRCVATNMGASASC 228
Qy 458 -----TAGLAVG---GVLLALLGGCGYFAKRLDRNKGVQAHHNHFQSDR 501
Db 229 ELTSLVTEPPQGRVAGALIGVLLGLLTV-----AARCLVRFQKER 270
Qy 502 GAKKKRP---SDLMQEA 515
Db 271 GKPKRETYGSGDLREDA 287

RESULT 37
US-10-216-163-236
; Sequence 236, Application US/10216163
; Publication No. US20030149239A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc

; APPLICANT: Gertieen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530PIC3
; CURRENT APPLICATION NUMBER: US/10/216,163
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 236
; LENGTH: 327
; TYPE: PRT
; ORGANISM: Homo sapien
US-10-216-163-236

Query Match 3.4%; Score 98.5; DB 12; Length 327;
Beet Local Similarity 19.7%; Pred. No. 0.92;
Matches 86; Conservative 43; Mismatches 107; Indels 201; Gaps 20;

Qy 127 LPG-----GFNINFTVPSGORIS--PPMELLEKNINIKASTDLCRCACFAFTVAMDKNK 181
Db 4 LPGPFLCALGLFLCLSLGLAVEVVKPTPEPL-----STPLGKTABLT----- 44
Qy 182 ATKRYRPFVYDSKRLCHILVYSQMLEGKKYCSVKGEPPDLTWYCFPRKSVTEHHLI 241
Db 45 -----C-----TYSTVSDSPALFVSGFVQPGKPRISHPIL 75
Qy 242 YGSAYGENPDPAFISKCPNQLRGYRFGVKKGRCLDTYELTDYIERVESKAQCWVKT 301
Db 76 YFT-----NGHLYPTGSKSKRVSLQNPPTV----- 101
Qy 302 ENDGVASDQPHTYPLTQASWMDWMLHQSOPHSGVGRNYGFYVDTTGEKCALSDQ 361
Db 102 ---GVA---TLKLTID-----VHPSD-----TGYLCOVNNP 126
Qy 362 VPDCLVSDSAVSYTAAGLSLEETPNFIIPSNP-----SVTPPTETALQCTADK----- 411
Db 127 -PDPYTNGLGLINLTV-----LVPSNPFLCSGSGQTSVGSSTALRCSSSGAKRP 175
Qy 412 -----PDPSPGACDVQACKROKTSVGGQIQSTSVDTCTAD-----EONEGCS--- 453
Db 176 VYNNWRLGTFTPTSPGSMVQ-----DEVSGQLITLNLSTSGTYRCVATNMGASASC 228
Qy 454 -----NTALTAGLAVG---GVLLALLGGCGYFAKRLDRNKGVQAHHNHFQSDR 501
Db 229 ELTSLVTEPPQGRVAGALIGVLLGLLTV-----AARCLVRFQKER 270

OY 502 GAKKRP---SDLMQEA 515
Db 271 GKXPKETVGGSDLRDA 287

RESULT 38

US-10-227-884-236
Sequence 236, Application US/10227884
Publication No. US20030027988A1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Deenoyers, Luc
APPLICANT: Gerritsen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
APPLICANT: Wood, William I.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
FILE REFERENCE: P3530PCT9
CURRENT APPLICATION NUMBER: US/10/227,884
PRIOR FILING DATE: 2002-08-26
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
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PRIOR APPLICATION NUMBER: 60/069873
PRIOR FILING DATE: 1997-12-17
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/079294
PRIOR FILING DATE: 1998-03-25
PRIOR APPLICATION NUMBER: 60/079556
PRIOR FILING DATE: 1998-03-26
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PRIOR FILING DATE: 1998-04-15
PRIOR APPLICATION NUMBER: 60/081955
PRIOR FILING DATE: 1998-04-15
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PRIOR FILING DATE: 1998-04-22
PRIOR APPLICATION NUMBER: 60/084441
PRIOR FILING DATE: 1998-05-06
PRIOR APPLICATION NUMBER: 60/085323
PRIOR FILING DATE: 1998-05-13
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PRIOR FILING DATE: 1998-05-15
PRIOR APPLICATION NUMBER: 60/086392
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PRIOR APPLICATION NUMBER: 60/089532
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PRIOR APPLICATION NUMBER: 60/089905
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PRIOR APPLICATION NUMBER: 60/090472
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090557
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PRIOR APPLICATION NUMBER: 60/090691
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PRIOR APPLICATION NUMBER: 60/090695
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PRIOR FILING DATE: 1998-07-07
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PRIOR FILING DATE: 1998-08-10
PRIOR APPLICATION NUMBER: 60/096146
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PRIOR FILING DATE: 1998-09-09
PRIOR APPLICATION NUMBER: 60/099598
PRIOR FILING DATE: 1998-09-09
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PRIOR APPLICATION NUMBER: 60/099811
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PRIOR APPLICATION NUMBER: 60/099812
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PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/149638
PRIOR FILING DATE: 1999-08-17
PRIOR APPLICATION NUMBER: 60/151733
PRIOR FILING DATE: 1999-08-31
PRIOR APPLICATION NUMBER: 60/164418
PRIOR FILING DATE: 1999-11-09
PRIOR APPLICATION NUMBER: 60/166361
PRIOR FILING DATE: 1999-11-16
PRIOR APPLICATION NUMBER: 60/169445
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169495
PRIOR FILING DATE: 1999-12-07
PRIOR APPLICATION NUMBER: 60/169835

Query Match 3.4%; Score 98.5; DB 15; Length 327;

Beet Local Similarity 19.7%; Pred. No. 0.92;

Matches 86; Conservative 43; Mismatches 107; Indels 201; Gaps 20;

Qy 127 LFG---GFNFVTPSGORIS-PPMELLEKNISIKASTDLCRCAEFAFTVAMDKNK 181
Db 4 LRGPLCALGLFLSLGSLAVEVKYFTEPL-----STPLGKTAELT----- 44
Qy 182 ATKRYRPFVYVDSKRLCHILVYSWQJMEGKKYCSVKGEPDPLTWYCFKPRKSVTEHHLI 241

Db 45 -----C-----TYSTSVGDSFALFWSFVQPKRISHPDL 75
Qy 242 YGSAVGENPDFAFISKCPNOLRGYRFGWKGRCLDYTELTDYIEVESKAOQWVTF 301
Db 76 YFT-----NGHLVPTGSKSRVSLLOQPPV----- 101
Qy 302 ENDGVASDQPHYPTLTSQASWMDWPLHOSDQPHSGVGRVYGYVDTTGEKCALSDQ 361
Db 102 ---GVA-----TLKLTU-----VHPSD-----TGTYLCQVWNP 126
Qy 362 VPDCLVSAVSTTAAGSLSEETNFIIPNP-----SVTPPIETALQCTADK----- 411
Db 127 -PDFYVNLGLINLTV-----LVPPSNPLCSGSGQTSVGSTALRCSGSGAKP 175
Qy 412 -----FPDSGACDVQACXKQKTSQVGOIQSTSVDCAD-----EQNEGCS--- 453
Db 176 VYNWRLCTFFTPBPGSNVQ-----DEVGQLITNLSITSGTRCAVTNQGASNC 228
Qy 454 -----NTALJAGLVG---GVLLALLGGCCYFAKRLDRNKGVOAHHHEHFGSDR 501
Db 229 ELTSLVTEPSQGRVAGALIGVLGLLTV-----AFCVLRFQKER 270
Qy 502 GAKKRP---SDLMQEA 515
Db 271 GKRPETVYGSDDLREDA 287

RESULT 39
US-10-230-163-236
Sequence 236, Application US/10230163
Publication No. US20030036635M1
GENERAL INFORMATION:
APPLICANT: Baker, Kevin P.
APPLICANT: Deenoyers, Luc
APPLICANT: Gerltisen, Mary
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Smith, Victoria
APPLICANT: Stephan, Jean-Philippe F.
APPLICANT: Watanabe, Colin L.
TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
TITLE OR INVENTION: ACIDS ENCODING THE SAME
FILE REFERENCE: P3530PIC96
CURRENT APPLICATION NUMBER: US/10/230,163
CURRENT FILING DATE: 2002-08-28
PRIOR APPLICATION NUMBER: 10/119,480
PRIOR FILING DATE: 2002-04-09
PRIOR APPLICATION NUMBER: 60/059113
PRIOR FILING DATE: 1997-09-17
PRIOR APPLICATION NUMBER: 60/062287
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/063549
PRIOR FILING DATE: 1997-10-28
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PRIOR FILING DATE: 1997-12-17
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PRIOR APPLICATION NUMBER: 60/082804

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1. PRIOR FILING DATE: 1999-08-31
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 8. PRIOR APPLICATION NUMBER: 60/169495
 9. PRIOR FILING DATE: 1999-12-07
 10. PRIOR APPLICATION NUMBER: 60/169835

Query Match	3.4%	Score 98.5	DB 15	Length 327
Best Local Similarity	19.7%	Pred. No. 0.92		
Matches	86	Conservative	43	Mismatches 107
				Indels 201
				Gaps 20

[illegible]

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RESULT 40
US-10-230-338-236
/ Sequence 236, Application US/10230338
/ Publication No. US20030044934A1
/ GENERAL INFORMATION:
/ APPLICANT: Baker, Kevin P.
/ APPLICANT: Deenoyere, Luc
/ APPLICANT: Gerritsen, Mary
/ APPLICANT: Goddard, Audrey
/ APPLICANT: Godowski, Paul J.
/ APPLICANT: Grimaldi, J. Christopher
/ APPLICANT: Gurney, Austin L.
/ APPLICANT: Smith, Victoria
/ APPLICANT: Stephan, Jean-Philippe F.
/ APPLICANT: Watanabe, Colin L.
/ APPLICANT: Wood, William I.
/ TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEOTIDE SEQUENCES
/ TITLE OF INVENTION: ACIDS ENCODING THE SAME
/ FILE REFERENCE: P2530P1C92
/ CURRENT APPLICATION NUMBER: US/10/230.338
/ CURRENT FILING DATE: 2002-08-28
/ PRIOR APPLICATION NUMBER: 10/119,480
/ PRIOR FILING DATE: 2002-04-09
/ PRIOR APPLICATION NUMBER: 60/059113
/ PRIOR FILING DATE: 1997-09-17

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2  PRIOR FILING DATE: 1997-10-17
3  PRIOR APPLICATION NUMBER: 60/065549
4  PRIOR FILING DATE: 1997-10-17
5  PRIOR APPLICATION NUMBER: 60/064103
6  PRIOR FILING DATE: 1997-10-31
7  PRIOR APPLICATION NUMBER: 60/069873
8  PRIOR FILING DATE: 1997-12-17
9  PRIOR APPLICATION NUMBER: 60/078910
10 PRIOR FILING DATE: 1998-03-20
11 PRIOR APPLICATION NUMBER: 60/079294
12 PRIOR FILING DATE: 1998-03-25
13 PRIOR APPLICATION NUMBER: 60/079555
14 PRIOR FILING DATE: 1998-03-26
15 PRIOR APPLICATION NUMBER: 60/079728
16 PRIOR FILING DATE: 1998-03-27
17 Remaining Prior Application data re
18 NUMBER OF SEQ ID NOS: 246
19 SEQ ID NO: 236
20 LENGTH: 327
21 TYPE: PRT
22 ORGANISM: Homo Sapien
23 US-10-230-338-236

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Query Match	3.4%;	Score 98.5;	DB 15;	Length 327;
Best Local Similarity	19.7%;	Pred. No. 0.92;		
Matches	86;	Conservative	43;	Mismatches 107;
				Indels 201;
				Gaps 20

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QY      127 LPP-----GNNLFVVPVSGGRIS-PEPMELLEKNNSIKASTDLCGRCAEFAFTYAMDKNK 181
D      4  LPPFLCGALLPFLCISGLAEVKKVTEPL-----STPLGTAELT----- 44
QY      182 ATKIRPYFVYDSKKLCHILVYSQMLEGKKYCSYKGEPPDLTYCEKRPKSTVENHLL 241
D      45 -----C-----TYSTSVGSPFALEMSFWQGPPISESHPL 75
QY      242 YGSAYVGENPDARFISKCPNQLRGYRFWMKKGCCLDTLDTLVIERVESKAQCWKT 301
D      76 YFT-----NGHLTYTGSKSKRVSLQNPVY----- 101
QY      302 ENDGVASDPHTYPLTSSQASWNDMMPLHQSDQPHSGGVGRNYGYVDTTGEKCALSDQ 361
D      102 --GVA--TLKLTLD-----VHPSD-----TGYTLCQVNNP 126
QY      362 VPDCLVSDSAASYTAAGSLSEETNFIIPENP-----SYTPPTPETALQCTADK----- 411
D      127 -PDFTYTNGLCLNLTV-----LVPSNPICSGSGCGYSGVSGSTALRCSSEGA PKP 175
QY      412 -----FDPISFACDVQACKROKTSYCVSGQIISTSVDTAD-----EONECGS-- 453
D      176 VYNNVRLTGFFPIPSGSMWQ-----DEVSGQILITNLSTSSGTYRCVATNMGSAASC 228
QY      454 -----NTLLINGLAVG--GYLLIALLGGCGYFAKRLDRNKGVOAAHHHEHFOSDR 501
D      229 ELTLSVTBESQORVAGVALIGVLLGVTLLTSV-----AAFCLVRFQEK 270
QY      502 GAKKKR---SDLMOEA 515
D      271 GKPKKETYGSDLPREDA 287

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Search completed: October 2, 2003, 16:01:31
Job time : 73 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 2, 2003, 15:46:34 ; Search time 43 Seconds
(without alignments)
1209.936 Million cell updates/sec

Title: US-10-039-770A-1
Perfect score: 2922
Sequence: 1 MGLVGVQVLTVLVADCTIFA.....EAEENIODEGTHWVSGDY 541

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: pir76:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	447	15.3	562	2 A44944	apical membrane an
2	431	14.8	622	2 A44986	apical membrane an
3	431	14.8	622	2 A32499	apical membrane an
4	421.5	14.4	563	2 A39238	66k merozoite surf
5	415	14.2	622	2 A44986	apical membrane an
6	412	14.1	622	2 A44986	apical membrane an
7	410	14.0	622	2 C44986	apical membrane an
8	398.5	13.6	558	2 A44964	apical membrane an
9	127	4.3	2364	2 A56577	microtubule-associ
10	125	4.3	863	2 S06017	neuraxin - rat
11	120	4.1	1701	1 T09127	probable erythrocy
12	120	4.1	2464	1 QRMSP1	microtubule-associ
13	112	3.8	993	2 T09129	probable erythrocy
14	111	3.8	600	2 T34757	probable oligopept
15	109	3.7	724	2 A48569	antigen Emu10 - Bi
16	108	3.7	768	2 T00073	hypothetical prote
17	107.5	3.7	1104	2 T38869	transcription fact
18	107	3.7	1009	2 T48727	retinoblastoma bin
19	106	3.6	415	2 A35560	lysosomal membrane
20	104.5	3.6	6658	2 T13931	proectin - fruit
21	104	3.6	1255	1 A24571	protein-tyrosine k
22	104	3.6	1611	2 T38236	hypothetical prote
23	103	3.5	360	2 S69063	probable membrane
24	103	3.5	1332	2 T23024	hypothetical prote
25	102	3.5	3002	2 A47221	fibrillin 1 precur
26	101.5	3.5	287	2 A60643	antigen 5401 - Rim
27	101.5	3.5	320	2 S07296	plastoquinol-plas
28	100.5	3.4	715	2 T14812	hypothetical prote
29	99.5	3.4	732	1 J00132	acylaminoacyl-pept

30	99.5	3.4	1606	2 T49219	translacion initia
31	99	3.4	2331	2 S44054	genome polyprotein
32	98	3.4	444	2 E65203	probable dehydroge
33	98	3.4	521	2 A1525	internalin like pr
34	97.5	3.3	1280	2 B95031	alkaline amylopull
35	97.5	3.3	2871	2 A55624	fibrillin-1 precur
36	97	3.3	468	2 B40228	neuraxin I-beta pr
37	97	3.3	694	2 F97279	TPR-repeat-contain
38	97	3.3	1507	2 A40228	neuraxin I-alpha p
39	96	3.3	1020	2 B86414	hypothetical prote
40	96	3.3	1256	2 G97902	alpha-amyase (EC
41	95.5	3.3	320	1 C9R2	plastoquinol-plas
42	95.5	3.3	376	2 C81272	probable aminotran
43	95.5	3.3	482	2 JC5092	E-selectin - pig
44	95	3.3	357	1 TVH02	transforming prote
45	95	3.3	571	2 D90157	hypothetical prote

ALIGNMENTS

RESULT 1

A44944
Apical membrane antigen 1 precursor - Plasmodium fragile
C:Species: Plasmodium fragile
C:Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 11-May-2000
C:Accession: A44944
R:Peterson, M.G.; Nguyen-Dinh, P.; Marshall, V.M.; Elliott, J.F.; Collins, W.E.; Anders, M.O. Biochem. Parasitol. 39, 279-284, 1990.
A>Title: Apical membrane antigen of Plasmodium fragile.
A:Reference number: A44944; MUID:90205978; PMID:2181309
A:Accession: A44944
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-562 <P>
A:Cross-references: GB:M29898

Query Match 15.3%; Score 447; DB 2; Length 562;
Best Local Similarity 25.9%; Pred. No. 5.9e-27;
Matches 159; Conservative 91; Mismatches 231; Indels 132; Gaps 26;

QY	6	VQVLLVAVDCTIF-----ASGLSSSTRS---RESQTLASISGPNPQANVENKT	52
DB	4	IYCLIFLSAQCLVHMGKEPQKPSRLTRSAKNVLEQEPWVERSTRMSNPW-----KA	57
QY	53	FMERFNLTHHQSGIYVDIGDQKVDGTLVEEPAGLCPIMKCHIELQPDLLPYRNPLE	112
DB	58	FMEKYDIEKTHSSGIRVDLGDAEAGNSYRIPAKCPVFGKGIIVQNSE-----VSFLT	112
QY	113	DVPT-EKEXKQSGNPLPGFNLNFTPSGQRISPPPM---ELLEKNSINIKASTDLGRCA	167
DB	113	PVAFGNQKLKDGCFAPF-----QANDHISISISIGNLBERKENNDLKKNDLALCK	163
QY	168	EPAFKTV-AMDKNKATRYRPFYVDSKRIKCHILLYVSMQMEGKYCSVKGPEPDLTWY	226
DB	164	THAASFVEMDKN---SSYRHPAVYDEDKICMYLYLSAQNMGPBYCSKDAENKD-AMF	219
QY	227	CFKRRKSTENHLLIYGSAVYGEN-PDAFISCKGNQMLRGRRGVWKKRGCLDYTELDT	285
DB	220	CFKDKMETFDH-----LAYSKNVVDWQNKCRKNGSKFGIWDNGCEELPYVDV	274
QY	286	VIERVESKAQCVMVFENDGVASDQPHYPLTISOASWMDWMLHQSDQPHSGV-----	339
DB	275	---QAKDRECNRIVFE--ASASQPPQY-----BEELDYKIQIGFQNGQMIKSAFL	325
QY	340	-----GRNYGFYVDITTECK-CALSDQVPDCLVSSAASVYPAAG---SLS	382
DB	326	PVGAFNSDNFKSKRGVWMAFDT--ENKVCYLFNAKPTCLINDKNFIATATLSHPQFVD	383
QY	383	EETNFIIPSN-----PSVTPTPTPTALQCTADKKPPDSGA	418
DB	384	NEPFSIYKDEMEREMRKESRNSMLVNDKARIYLPRIISNDKSLCKPCAPAEHITNST	443

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Qy 419 CDVQCKKQKTSV--GGQIOSTSVDTCTADE-----QNECGSNLTLLAGLAVGVLL 468
Db 444 CNFYVC-----NCVEKRAEIKENNEVAIKEEFKQDYQAQGSCKOMLIIIGITGVGV 498
Qy 469 LALLGGCGYFAKRLDRNKGVQAHHHEHFQSDRGARKKRPDLMOEAPSFMDAEENIE 528
Db 499 VALLSMFYFRKKANDK-----YDKMQDAQGVGKPTTRKQEMLDPEASFWGEEK--R 548
Qy 529 ODGEHVMVEGDY 541
Db 549 ASHTTPVLMKEPY 561

RESULT 2
B44986
Apical membrane antigen 1 - malaria parasite (Plasmodium falciparum) (strain Thai Tn)
C.Species: Plasmodium falciparum
C.Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 09-Jun-2000
C.Accession: B44986
R.Thomas, A.W.; Waters, A.P.; Carr, D.
Mol. Biochem. Parasitol. 42, 285-288, 1990
A.Title: Analysis of variation in PF83, an erythrocytic merozoite vaccine candidate anti
A.Reference number: A44986; MUID:91101665; PMID:2270110
A.Accession: B44986
A.Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A.Molecule type: DNA
A.Residues: 1-622 <THO>
A.Cross-references: GB:M34553
C.Keywords: membrane protein; surface antigen

Query Match 14.8%; Score 431; DB 2; Length 622;
Best Local Similarity 26.7%; Pred. No. 1.2e-25;
Matches 153; Conservative 81; Mismatches 209; Indels 130; Gaps 25;

Qy 41 GNPQANVEMKTFMERFNLTHHSGIYVDLGQDKVDGTLYPEAGLCPIWGKHIELQ 100
Db 107 GNPW-----TEYMAKYDIEVHGSGIRVDLGEDAVAGTQYRLPSGKCPVFGKGIIE 160
Qy 101 PDRLPYRNFLVDVTE-KEYKOSGNPLDGGFNLNFTVSGORISFPFME---LLEKSN 155
Db 161 S-----KTFPLTPVATENODLKDGFAPF-----PTEPLISMPTLDKMKHLKXDE 206
Qy 156 NIKASTDLGRCAEFKATVAMDKNNKATKYRPFYVDSKKRLCHILYVSMQMEGKYSV 215
Db 207 YKANLDELTLCSHAGNM--PNNDKSNYKIPAVDDDKCHILYIAQENNGRYCN- 264
Qy 216 VKGEPPDLTWYCFKPKRK-SVTENHHLIYGSAYGEN-PDAFISKCPNQLRGYRGVWK 273
Db 265 -KDESKRNMFCRPAKDLFENY-----TYSKAVVDMWEKVCPRKQLQNAKFGLVND 317
Qy 274 GRCLDYTELDTYIEVESKAQCVKTFENDGVAASQPHYR--LTSQASNDMWPF----- 327
Db 318 GNCEIDIPHYNEF--SANDLFECNKLVFELS--ASDQPKQYEQHLDYERIKIEGFKNKA 372
Qy 328 -----LHOSQPHSGGVGRNYGFYVDTTEGKCALSDQVPCIVSASAVSYT 376
Db 373 SMKSAFLPTGAFKARVYKSGKGYMGNVNTETO--KCEIFNVKPTCLINNSSIATTT 429
Qy 377 AAGSLSEETPNFLIPSN-----PSVTPPTPETAL 405
Db 430 ALSHPREVENNF--PCSLYKDEIKKEIERESKRIRKLNDDDEGNKKIAPRIFISDDKSL 487
Qy 405 LOCTADKFPDSFGACVQACKROKTSQVGGIOSTS-----VDCIAD--EQNECG 452
Db 488 LKCPDPEIVSNSTCNFVCK-----CVERRAVTNNNEVVVEKYKDEYADIPKHPY 542
Qy 453 SNTALI-----AGLAVGVLLALLGGCYFAKRLDRNKGVQAHHHEHFQSDRGARKKRP 508
Db 543 DNKKIIIASAAVAVALTILM-----VLYKR-----KNAEKYDKMDPEQYIGKSTR- 591
Qy 509 SDLMQAEPSFMDAEENIEODGEHVMVEGDY 541
Db 592 NDEMIDPEASFWGEEK--RASHTTPVLMKEPY 621
```

```
RESULT 3
A32499
Apical membrane antigen 1 - malaria parasite (Plasmodium falciparum)
C.Species: Plasmodium falciparum
C.Date: 12-Oct-1989 #sequence_revision 12-Oct-1989 #text_change 09-Jun-2000
C.Accession: A32499
R.Petersen, M.G.; Marshall, V.M.; Smythe, J.A.; Crewther, P.E.; Lew, A.; Silva, A.; Ande
Mol. Cell. Biol. 9, 3151-3154, 1989
A.Title: Integral membrane protein located in the apical complex of Plasmodium falciparu
A.Reference number: A32499; MUID:89384584; PMID:2701947
A.Accession: A32499
A.Status: preliminary
A.Molecule type: DNA, mRNA
A.Residues: 1-622 <PBT>
A.Cross-references: GB:M27133; NID:9160072; PID:9160073
C.Keywords: membrane protein; surface antigen

Query Match 14.8%; Score 431; DB 2; Length 622;
Best Local Similarity 26.2%; Pred. No. 1.2e-25;
Matches 149; Conservative 86; Mismatches 212; Indels 122; Gaps 24;

Qy 41 GNPQANVEMKTFMERFNLTHHSGIYVDLGQDKVDGTLYPEAGLCPIWGKHIELQ 100
Db 107 GNPW-----TEYMAKYDIEVHGSGIRVDLGEDAVAGTQYRLPSGKCPVFGKGIIE 160
Qy 101 PDRLPYRNFLVDVTEKEYKOSGNPLDGGFNLNFTVSGORISFPFME---LLEKSN 156
Db 161 SN-----TTFPLTPVATGNQYLDK-----GGFAPF-----PTEPLISMPTLDKMKHLYKXNY 207
Qy 157 IKASTDLGRCAEFKATVAMDKNNKATKYRPFYVDSKKRLCHILYVSMQMEGKYSV 216
Db 208 VANLDELTLCSHAGNM--PNNDKSNYKIPAVDDDKCHILYIAQENNGRYCN- 264
Qy 217 KGEPPDLTWYCFKPKRSYTENHHLIYGSAYGEN-PDAFISKCPNQLRGYRGVWKGR 275
Db 265 KDESERNMFCRPAKDLISFQNY-----TYSKAVVDMWEKVCPRKQLQNAKFGLVND 319
Qy 276 CLDYTELDTYIEVESKAQCVKTFENDGVAASQPHYR--LTSQASNDMWPF----- 327
Db 320 CEDIPHYNEFSAIDFE--CNKLVFELS--ASDQPKQYEQHLDYERIKIEGFKNKAS 373
Qy 328 -----LHOSQPHSGGVGRNYGFYVDTTEGKCALSDQVPCIVSASAVSYT 377
Db 374 MKSAFLPTGAFKARVYKSGKGYMGNVNTETO--KCEIFNVKPTCLINNSSIATTA 430
Qy 378 AAGSLSEETPNFLIPSN-----PSVTPPTPETAL 405
Db 431 LSHPREVENNF--PCSLYKDEIKKEIERESKRIRKLNDDDEGNKKIAPRIFISDDKSL 488
Qy 406 OCTADKFPDSFGACVQACKROKTSQVGGIOSTSVDCTA-----DEQNECGS----- 454
Db 489 KCPDPEIVSNSTCNFVCK-----CVERRAVTNNNEVVVEKYKDEYADIPKHPY 543
Qy 455 --TALIAGLAVGVLLALLGGCYFAKRLDRNKGVQAHHHEHFQSDRGARKKRPDL 512
Db 544 KKKIIIASAAVAVALTILM--VLYKR-----KNAEKYDKMDPEQYIGKNSR-NDKM 595
Qy 513 QEAPSFMDAEENIEODGEHVMVEGDY 541
Db 596 LDPEASFWGEEK--RASHTTPVLMKEPY 621

RESULT 4
A39238
66k merozoite surface antigen precursor - Plasmodium knowlesi
C.Species: Plasmodium knowlesi
C.Date: 13-Sep-1991 #sequence_revision 13-Sep-1991 #text_change 07-Feb-1997
C.Accession: A39238
R.Waters, A.P.; Thomas, A.W.; Deane, J.A.; Mitchell, G.H.; Hudson, D.E.; Miller, L.H.; M
J. Biol. Chem. 265, 17974-17979, 1990
A.Title: A merozoite receptor protein from Plasmodium knowlesi is highly conserved and d
```

A:Reference number: A39238; MUID:91009268; PMID:2211675
 A:Accession: A39238
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-563 <WMT>
 A:Cross-references: GB:J05631
 C:Keywords: surface antigen

Query Match 14.4%; Score 421.5; DB 2; Length 563;
 Best Local Similarity 24.6%; Pred. No. 5.9e-25;
 Matches 148; Conservative 96; Mismatches 250; Indels 107; Gaps 24;

```

QY 6 VOVLIVVADCTTASGL---SSSTRRESQTLASSTSGNPQANVEN---KTFMEREN 58
DB 4 IYVILFISAQCLVMGKCCERNQKTRTLRSANNASLEKGPILERSIRMSPMKAFMEKYD 63
QY 59 LTHHOSGIYVDLQDQDEVDGTLREPAICPIWGKHIELQOPRLPFRNNFLDVPF-E 117
DB 64 LERHNSGIRIDLEDDEAVGNSKTRIPAGKCPVFGKIVENS---VSFLTPVATGA 118
QY 118 KEYKQSNPLPGGFNLNFTPSGORISPPFM---ELLEKSNIKASTDLGRCAEFAPKT 173
DB 119 QRLKEGFAFPN-----ADHISITITANLKERKENADLMKLDLCTHAASF 169
QY 174 VANDKNNKATKRYRPFYVDSKRLCHILYVSMQMEKKYCSVKGEPPDLTWYCFKPKRS 233
DB 170 VIAEDQN--TSYRPAVYDEKTKCYMLYLSAQENMGPRYCSPPSQND-AMFCFKPKDN 226
QY 234 VTEHHHLYGSAVYGENPDATISKCPNALAGYRFGWKRCCLDYTELDTVIERVESK 293
DB 227 -EKFDNLVYLSKVNND--WENKCPKRLNAGFGLWVDCBEI-----PYNEVEAR 277
QY 294 A--QCWVTEFNDGVASDQPHTY--PLTSQASNDMPHLQSDQPHSG----- 337
DB 278 SLRCKNIVFE--ASADQPRQYEEELTAYEKIOEGFRQNRDIAKAFLEVGAFNSDNF 335
QY 338 -GGRNRYGFYVDTTGSKCALSDQVPCVSDSAVSYTAAG--SLSEETPNFIIPSN 393
DB 336 KSKRGYVWMAFDSV--NNKCYIFNTKPTCLINDKQFATLASHQEVNDFFPSIYDE 394
QY 394 -----PSVTPPETALQCTADKFPDSGACVQACQOKT 429
DB 395 IEREIKQSRNNLYSVDKERIVLPRIFFISTDKESIKCPCEPHISNCTCFYVC----- 449
QY 430 SCV--GGQIOSTS-----VDCTADEONECGSN--TALIAGLAVGVLLALLGGCYFAK 480
DB 450 NCVKRAEIKENNVIIKEPKEDYENDGKHKMLIITIGTAVCAVAVASLFFPRK 509
QY 481 RLDRNKGVQAHHHEFQSDRGARKRPSDLMQEAEPSPFMDAEENIEODETHVWEGD 540
DB 510 KAQDDK-----YDKWDQAEAVGKTANTRKDEMLDPBASFWGDEK---RASHTTIVLMKRP 561
QY 541 Y 541
DB 562 Y 562

```

RESULT 5
 D44986
 apical membrane antigen 1 - malaria parasite (Plasmodium falciparum) (strain 7G8)
 C:Species: Plasmodium falciparum
 C>Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 09-Jun-2000
 C:Accession: D44986
 R:Thomas, A.W.; Waters, A.P.; Carr, D.
 Mol. Biochem. Parasitol. 42, 285-288, 1990
 A:Title: Analysis of variation in Pf83, an erythrocytic merozoite vaccine candidate anti-
 A:Accession: D44986
 A:Reference number: A44986; MUID:91101665; PMID:2270110
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
 A:Molecule type: DNA
 A:Residues: 1-622 <THO>
 A:Cross-references: GB:M34555
 C:Keywords: membrane protein; surface antigen

Query Match 14.2%; Score 415; DB 2; Length 622;
 Best Local Similarity 25.8%; Pred. No. 2.2e-24;
 Matches 147; Conservative 82; Mismatches 218; Indels 122; Gaps 23;

```

QY 41 GNPFQANVEKTFMERENLTHHOSGIYVDLQDQDEVDGTLREPAICPIWGKHIELQ 100
DB 107 GNPF-----TEYMAKDIEKVGSGIRVLDGDAVAGTQYRLPSGKCPVFGKIIEN 160
QY 101 PDRLPYNNFLDVPF-EKEKYKQSNPLPGGFNLNFTPSGORISPPFM---ELLEKNS 155
DB 161 SN-----TTLKPVATGNQDLQDGFAP-----PTNPLISPMTLDMRPYKNE 206
QY 156 NIKASTDLGRCAEFAPFVAMDKNNKATKRYRPFYVDSKRLCHILYVSMQMEKKYCS 215
DB 207 YVKNLDELITCSRAAG--NMPDQKNSNRYKPAVYVNDKCHILYIAQENNGPRCN 264
QY 216 VKGEPPDLTWYCFKPKRSVTENHHLYGSAVGEN--DAFISKCPNALRGYRFGWKKG 274
DB 265 -KDSKNSMFCFRPAKDKSFQNY-----TYSKNVVDNMEKVCPRKULENAKFGWLWDG 318
QY 275 RCLDYTELDTVIERVSKAQCWKTPENDGVASDQPHTY--LTSQASNDMP----- 327
DB 319 NCEDI PHVNEF--SANDLFCNKLVFELS--ASDQPRQYEQHLTDYKIKEGKKNVAS 373
QY 328 -----LHQSOPHSGGVGRNRYGFYVDTTGSKCALSDQVPCVSDSAVSYTA 377
DB 374 MIKSAFLPTGAFAKDRKSKGKGYNMGYNRKTO--KCELFNVKPTCLINNSSIATTA 430
QY 378 AGSLSEETPNFIIPSN-----PSVTPPETAL 405
DB 431 LSHPEVEHNF--PCSLYKDEIKKEIERESKRIKLANDNDEGNKIIAPRIFFISDDKSL 488
QY 406 QCTADKRPDSFGACDVQACRKQTS CVGQIOSTSVCTA-----DEONECGSN----- 454
DB 489 KCPCDPRIVNSNTGNFVCK-----CVKRAEVTSNNEVVVKEEYKQEDVADIPHKPTTD 543
QY 455 -TALIAGLAVGVLLALLGGCYFAKRLDRNKGVQAHHHEFQSDRGARKRPSDLM 512
DB 544 KMKIITISSAANVAVLAILM---VLYLKR-----KGNAEKDKMDPEODYGSNSR-NDEN 595
QY 513 QEAEPSPFMDAEENIEODETHVWEGDY 541
DB 596 LDPEASFWGDEK---RASHTTIVLMKRP 621

```

RESULT 6
 A44986
 apical membrane antigen 1 - malaria parasite (Plasmodium falciparum) (strain CAMP)
 C:Species: Plasmodium falciparum
 C>Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 09-Jun-2000
 C:Accession: A44986
 R:Thomas, A.W.; Waters, A.P.; Carr, D.
 Mol. Biochem. Parasitol. 42, 285-288, 1990
 A:Title: Analysis of variation in Pf83, an erythrocytic merozoite vaccine candidate anti-
 A:Accession: A44986
 A:Reference number: A44986; MUID:91101665; PMID:2270110
 A:Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tran
 A:Molecule type: DNA
 A:Residues: 1-622 <THO>
 A:Cross-references: GB:M34552
 C:Keywords: membrane protein; surface antigen

Query Match 14.1%; Score 412; DB 2; Length 622;
 Best Local Similarity 26.2%; Pred. No. 3.8e-24;
 Matches 150; Conservative 80; Mismatches 214; Indels 128; Gaps 25;

```

QY 41 GNPFQANVEKTFMERENLTHHOSGIYVDLQDQDEVDGTLREPAICPIWGKHIELQ 100
DB 107 GNPF-----TEYMAKDIEKVGSGIRVLDGDAVAGTQYRLPSGKCPVFGKIIEN 160
QY 101 PDRLPYNNFLDVPF-EKEKYKQSNPLPGGFNLNFTPSGORISPPFM---ELLEKNS 155

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Db 161 SN-----TFLKPAVATGNQDLKDGFAFP-----PTREPLISPMTLNGMRDPFYKNE 206
Qy 156 NIKASTDLGRCAFAFKTVAMDKNKATKYRYPFYVDSKKRLCHILYVSMQMEGKYYCS 215
Db 207 YVKRLDELTLCSRNA-GNMNPDKQON--SNKYKPAVYDDKDKCHILYIAQENNGPRYCN 264
Qy 216 VKGEPPDLTWYCFKPKRSVTENHLLYGSAYGEN-PAFISKCPNOALRGYRFGVWK 274
Db 265 -KDESKRSMFCFRPAKDKSFQNY-----TYLSKVVVNMEKVCPRKLENAKRGLWVDG 318
Qy 275 RCLVTELTDTVIERVESKAQCVKTFENDGVAADQPHYTP--LTSQASWMDWMP----- 327
Db 319 NCEDIPHYNER---SANDLPECNKLVEFELS--ASQPRQYEHQHLTDYEKIKEGFNKNAS 373
Qy 328 -----LHSDQPHSGVGRNRYGYVDTTGEKCALSDQVPCLVSDSAVSYTA 377
Db 374 MIKSAFLPTGAFAKDRYKSHGKGYWGNVNRKT--HKCEIFNVKPTCLINNSYIATTA 430
Qy 378 AGSLSEETPNFPIPSN-----PSVTPTPTETA 405
Db 431 LSHPIEVNNF--PCSLYKNEIMKEIERESKRKIKLNDNDEGNKKIAPRIFISDKDSL 488
Qy 406 OCTADKFPDSFGACDVQACKRQKTSVCGGQIOSTS-----VDCTAD--EQNEGCS 453
Db 489 KCPDPEMVNSSTCRFFVCK-----CVERRAEVTSNNEVYKKEVXDYADIDPEHKPTY 543
Qy 454 NTALI-----AGLAVGVLLALLGGCYFPAKRLDRNKGYOAAHNEHFGSDRGARKRPS 509
Db 544 NMKIIIASAVALATILMV-----YLYKR-----KGNAEKYDKMDQPODYGKSTSR-N 592
Qy 510 DLMQEAEPFWDABEENIEQDETHVWEGDY 541
Db 593 DEMLDPEASFWGEEK--RASHTPVLMEXPY 621

```

RESULT 7

```

A: apical membrane antigen 1 - malaria parasite (Plasmodium falciparum) (strain FCR 3)
C: Species: Plasmodium falciparum
C: Date: 28-Apr-1993 #sequence_revision 28-Apr-1993 #text_change 09-Jun-2000
A: Accession: C44986
R: Thomas, A.W.; Waters, A.P.; Carr, D.
Mol. Biochem. Parasitol. 42, 285-288, 1990
A: Title: Analysis of variation in Pf83, an erythrocytic merozoite vaccine candidate anti-
A: Reference number: A44986; MUID:91101665; PMID:2270110
A: Accession: C44986
A: Status: preliminary; nucleic acid sequence not shown; not compared with conceptual tra
A: Molecule type: DNA
A: Residues: 1-622 <THO>
A: Cross-references: GB:M34554
C: Keywords: membrane protein; surface antigen

```

```

Query Match 14.0%; Score 410; DB 2; Length 622;
Best Local Similarity 26.0%; Pred. No. 5, 4e-24;
Matches 149; Conservative 80; Mismatches 214; Indels 130; Gaps 25;

Qy 41 GNPQANVEMKTFMERFNLTHHQSIGIYVDLGDKVEDGTLREPRGLCPIMKHILOP 100
Db 107 GNPW-----TEYAKYDIEVYHSGIRVLDGEDAVAGYQYRLPBGKCPVFGKGIILIN 160
Qy 101 PRLPLRNNFLEVPF-EKEYKQSGNPLDGGFNLNFTVPSGORISFPME---ELLEKNS 155
Db 161 SN-----TFLKPAVATGNQDLKDGFAFP-----PTNPLISPTTLNGMRDPFYKNE 206
Qy 156 NIKASTDLGRCAFAFKTVAMDKNKATKYRYPFYVDSKKRLCHILYVSMQMEGKYYCS 215
Db 207 YVKRLDELTLCSRNA--MNPNDKSNKYKPAVYDDKDKCHILYIAQENNGPRYCN 264
Qy 216 VKGEPPDLTWYCFKPKR-SVTENHLLYGSAYGEN-PAFISKCPNOALRGYRFGVWK 273
Db 265 -KQSKRSMFCFRPAKDKLFENY-----TYLSKVVVNMEKVCPRKLENAKRGLWVD 317
Qy 274 GRCLDTLTDTVIERVESKAQCVKTFENDGVAADQPHYTP--LTSQASWMDWMP----- 327

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Db 318 GNCEDIPHYNER---SANDLPECNKLVEFELS--ASDQPRQYEHQHLTDYEKIKEGFNKNNA 372
Qy 328 -----LHSDQPHSGVGRNRYGYVDTTGEKCALSDQVPCLVSDSAVSYTA 376
Db 373 SMKSAFLPTGAFAKDRYKSHGKGYWGNVNRKT--HKCEIFNVKPTCLINNSYIATTA 429
Qy 377 AGSLSEETPNFPIPSN-----PSVTPTPTETA 404
Db 430 LSHPIEVNNF--PCSLYKNEIMKEIERESKRKIKLNDNDEGNKKIAPRIFISDKDSL 487
Qy 405 OCTADKFPDSFGACDVQACKRQKTSVCGGQIOSTS-----VDCTAD--EQNEGCS 452
Db 488 KCPDPEMVNSSTCRFFVCK-----CVERRAEVTSNNEVYKKEVXDYADIDPEHKPTY 542
Qy 453 NTALI-----AGLAVGVLLALLGGCYFPAKRLDRNKGYOAAHNEHFGSDRGARKRPS 508
Db 543 NMKIIIASAVALATILMV-----YLYKR-----KGNAEKYDKMDQPODYGKSTSR 591
Qy 509 DLMQEAEPFWDABEENIEQDETHVWEGDY 541
Db 592 DEMLDPEASFWGEEK--RASHTPVLMEXPY 621

```

RESULT 8

```

A: apical membrane antigen 1 - Plasmodium chabaudi adami
C: Species: Plasmodium chabaudi adami
C: Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 09-Sep-1997
A: Accession: A44964
R: Marshall, V.M.; Peterson, M.G.; Lew, A.M.; Kemp, D.J.
Mol. Biochem. Parasitol. 37, 281-283, 1989
A: Title: Structure of the apical membrane antigen 1 (AMA-1) of Plasmodium chabaudi.
A: Reference number: A44964; MUID:90114335; PMID:2608101
A: Accession: A44964
A: Status: preliminary
A: Molecule type: DNA
A: Residues: 1-558 <MAR>
A: Cross-references: GB:M25248; NID:G160076; PID:G160077
C: Keywords: membrane protein; surface antigen

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Query Match 13.6%; Score 398.5; DB 2; Length 558;
Best Local Similarity 25.8%; Pred. No. 3, 7e-23;
Matches 147; Conservative 86; Mismatches 202; Indels 135; Gaps 24;

Qy 42 NFPQANVEMKTFMERFNLTHHQSIGIYVDLGDKVEDGTLREPRGLCPIMKHILOP 101
Db 53 NPWE-----KMEKYDIEKVGSGIRVLDGEDAVENQDYRIRPBGKCPVWGKGIITONS 106
Qy 102 DRLPYRNNFLEVPF-EKEYKQSGNPLDGGFNLNFTVPSGORISFPME---LLEKNSN 156
Db 107 -----KVSFLRVATGNQKVRBGLAFP-----QDVNMSITIDNLKLMYKHKE 152
Qy 157 IKASTDLRCAFAFKTVAMDKNKATKYRYPFYVDSKKRLCHILYVSMQMEGKYYCSV 216
Db 153 ILALNDMSLCAGHA--SFVPGTNNVTAVRHRAVYDDKDKCHILYIAQENNGPRYCS- 209
Qy 217 KEPPDLTWYCFKPKRSVTENHLLYGSAYGENPDAFISKCPNOALRGYRFGVWKGR 276
Db 210 NEEDENOPFCFTPKR-DEYKSLSYLTGNLEED--WETSCPNKSIQNAKGVWVDGVC 265
Qy 277 LDY--TELDTVIERVESKAQCVKTFENDGVAADQPHYTP----- 314
Db 266 SEYQKEVHND-----KTLLEGNOIVFNES--ASQPRQYEHQHLTDYAKIRRGIVDRNG 318
Qy 315 -----PLTSQASWMDWMP-LHSDQPHSGVGRNRYGYVDTTGEKCALSDQVPCLV 367
Db 319 LIGBALPFGS-----YRADQVSKSGKGYWANYDKKTK--KCYIFNKPTCLTI 365
Qy 368 SDSAASVSYTAASLSSEETPNFPIPSN-----PSVTPTPTETA 400
Db 366 NDKDFVATTAALSL-EEGQESFPDIIYKKKIAEIKVNNVNRNNGNDTIKPRIFISD 424

```


A:Residues: 1-1701 <KAP>
A:Cross-references: EMBL:AF031886, NID:g2947227, PID:g2947228
A:Experimental source: subspecies yeoelli, strain YM
C:Genetics:
A:Gene: maeb1
A:introns: 62/1, 1648/1, 1674/2, 1697/1
C:Keywords: alternative splicing, cell binding, erythrocyte invasion

Query Match 4.1%; Score 120, DB 2, Length 1701,
Best Local Similarity 18.8%; Pred. No. 1.2;
Matches 87, Conservative 52, Mismatches 151, Indels 172, Gaps 21,

QY 34 TLSASNSGPFQANVEMKTFMERENLTTHH-----QSGLYYDLGDDEVD--- 78
DB 18 TFSIRAIADNP-----OEDFMDRFDILNNHNWIKWTNKSGLAQGNLKFDIYDENDISSKL 71
QY 79 -----GTLYPEAGLCPIWGKA-----I 96
DB 72 NSLENARLCPRNEKNKNIYR---GSCPDYGKTFMSMDLDKDEXSEDFLEISLGCLKLLI 128
QY 97 ELQQPRL-----PYRNPLEDYPTKEY-----KQSGNPLFGFNVL 133
DB 129 DVEIPVMWSGLAMYQGLFANCPCYDKNHVNDIKNEKEYDMCFDKFYSNKD----- 178
QY 134 NFVTPEGQGISPPMELLEKNSTIKA---STDLDRCAEFAKTAMDKNKATKYRY--- 187
DB 179 ----ISTRIKKYP--LISKITYPGSHGLGRLSNTPEPLHIYNPINYRTQKRYPKL 231
QY 188 -----PFVVDSKKRLCHILYVSMQLMEGGKYSVK 217
DB 232 VETLEDCSISHCIIGCPFPDDFDNKRCERDLPVARPNHKTKCELIIGTH----BEKTTNGN 287
QY 218 GEPPDLTWYCFFPKRKSVTENHHLYGSAYGVENPDPAFISK-PNOALRGYRFV--WKKG 274
DB 288 SDNSRRNGRCFSSIKK-EKGMWTYASSFL-RPD-YETKCPRPYPLNNSEGFYNYNG 343
QY 275 RCLDIYELDTIVIERVSKAQCVKTPENDGVASDQPTTPLYTSQSNWDMPHLQSDDP 334
DB 344 NESPSFKLYD---NSVISFEKEIEKLF-NFYVANEDPE--EKRRNMYLGWVWLGNKQNKL 397
QY 335 HSGCGVRNRYGYVDTTGEGKCALSDQVPDCLVSDAVAASYT 376
DB 398 NS-----MNDLGVALLKEKFTCVLKKQNTYSP 426

RESULT 12
ORMSPI
microtubule-associated protein MAP1B - mouse
N:Alternate names: microtubule-associated protein MAP1(X); microtubule-associated protei
C:Species: Mus musculus (house mouse)
C:Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 01-Sep-2000
C:Accession: S07549, S44387, A33645
R:Noble, M.; Lewis, S.A.; Cowan, N.J.
J:Cell Biol. 109, 3367-3376, 1989
A>Title: The microtubule binding domain of microtubule-associated protein MAP1B contains
A:Reference number: A33645; MUID:90094539; PMID:2480963
A:Accession: S07549
A:Molecule type: mRNA
A:Residues: 1-2464 <NOB>
A:Cross-references: EMBL:X51396; NID:952999; PIND:CAA35761.1; PID:g533000
R:Sanchez, C.; Padilla, R.; Paciucci, R.; Zabala, J.C.; Avila, J.
Arch. Biochem. Biophys. 310, 428-432, 1994
A>Title: Binding of heat-shock protein 70 (hsp70) to tubulin.
A:Reference number: S44387; MUID:94234720; PMID:8179328
A:Accession: S44387
A>Status: preliminary
A:Molecule type: Protein
A:Residues: 653-663, 'IC' <SAN>
C:Superfamily: microtubule-associated protein MAP1B
C:Keyword: microtubule binding, phosphoprotein, tandem repeat
E:589-786/Domains: microtubule binding #status experimental <MTB>
E:589-592, 639-642, 649-652, 655-658, 660-663, 668-671, 674-677, 679-682, 683-686, 687-690, 691-69
R-K-E/D-X)

F:1861-2064/Region: 17-residue repeats
F:91, 116, 351, 888, 1124, 1153, 1168, 1208, 1662, 1877, 1918, 2003, 2030, 2054, 2083/Binding site: ph
P:1747, 969, 1336, 1563, 1563, 1702, 1708, 1990, 2057, 2063, 2419/Binding site: phosphate (Thr) (co
F:1953/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 4.1%; Score 120; DB 1; Length 2464;
Best Local Similarity 19.3%; Pred. No. 2;
Matches 98; Conservative 53; Mismatches 174; Indels 184; Gaps 22;

Dy 15 DCTFASGLSSSTRRESQTLASTSGNPQANVEKTFMERFN-----LTHHQ 64
Db :
1754 EMSLVASLASSEKVOSELEGEKLSPKSDISPLTPRESSFLYSPGFSDSTAARATAAHQAS 1813
Dy 65 SGIVVDLGDDKXVDGTLNREPAG----LCPIKGKHIELQDPRLPYRNNPLEDVPTKE 119
Db :
1814 SSEPIDAAT-----AEVIGFRSSMLFTDMHIALNR-----DLTTSSV 1852
Dy 120 YKSGNPLPGCFNLNFVTPESGORISP----- 145
Db :
1853 EKDSGGKTGPDNVYAQKNENAGSPDEEDDYDESQEKTRTHDVVRYYEKTERTIKSP 1912
Dy 146 ---FPMELEKXNSNIKASTDLGRCAEFAPKYV-----ANDKNNKATV-----YRY 187
Db :
1913 CDGSGYEETIEKTY--KTPEDCGYTCETTEKTRTPREGGSYEISEKTKTRTPVESGYTY 1970
Dy 188 PNYVOSKRLL-----CHILYSQM-----EGKY---GSVK-GEP 220
Db :
1971 EXTERSRRLLDISNGYDTEDGHTLDGCSYSETTEKTSPPESSESYSYSTKPTRS 2030
Dy 221 PDLTWYCFPKRSXTENHHLIYGSAAYGENPDFAISKPNALRGYFGWKKGRCLDYT 280
Db :
2031 POTSAYCYTMEKITTPC---ASTYSYERSD-----RC--YT 2063
Dy 281 ELTDIVIERVESKAQCWKVFENDVASDQPHTYPLTQSASWN--DWM---PLHQSQOP 334
Db 2064 TEKKSPSEARQVDPCLVASCE-----FKHPKTELSPSFINPNPLEWFAGEPTEESEKP 2118
Dy 335 --HSGGVGNNGFYVYDTTGEGKCALSDQVPDCLVDSA-----AVSYRAA 378
Db 2119 LTQSGAPPSPG-----GKOQRCCDETPTPSVSSESAPSQTSDVPPETECPSTAD 2171
Dy 379 GSLSEETPMFIIPSNPSVT-----PPTP 401
Db 2172 ANIDSEDESETIPTDKTVLYKMDPPAP 2200

RESULT 13
T09129
probable erythrocyte-binding protein MAEBL - Plasmodium berghei (fragment)
C:Species: Plasmodium berghei
C:Date: 11-Jun-1999 #sequence, revision 11-Jun-1999 #text_change 21-Jul-2000
C:Accession: T09129
R:Kappe, S.H.I.; Noc, A.R.; Fraser, T.S.; Blair, P.L.; Adams, J.H.
Proc.Natl.Acad.Sci.U.S.A. 95, 1230-1235, 1998
A:Title: A family of chimeric erythrocyte binding proteins of malaria parasites.
A:Reference number: Z16577; PMID:98115903; PMID:9448314
A:Accession: T09129
A:Status: preliminary; translated from GB/EMBL/DDDBJ
A:Molecule type: DNA
A:Residues: 1-993 <KAP>
A:Cross-references: EMBL:AF031887; NID:g2947229; PIDN:AAC05367.1; PID:g2947230
A:Experimental source: strain ANKA
C:Genetics:
A:Gene: maeb1
A:introns: 62/1
C:Keywords: alternative splicing; cell binding; erythrocyte invasion; malaria

Query Match 3.8%; Score 112; DB 2; Length 993;
Best Local Similarity 20.4%; Pred. No. 2.3;
Matches 91; Conservative 49; Mismatches 135; Indels 170; Gaps 24;

Dy 53 FWERFULTHHH-----QG-----LY-----VDLGDDKXVDGTLX 82
Db :

Db 31 FMDRDLANHNHNTKNTSGSLGKDFKFDIYDEDNINSKENTLESQALCSNHENDG-1Y 89
 QY 83 REPAGLCPIWGRH-----IELQPDRL-----104
 Db 90 R---GSCPDYGTPEMNLDKOEYNEDFLNEISLGLNKKLIDLEIPVMSGLAYQGLF 146
 QY 105 ---PYRNNFLEDVPEKEY-----KOS-----GNPLFGFNL 133
 Db 147 ANCPDKHNDIKKEKEYDMCFDKFYNNKONISTRIKKOLLISKYTFGSGGLGRLGS 206
 QY 134 NFVTPSGGRISPPFMELEKNSNIKA-----STDGRCHEFAFKIVA 175
 Db 207 N-----TEYFPHITNPTEYNTTKQMRPKLVETLEDCSIYHCHGPCD-----250
 QY 176 MDKNKATKRYRYPFYDSKKRLCHILYVSMQLEGGKCYSGVGPBPDLTWYCFKPKSVT 235
 Db 251 RDPDKCR-DLPVAFNHTKECIIIGH---EKKTKNCSNDSRRNGCFSSIK-E 304
 QY 236 ENHHLIYSANVGENPDAPFISK-PNQLRGYRGV-WKGRCLDYELTD-TVIERVE 291
 Db 305 KGKMTYVSSFL-RPD-YETKCPRPYPLNNSFEGFYNNYTKCESPTKLYDNTVI---357
 QY 292 SKAOCWVTFENDGVASDQPHYPLTSGASNDWMLHQSQPHSGGVGRNYGYVDTT 351
 Db 358 SPNOIEKLF-SFYANENPD-QKRSNYLWGVWLENKONKLS-----MN 401
 QY 352 GEGKCALSDQVDDCLVSDAAVSYT 376
 Db 402 DLGVCVLKERPTCVLKKONYST 426

RESULT 14

probable oligopeptide-binding lipoprotein - Streptomyces coelicolor
 C:Species: Streptomyces coelicolor
 C>Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change 17-Mar-2000
 C:Accession: J34757
 R:Murphy, L.; Harris, D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, August 1998
 A:Reference number: Z21556
 A:Accession: J34757
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-600 <MOR>
 A:Cross-references: EMBL:AL01184; PIDN:CAA20180.1; GSPDB:GN00070; SCOEDB:SC2A11.11
 A:Experimental source: strain A3(2)
 C:Genetics:
 A:Gene: SCOEDB:SC2A11.11
 C:Superfamily: dipeptide transport protein

Query Match 3.8%; Score 111; DB 2; Length 600;
 Best local similarity 21.4%; Pred. No. 1.4; Indels 80; Gaps 14;
 Matches 59; Conservative 38; Mismatches 99;
 QY 15 DCTTFASGLSSSTRSQSQTSLASTSGNPFQANVEMKTF---MERFNLTHHSGIYDL 71
 Db 305 DIDLQGTGLSPQGRITALKHKANLD-NPVGYIRYAFPGNVKPFQDNIHCKAVLY---360
 QY 72 GQDEVDGTLYRBPAGLCPIWGRHIELQPDRLPYRNNFLEDVPEKEYKOSGNPLPG-130
 Db 361 GAD-----HVSLO-----TARGGVAGGD 379
 QY 131 FNLNFTPS-----GORISPPFMELEKNSNI-KASTDLGRCAE-FAKTVAMDKNKAT 183
 Db 380 IGTMLPFAVPSGQKIDPIEMSGANKKNGEAKELKACNPNKGKTTIYAVRNKPV 439
 QY 184 KY-RYPVYDSKKLCHILYVSMQLEGGKCYSGVGPBPDLTWYCFKPKSVTENHLY 242
 Db 440 EVATAESLQASLKKVG-IDVEIDQYDSQYASVIGSPNV-----QKKG-----Y 483
 QY 243 GSAVGENPDAPFISCPNQLARGYRGVWKKGRCLD 278
 Db 484 GIITMGWGPDE-----PSVOGYGLPLMHSYDILD 512

RESULT 15

A48569
 antiGen Eml100 - Eimeria maxima
 C:Species: Eimeria maxima
 C>Date: 01-Dec-1993 #sequence_revision 18-Nov-1994 #text_change 20-Mar-1998
 C:Accession: A48569
 R:Parmentier, L.; Hug, D.; Humbelin, M.; Weber, G.
 Mol. Biochem. Parasitol. 57, 171-174, 1993
 A>Title: Sequence of a major Eimeria maxima antigen homologous to the Eimeria tenella m...
 A:Reference number: A48569; MUID:93149203; PMID:842611
 A:Accession: A48569
 A:Status: preliminary
 A:Molecule type: nucleic acid
 A:Residues: 1-724 <PAS>
 A:Cross-references: GB:M9058; NID:g158890; PID:g158891
 A>Note: Sequence extracted from NCBI backbone (NCBI:123776, NCBI:P.123777)
 C:Superfamily: thrombospondin type 1 repeat homology; von Willebrand factor type A repeat
 F:45-218/Domain: von Willebrand factor type A repeat homology <VWA2>
 F:238-296/Domain: thrombospondin type 1 repeat homology <THR1>
 F:309-371/Domain: thrombospondin type 1 repeat homology <THR2>
 F:372-432/Domain: thrombospondin type 1 repeat homology <THR3>
 F:433-493/Domain: thrombospondin type 1 repeat homology <THR4>
 F:494-556/Domain: thrombospondin type 1 repeat homology <THR5>
 F:560-610/Domain: thrombospondin type 1 repeat homology <THR6>

Query Match 3.7%; Score 109; DB 2; Length 724;
 Best local similarity 21.0%; Pred. No. 2.6;
 Matches 73; Conservative 36; Mismatches 123; Indels 116; Gaps 17;

QY 211 KKYCVKGEF-----PDLTWYC-----FKPKSVTENHLYGSAY-----V 247
 Db 367 KSPPEVQOQPGPWSMDSCATCGGTRRYRREGEYRPGELFGQTLQAGLDVRENDTC 426
 QY 248 GENDPAFISCPNQLARGYRGVWKKGRCLDYELTVIERV-----ESKAOCWKTF 301
 Db 427 NENP-----CPVDA-----TCGWEFTESD-CRVCYGGGTERRRRPPWLDA 466
 QY 302 ENDGVASDQPHYPLTJQ-----AAMNDWMLPHQSDQPHSGGVGRNYGYV 347
 Db 467 QFGGRSCSQQHPGPTSSVECHNPPCPVDEYVGEWEGPC-SEQ-----CGRGROPRY 519
 QY 348 ----VDTTGEGKCALSPQVDPCLVSDAAVSYTAGSLSEETPNFIIPNSVTPPTPET 403
 Db 520 RGPLQDAMRGKTIIEQ-----NAGVEBQKILKVERPCNDVPCGCTLPFTBWT 571
 QY 404 ALQ-CTADKPEPSGACDV-QACK---ROKTSQ----- 431
 Db 572 ACESCSGTRFDSWVAFDYDDRCQNPTHEESCDAVCESASGGVGGAGAGGGGGG 631
 QY 432 -VGQIOTSTVDTCTADQNEGSGNTALAGLAVGVLLALLGGGCTF 478
 Db 632 SAGEGSGNAGPGEDEKESKGFPTAAVAGVAGVLAIA-AGAGAFY 678

RESULT 16

hypotheical protein KIA0527 - human (fragment)
 C:Species: Homo sapiens (man)
 C>Date: 22-Jan-1999 #sequence_revision 22-Jan-1999 #text_change 21-Jul-2000
 C:Accession: T00073
 R:Nagase, T.; Ishikawa, K.; Miyajima, N.; Tanaka, A.; Kotani, H.; Nomura, N.; Ohara, O.
 DNA Res. 5, 31-39, 1998
 A>Title: Prediction of the coding sequences of unidentified human genes. IX. The complet...
 A:Reference number: Z14086; MUID:98290545; PMID:9628581
 A:Accession: T00073
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-768 <NAG>
 A:Cross-references: EMBL:AB011099; NID:g3043577; PIDN:BAA25453.1; PID:g3043578
 A:Experimental source: Brain; clone HG2246
 C:Genetics:

A>Note: KIA0527

Query Match 3.7%; Score 108; DB 2; Length 768;
 Best Local Similarity 22.0%; Pred. No. 3.3;
 Matches 105; Conservative 38; Mismatches 160; Indels 174; Gaps 23;

QY 97 ELQGDRLPY-----RNNFLD-----VPTKEVYKQSGNPLPGGFNLNFPVPSGQRISP----- 145
 DB 382 EAPKQDRLVSVISVGEMNARDKVFVPT-----TSSP-GAGSSVPADSPGSHLLQKHLFW 434
 QY 146 FPMELLENKSNIKASTDLGRCAEFAKTVAMDKNKATKYRPFYVDSKSKRLCHILYVSM 205
 DB 435 FPAEAFHKRGLEKEVD-----DTKK----- 455
 QY 206 QLMESKRYCSYK--GEPPDLTWYCFKPKRSVTENHHLIYGA-----YGENP----D 252
 DB 456 QPSADNHSVGLVNGEP-----ETKVLYGNTDPSGPFVSKNDSKAGD 499
 QY 253 AFISCPNALRGYAF--GVWKGRCLDYTELTDVIEVESKACQWTFENDGVASDQ 310
 DB 500 PIVSSSDSSWLDGYFVPTDAMRK-----TEABEEDGDRGDSVGLDENLVLPDQ 550
 QY 311 P-----HTYPLTQASWMDWMPPLHQSODPHSGGVGRNYGYVYDT 350
 DB 551 PIVLVKKPKSSTLTPSEGTHSSVLPQMLDVEALALRPVNASFEGIGDGDLLTKYST 610
 QY 351 -----TSGKCALSDQVPCDCLVSDSAVSYTAAGSLF-----ETPNFIISNPSV 396
 DB 611 LPMRFTEE-----SPMATLSYELTSTLEILTNTVTKQTPNHIPSTIMAT 656
 QY 397 TPPTPEETLQCTADKFP-----DSFGACQVQACKQKTSQVCG--QIGSTVDTCADEQN 449
 DB 657 TOPVEVETVPEIQDSEFPYLSDFE-----QEGCGPASELHATLESCTCGD--- 704
 QY 450 ECG--SNTALLAGLVGLLALLGGCYFAKRLDRNK-----GVQAHHHE 496
 DB 705 GCPGLSRGVATITVTLCLLLLAGVGNWGVGRKQHSVYKLVNGQRQARHYNQ 761

RESULT 17

13869 transcritpion factor NF1 (imported) - human
 C:Species: Homo sapiens (man)
 C:Date: 06-Sep-1996 #sequence_revision 06-Sep-1996 #text_change 02-Sep-2000
 C:Accession: I38869
 J.Song, Z.; Krishna, S.; Thanos, D.; Strominger, J.L.; Ono, S.J.
 J. Exp. Med. 180, 1763-1774, 1994
 A:Title: A novel cysteine-rich sequence-specific DNA-binding protein interacts with the
 n and functions as a transcriptional repressor.
 A:Reference number: I38869; MID:95053707; PMID:7964459
 A:Accession: I38869
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Accession: I38869
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-1104 <RES>
 A:Cross-references: EMBL:U15306; NID:g563216; PIDN:AAA69517.1; PID:g563217
 C:Superfamily: RING finger homology
 F:338-398/Domain: RING finger homology <RRN>

Query Match 3.7%; Score 107.5; DB 2; Length 1104;
 Best Local Similarity 19.7%; Pred. No. 6.1;
 Matches 103; Conservative 61; Mismatches 159; Indels 199; Gaps 29;

QY 85 PVLGLCPWGHKIELQOPDLRPLPRNNFLDVPTEKEVYKQSGNPLPGGFNLNFPVPSGQRIS 144
 DB 579 PCGQTPVLSQLELGSS-----RKTCDMPVPCG--KVGCKPLPCG-SLDFHTCEBKCH 630
 QY 145 PPMELLENKSNIKASTDLGRCAEFAKTVAMD-----KNNKATKYRPFYVDSKSKRL 197
 DB 631 EBDGCEVSTSVISC-----RC--SFRKTELPCTSLKSEDAI-----PMCKRCKKKL 677
 QY 198 CHILYVSMQLMGSKYCSVKGEPDLTWYCFKPKRSVTENHHLIYGSAYVGENPDAFISK 257
 DB 678 C-----GRHKCN-----IC-----CVDKEH-----K 694

QY 258 CPNALRGREGVWK-----KGRCLDYTELTDVIERVESKACQWTFENDGVASDQ 311
 DB 695 CPLNGRRLRGHLRCEBPCRHNC-----QTCWQASFDB----- 729

QY 312 HTYPLTQASWMDWMP-----LHSDQD--HSGG----- 338
 DB 730 -----LTCGASVYRPPGCTRPPECTQTGARHNECDHPYVHSHSEKRCPTFLTK 785
 QY 339 --VGR-----NYGYVYDT-----GEGKALSDQVPCDCLVSDSAVSYTAAGS 380
 DB 786 WCMGHEFRSNI PCHLVDISGLPCSATLPCGMKCRCLCHKGBCLYDE----- 834
 QY 381 LSEETPNFIISNPSVPTPEETLQCTADKFPDSFGACDVQAC--RQKTSQVSGQIGST 439
 DB 835 -----PCQPCCTPRADCGHPCAPCHTS--PCPVYACKAKVELQCEGR-RKE 881
 QY 440 SVDCTADQNECGSNTALLAGLVGLLALLGGCYFAKRLDRNKGVQAHHHEFQS 499
 DB 882 MVIC-----SEASVYQRIAIMASAKITDQLGSGVETSLTKRK-KEVHQARLECBEC 935
 QY 500 DRGARKKRPD--LMOEAP-----SFWEAEENIED 530
 DB 936 SALKERKRLAEAFHISEDSPFNIRSSGSKFSDSLKEDARKD 977

RESULT 18

148727 retinoblastoma binding protein 2 related protein (imported) - Neurospora crassa (fragment)
 N:Alternate names: protein 804.10
 C:Species: Neurospora crassa
 C:Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 03-Nov-2000
 C:Accession: T48727
 R.Schultz, U.; Aigun, V.; Hehnel, J.; Brandt, P.; Farciann, B.; Holland, R.; Nyakatura,
 submitted to the Protein Sequence Database, April 2000
 A:Reference number: Z24541
 A:Accession: T48727
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-1009 <SCH>
 A:Cross-references: EMBL:AL353819; GSPDB:GN00112; NCSP:8D4.10
 A:Experimental source: cosmid contig 8D4; strain 74
 C:Genetics:
 A:Gene: NCSP:8D4.10
 A:Map position: 2
 A:Insertions: 153/2; 480/1
 C:Superfamily: human retinoblastoma binding protein 2

Query Match 3.7%; Score 107; DB 2; Length 1009;
 Best Local Similarity 19.4%; Pred. No. 5.9;
 Matches 111; Conservative 97; Mismatches 191; Indels 172; Gaps 29;

QY 18 IFAGLSSTNS-RESQTLASTSGNPQAVENKTEMERENLTHHOSGIYVDGDK 76
 DB 13 VAAAGTSNNASARASPVYTHSS-----NGSKTAAVNSNGYHPPIPSLSPKSEP 66
 QY 77 VD-GTVLPEPAGLCIWKHIELQOPDLRPLPRNNFLDVPTEKEVYKQSGNPLPGGF 131
 DB 67 LDLSNVER-----QOPTACKPEPSKKKPNHLEBAPSTCPLEEWK----- 109
 QY 132 NLNFTPSGQRISPPMELLENKSNIKASTDLGRCAEFAKTVAMDKNKATKYR 187
 DB 110 -----PFYIRKIT--PASKGIGLKIIIPESWMDPAIDTEVRSIARQ 152
 QY 188 PFVDSKRLCHILYVSMQLMGSKYCSVKGEPDLTWYCFKPKRSVTENHHLIYGSAY 247
 DB 153 PFHFRTRQ-----ELNSIEGSSRANIN-----YIDALQFHRQHGNNLTRLPV 197
 QY 248 GENP-DATISCPNALGY-----RFGVKK--GRCLDYTELTDVIERVESKACQWTF 300
 DB 198 DKRPDLRLKAVARAGFDVCLKKWAEIGRLGYSGLKMSLSLSLKSYSQKMLCP 257
 QY 301 FEN-----DGVASDQPTY--PLTSQASWMDWMPLEHSD--QPHSGGVGRNYGYVYDT 351

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Db      258 YEDYIRVAKPGVHQLELEYGGLTPSPAPS---PMKSMNAQTPPDLGSESPSRPTPA 314
Oy      352 GEGKCALSDQVDCVSDSAAV-----SYTAAGSLSEETPNFIIPNSV 396
Db      315 VNGHAKDSDR--DYMTDAPSPAPVKSFGTAINTGFTALNSFTSINRLAASAI 372
Oy      397 TP-----PTPETALCTADKFPDSFGACDVQACRKQKTSVCGGQISTSVDTAD----- 446
Db      373 TPLSSAKNTPPEVR-----PSAAGS---SELKQ-----LSFDTSDAKKE 410
Oy      447 -----EQNECGSNTALLINGLVGVLLALLAGCGCYPAKRLDRKNGVQAHHHEFGSDR 501
Db      411 SSVDDKDEAGSR-----SKRLKKGR-----SYHFPHLQAYQ 443
Oy      502 GARKK-----RPSDLMOEAEP-----FWDEAE 525
Db      444 GSRAEACGAARSLYCEARTSPHLFWNLCS 474

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RESULT 19
A:Species: lysosomal membrane glycoprotein 2 precursor - mouse
C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 20-Aug-1999
C:Accession: A35560
R:Cha, Y.; Holland, S.M.; August, J.T.
J. Biol. Chem. 265, 5008-5013, 1990
A:Title: The cDNA sequence of mouse LAMP-2. Evidence for two classes of lysosomal membra
A:Reference number: A35560; MUID:90202978; PMID:2318880
A:Accession: A35560
A:Status: not compared with conceptual translation
A:Residues: 1-415 <CHA>
A:Cross-references: GB:J05287; NID:g198708; PIDN:AAA9412.1; PID:g293693
C:Superfamily: lysosome-associated membrane protein
C:Keywords: glycoprotein; membrane protein
F:1-25/Domain: signal sequence #status predicted <SIG>
F:26-415/Product: lysosomal membrane glycoprotein 2 #status predicted <MAT>

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Query Match      3.6%; Score 106; DB 2; Length 415;
Best Local Similarity 21.1%; Pred. No. 2;
Matches 71; Conservative 24; Mismatches 91; Indels 150; Gaps 15;

Oy      277 LDYTELTLTVIERVESKAQCWKTFFENDVASD-----QPHYPLTQSAQWMDWPLHQ 330
Db      112 LSYNTSDTVFPGAAKGVHVKPBNFKVPLDVFKNSTVLTNLTIVV--QKTMGHL 169
Oy      331 SDQPHSGVGNRYGYVDTTGEGKCALSDQVDCVSDSAVSYTAAGSLSEETPNFI 390
Db      170 QAFVQNGTVSKN-----EQVCE-EDQPTTV-----APIHTTAPS-----TTTTLT 210
Oy      391 P-SNPSVTP-PTPETA-----LOCTADKFPDSF-----GAC 419
Db      211 PTFSTPTPTPTPTVGNYSIRNGNTTCLLATWGLQLTITEKVPPIFINPATNTFTTSC 270
Oy      420 DVQA----- 423
Db      271 QPQSAQLRLANSQIKYLDLIRAVKNEKRFYKEVNVMTYLANGSAFNISKNLSEFWAPL 330
Oy      424 -----CKRQKTSVCGGQIQ-----STVSDCTADEQNECGSNTALLAG 460
Db      331 GSSVYCNKEQVLSVBARFOINTFNLKVPFNTKGTQTADDCADENFL--VPLAVG 387
Oy      461 LAVGVLALLALLGGCGCYPAKRLDRKNGVQAHHHEHE 496
Db      388 AALGGVLLVLVL--AYPI-----GLKRHTTGYE 413

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RESULT 20
T13931
projectin - fruit fly (Drosophila melanogaster) (fragment)
C:Species: Drosophila melanogaster

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C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 17-Nov-2000
C:Accession: T13931
R:Daley, J.; Southgate, R.; Ayme-Southgate, A.
J. Mol. Biol. 279, 201-210, 1998
A:Title: Structure of the Drosophila projectin protein: isoforms and implication for pro
A:Reference number: Z17815; MUID:96300339; PMID:9636710
A:Accession: T13931
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-6658 <DAL>
A:Cross-references: EMBL:AF047475; NID:g3337430; PID:g3337431; PIDN:AAC27550.1
C:Genetics:
A:Gene: projectin
A:Cross-references: FlyBase:FBgn0005666
A:Map position: 4
A:Note: intron positions not resolved (incomplete sequence)
C:Keywords: muscle

```

```

Query Match      3.6%; Score 104.5; DB 2; Length 6658;
Best Local Similarity 19.0%; Pred. No. 1.4e+02;
Matches 76; Conservative 49; Mismatches 123; Indels 151; Gaps 20;

Oy      124 GNPLPGGNLNFVTPSGQRIISPPMELLEKNISIKASTDLGRC--EPAFTVAMDKNK 181
Db      2340 GSPIQG-----YIVEVDKYSPLWEKALETSSPTPTAVQGLIGNEYQFVALNKGNTL 2394
Oy      182 ATKRYRPFVYDSKRLCHILYV-----SMQLWEG--KKYCVKGP-PDLTWYC 227
Db      2395 SEBDSKIFYAKR-----YIAPKIDRLNRNTLSSGALKLDANITGQPAKRVW-- 2447
Oy      228 FKPRKVTENHLLIYGSAYVGENPDAF---ISKCPNALRG----- 265
Db      2448 -----KLSNHLQSGKNVTETPDYTKLVIRPQGTDSSEVLVTANTSGKSVLVNV 2501
Oy      266 -----YRFGV--WK-----GRCLDTLDTVIERVESQAQCWK 299
Db      2502 VITDKPPNPGLQISDVHKGCHLKKWRPSHDGTFIEYFQ-----IDKLEPTGCIW 2556
Oy      300 TFEKDVASDQPHRYPLTQSAQWMDWPLHQSDQPHSGVGNRYGYVDTTGEGKCAL 359
Db      2557 SCRSTAQVDVTGSP-----GNEYKFRVSAVNAEGE----- 2588
Oy      360 DQVDCVSDSAVSYTAAGSLSEETPNFIIPSNP-----SVTPPTPE-- 402
Db      2589 ---SQPLVGESIVA-----RNP-FDEPKREULKATDMDKHVDLAWTPEVIDG 2635
Oy      403 TALQCTADKFPDSFG---ACDVQA--CKRQKTSVCGGQ 435
Db      2636 SPISCIYIIEKQDKYKMERALDVADQCKATIPDLVEGQ 2674

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RESULT 21
A:Accession: A24571
A:Protein-cytosine kinase (EC 2.7.1.112) erbB2 precursor - human
N:Alternate names: c-erb-B-2 protein precursor; kinase-related transforming protein erbB
C:Species: Homo sapiens (man)
C:Date: 25-Oct-1987 #sequence_revision 06-Dec-1996 #text_change 11-Jun-1999
C:Accession: A24571; A25491; A41488; B41488; I55509; I57622
R:Yamamoto, T.; Ikawa, S.; Akiyama, T.; Semba, K.; Nomura, N.; Miyajima, N.; Saito, T.;
Nature 319, 230-234, 1986
A:Title: Similarity of protein encoded by the human c-erb-B-2 gene to epidermal growth f
A:Reference number: A24571; MUID:86118663; PMID:33003577
A:Accession: A24571
A:Molecule type: mRNA
A:Residues: 1-1255 <YAM>
A:Cross-references: GB:X03363; NID:g31197; PIDN:CAA27060.1; PID:g31198
R:Semba, K.; Kamata, N.; Toyoshima, K.; Yamamoto, T.
Proc. Natl. Acad. Sci. U.S.A. 82, 6497-6501, 1985
A:Title: A v-erbB-related protooncogene, c-erbB-2, is distinct from the c-erbB-1/epiderm
A:Reference number: A25491; MUID:86016729; PMID:2995967
A:Accession: A25491
A:Molecule type: DNA
A:Residues: 737-1031 <SEM>

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A:Cross-references: GB:M1167; NID:G182163; PIDN:AAA35808.1; PID:G553282
 R:Consensus, L.; Yang-Peng, T.L.; Liao, Y.C.; Chen, E.; Gray, A.; McGrath, J.; Seeburg, F
 Science 230, 1132-1139, 1985
 A:Title: Tyrosine kinase receptor with extensive homology to EGF receptor shares chromos
 A:Reference number: A44188; MUID:86070181; PMID:2999974
 A:Accession: A44188
 A:Molecule type: DNA
 A:Residues: 740-910 <CON1>
 A:Cross-references: GB:M12036; NID:G183988; PIDN:AAA35978.1; PID:G183989
 A:Accession: B44188
 A:Molecule type: mRNA
 A:Residues: 1-517, 'RALT', 522, 'S', 524-654, 'V', 656-1169, 'A', 1171-1255 <CON2>
 A:Cross-references: GB:M11730; NID:G183986
 R:King, C.R.; Kraus, M.H.; Atkinson, S.A.
 Science 229, 974-976, 1985
 A:Title: Amplification of a novel v-erbB-related gene in a human mammary carcinoma.
 A:Reference number: 159509; MUID:85272597; PMID:2992089
 A:Accession: 159509
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 832-909 <REX>
 A:Cross-references: GB:M29395; NID:G459807; PIDN:AAA35809.1; PID:G459808
 R:Tal, M.; King, C.R.; Kraus, M.H.; Ullrich, A.; Schlessinger, J.; Givol, D.
 Mol. Cell. Biol. 7, 2597-2601, 1987
 A:Title: Human HER2 (neu) promoter: evidence for multiple mechanisms for transcriptional
 A:Reference number: 157622; MUID:87286898; PMID:3039351
 A:Accession: 157622
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-191 <TAL>
 A:Cross-references: GB:M16792; NID:G183983; PIDN:AAA58637.1; PID:G553332
 C:Comment: Amplification and overexpression of this erbB-related gene occurs in about 30
 C:Genetics:
 A:Gene: GDB:ERBB2; NGL; NEU; HER-2
 A:Cross-references: GDB:120613; OMIM:164870
 A:Map position: 17q21.1-17q21.1
 A:Introns: 25/1; 75/3; 147/1; 883/3
 A:Note: the list of introns is incomplete
 A:Function:
 A:Description: catalyzes the phosphorylation of a peptidyl tyrosine residue by ATP
 C:Superfamily: epidermal growth factor receptor; protein kinase homology
 C:Keyword: ATP; autophosphorylation; duplication; glycoprotein; phosphoprotein; phospho
 kinase
 F:1-21/Domain: signal sequence #status predicted <SIG>
 F:22-1255/Product: protein-tyrosine kinase erbB2 #status predicted <MAT>
 F:22-553/Domain: extracellular #status predicted <EXT>
 F:70-304/Domain: EGF receptor extracellular domain repeat <BE1>
 F:395-605/Domain: EGF receptor extracellular domain repeat <EE2>
 F:654-675/Domain: transmembrane #status predicted <TM>
 F:676-1255/Domain: intracellular #status predicted <INT>
 F:718-983/Domain: protein kinase homology <KIN>
 F:726-734/Region: protein kinase ATP-binding motif
 F:68,124,187,259,530,571,629/Binding site: carboxylate (Asn) (covalent) #status predict
 F:686/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status predicted
 F:753/Active site: Lys #status predicted
 F:1139,1221,1222,1248/Binding site: phosphate (Tyr) (covalent) (by autophosphorylation)
 Query Match 3.6%; Score 104; DB 1; Length 1255;
 Best Local Similarity 22.5%; Pred. No. 14;
 Matches 108; Conservative 43; Mismatches 174; Indels 156; Gaps 27;
 QY 81 LYRBPAGLCPIGWKHLELOPDRPYRNNFLEDPTEKEKYGKSGNPLPGG---FNINPVT 137
 DB 256 LHNHNSGIC-----ELHCPALVYNTDTFESMPN-----PEGRTYFGASCVT 297
 QY 138 PSQGRISPFPMELLEKNKSNIKASTDLGRCAEFA---FKTVAMDKNKATKRYYPFYD 193
 DB 298 AC-----PYNVL-----STDVGSCTLVCPHNOEYTAEDGTORCKCKSPCA--- 339
 QY 194 KKRLLCH-----ILVSMQIMEGKKYC-----SVKGPPLTWYCEKPRK 232
 DB 340 --RVCYGLGMEHLREVAIVASNIQEPAGCKIFGSLAFPESPDGDPAANTAPLOEQL 397

QY 233 SVTEHHILYGSAYVGENPDAF--ISKCPN-QALRG-----YRFGV-WKKGR 276
 DB 398 QVFPLEITETLYLTISAMPBLSPLSVFQNLQVIRGHLHNGAYSLTLQIGISMLGRS 457
 QY 277 LDVLELDTVIERVESKAQCKVKTFFENDGASDQ---PHTYPLTSQASNMWMPPLQSD 332
 DB 458 L-RELGSGLALIHNNHLCFVHT-----VPMDDLFRNPH-----QAL-----LHTAN 498
 QY 333 QPHSGGVRRNGFYVDTTGE-----GKCALSDQ-----VPCLVSDSAVSYTAAG 379
 DB 499 RPEBCVGEGLACHQLCARGHCWGPFPQCVCNCSQFLRGECVECKVLOGLPREYVNR 558
 QY 380 SLSEETPNFIIPSNPSVTPPTPEALQCTAD-----K 412
 DB 559 HCLPCHPE-CQPGQSVTCFGE-ADQCVAHAYKDPFCVARCPSGVKPDLSYPIWK 616
 QY 413 PDSFGACDVQACKROKTSVCGGQIQSTSVCTADEQNECGSNYLLAGLAVGVLALL 472
 DB 617 PDEEGAC--QC-----PINCSTSCVDLDDKCGPAEOR--ASPLTSIIS--AVAGILLVVL 667
 QY 473 G 473
 DB 668 G 668
 RESULT 22
 T38236
 Hypothetical protein SPAC23A1.17 - fission yeast (Schizosaccharomyces pombe)
 C:Species: Schizosaccharomyces pombe
 C:Date: 03-Dec-1999 #sequence revision 03-Dec-1999 #text_change 03-Dec-1999
 C:Accession: T38236
 R:Murphy, L.; Harris, D.; Wood, V.; Barrell, B.G.; Rajandream, M.A.
 submitted to the EMBL Data Library, February 1998
 A:Reference number: Z21780
 A:Accession: T38236
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-1611 <MOR>
 A:Cross-references: EMBL:AL021813; PIDN:CAA1699.1; GSPDB:GN00066; SPDB:SPAC23A1.17
 A:Experimental source: strain 972h-, cosmid c23a1
 C:Genetics:
 A:Gene: SPDB:SPAC23A1.17
 A:Map position: 1
 Query Match 3.6%; Score 104; DB 2; Length 1611;
 Best Local Similarity 17.4%; Pred. No. 20;
 Matches 88; Conservative 73; Mismatches 160; Indels 184; Gaps 21;
 QY 105 PYRNNFLEDPTEKEKYGKSGNPLPGGFNIN-----FVTSQGR-ISPFMELLEKN 156
 DB 13 PYRSSFSDLEED-----PGQIVDVSNLDDGWYGTGYVSDGNKIKGSPMDTEPAED 67
 QY 157 IKASTDLGRCAEFAF---KTVAMDKNKATKRYRPFYVDSKKRLCHILVSMQIMEGK 212
 DB 68 ---AVFERASEMALHOPPTSVAHSRNSLSQY----- 97
 QY 213 YCSVAGEPDLTWYCEKPRKSTENHHLIYGSAYVGENPDAFISKCPNALRGYFGYWK 272
 DB 98 -----ASTI---RSIKTSINN-----TEHIGADTESILS----- 124
 QY 273 KGRCLDYELTDVIERVESKAQCKWKT---FENDGASDQPHYPLTSQASNMWMP 328
 DB 125 ---ANDFIDSTSEALTKIV---VDTLSAFQND--SNSRPHSLKNVEK-----L 166
 QY 329 HOSDQPHSGGVRRNGFYVDTTGEKCALSDQVDCLVSD----- 369
 DB 167 HTFSAPYL-----ISEETSCSTENDSLPLTATHTTTGGEAAT 205
 QY 370 SAAVSYTAAGSLSEET--PNFIIPSNPSVTPPTPEALQCTAD-----KPPDSFG 417
 DB 206 GAAVNTTTTHTTTSTNTSVIIPSNPSVFLVDCTHSQCPTLPLNATTOHSLRYIDNAS 265
 QY 418 ACIVQACKR-----QKTSVCGGQIOSTSVCTADEQNECG-----SNTALLIAGL 461

Db 266 ASATVLETRTPAASSTWATSSHQSPADSOAEELSKSQVAKODDPFVVSNTANSDP 325
 Qy 462 AVGGVLLALLAGGCGYFAKRLD-----RNGVQAHHHEHFQSDRGARKRP----- 508
 Db 326 ASSCKPAKPLTDLNPAFQKRLDPOKPKSQGSEISEQEBEDYDAESDEMHSPTSTHP 385
 Qy 509 -SDLMQEAEPSPFWEAEENIEQDGE 532
 Db 386 ESEPEPDQDEPSEKDEKNDKVEEEOE 410

RESULT 23

S69063

probable membrane protein YPR075c - Yeast (Saccharomyces cerevisiae)

N:Alternate names: hypothetical protein P9513.9

C:Species: Saccharomyces cerevisiae

C>Date: 22-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 06-Feb-1998

C/Accession: S69063

R/Couch, J.

A:Submitted to the EMBL Data Library, March 1996

A:Description: The sequence of S. cerevisiae cosmid 9513.

A:Reference number: S69057

A:Accession: S69063

A:Molecule type: DNA

A:Residues: 1-360 <COU>

A/Cross-references: EMBL:U51033; NID:g1230676; PID:g1230683; MIPS:YPR075c

C:Genetics:

A:Gene: SGD:OPY2

A/Cross-references: SGD:S0006279; MIPS:YPR075c

A:Map position: 16R

A:Keywords: transmembrane protein

F/96-112/Domain: transmembrane #status predicted <TM>

Query Match 3.5%; Score 103; DB 2; Length 360;

Best Local Similarity 23.4%; Pred. No. 2.8;

Matches 48; Conservative 23; Mismatches 58; Indels 76; Gaps 10;

Qy 350 TTGGKCALSDQVDPCLVSDSAVSYTAAGSLSEETPFIIIPSNPVTPTPTALQCTA 409
 Db 24 TRGSDGCVVCSTASCPV--CASGEYCVMTSL-----TC 55
 Qy 410 DKFPDSFGACDVOAKCRQKTSVCGQLOSTVDTCTADQNEGSGNTALIAGLA--VGV 466
 Db 56 DKCSTY-----CAKQSDS---QLSLSLSSSSSSSSNSNEMTSILVFTVIGVGA 104
 Qy 467 LLLALLGGCGCTFA-KRLDRNGVQAHHHEHFQSDRGARKRP-PSDLMQEAEPSPFWEAE- 524
 Db 105 MLIALV--ALYFINKRYWKPK-----RQKNKALKLEBASQSYGNEBEY 145
 Qy 525 -----ENIEODG-----ETHW 536
 Db 146 FDEDEDDDEDEDDGCMKRDESHITL 170

RESULT 24

T23024

hypothetical protein H02112.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C/Accession: T23024

R/McLay, K.

A:Submitted to the EMBL Data Library, March 1997

A:Reference number: Z19556

A:Accession: T23024

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-1332 <ML>

A/Cross-references: EMBL:292789; PIDN:CAB07215.1; GSPDB:GNO00022; CESP:H02112.1

C:GeneticCB:

A:Gene: CESP:H02112.1

A:Map position: 4

A:Introns: 12/3; 29/1; 60/3; 246/1; 449/1; 756/1; 849/1; 961/1; 1103/3; 1214/3
 Query Match 3.5%; Score 103; DB 2; Length 1332;
 Best Local Similarity 18.0%; Pred. No. 18;
 Matches 123; Conservative 74; Mismatches 237; Indels 248; Gaps 30;

Qy 37 ASTSGNPFQANVEKTFMERFNLTH-----HSGIYVD--L 71
 Db 386 SDTIVSPDENVRALKPKFRDRRKXHHKPSYGVNNGSYLENPFIPRHRSGRHDHRY 445
 Qy 72 GQDXEVD---GTLREPAAGLCPIWGKHELO---QPD--RLPYRNFLFVPEPEKXYQ 122
 Db 446 GYCPAIDSPFSTARFGAALSDQFKDYRRAMGKIQGDARKYDGNKRELIDEEF----- 500
 Qy 123 SGNPLPGFNLNFTPSGQRISPPMELKNSNIKASTDLGRCAEFKTVANDKNNKA 182
 Db 501 -----GPNKPFESNIEQVFP-----GNRSK--KQYG- 526
 Qy 183 TKRYPPFYVDSK-----RLCHILYVMQMEGKKYGSVKGPEPDLTWYCFKP 230
 Db 527 -PHDDPGYDEKTFDAKDLFGATRRKRSAYTEGQSYVGQSQNISARQAVNKKD--- 582
 Qy 231 KKSVTENHHLIYGAAYVGENDAFI-----SKCP-----NQLRGYRFGVWKGR 275
 Db 583 -QQYTFPTFLTFGDCF-----DQFIKSGNGINMAACPIGETPDKTLRS----- 626
 Qy 276 CLDYTELDTPYI-----ERVSKAQCVKTFENGVA-----SDQPHF----- 313
 Db 627 CSEFGVSTTIVAVTIGTQTSDDLSAPSEYEINGGVTTOSTWNDQPTTQAPNSYESYTT 686
 Qy 314 -----YPLTQASMNWMPFHQSDQPHSGGVGNV-----GFYYVDITG 352
 Db 687 QYSNDVPSTSAIIGRCSLDASGL--FSLGCSQKTIQCSGMAIVRCGSLYFNENIQ 745
 Qy 353 EGKCALSDQVDPCLVSDSAVSYTAAGSLSEETPFIIIPSNPVTPTPTETA----- 404
 Db 746 E--CTYRDEVCEGSCQSTSPVITTPGQDSSNYGIPSD--VPSITQTPVGDRCAYV 801
 Qy 405 -----LQCTADKRPDSFGACDVQAK-----RQKNSC----- 431
 Db 802 ASGLFDLGCSQKTIQCSDSASVRECEGSLYFDERSGSCRPDEVPKQTDVSSSSTVP 861
 Qy 432 -----VGGQIQTSTVD-----CTADQNEGSGNTALIAGLAVG 465
 Db 862 YLDPTTTPASPSDEPTTYSVAPYIPSVYVNVDTCTSLSDTHGCGSSFVFCG 921
 Qy 466 VLLIALLGGCGYFAKRLDRN-KGVQA-----AHHEHFQSDRGARKRP-PSDLMQEAEP 517
 Db 922 RLISS---GNCQLGEGYDPSVQCGRTFSEIPARACDEQVTTDGLVQLMPEYKTLBEVLT 978
 Qy 518 SFWEAEENIEQDETHWMBG 539
 Db 979 T--TEAATVANDGPTDTYITG 998

RESULT 25

A47221

fibrillin 1 precursor - human (fragment)

C:Species: Homo sapiens (man)

C>Date: 02-Jun-1995 #sequence_revision 25-Apr-1997 #text_change 02-Aug-2002

C/Accession: A47221; I54355; S17064; I59574; S17062; S62111; A34198

R/Corsos, G.M.; Chalberg, S.C.; Dietz, H.C.; Charbonneau, N.L.; Sakai, L.Y.

A:Title: Fibrillin binds calcium and is coded by cDNAs that reveal a multidomain structure

A:Reference number: A47221; MUID:94010947; PMID:7691719

A:Accession: A47221

A:Molecule type: mRNA

A:Residues: 1-337; 'T', 339-1029 <COR>

A/Cross-references: GB:X63556

R/Pereira, L.V.; D'Alessio, M.; Ramirez, F.; Lynch, J.; Sykes, B.; Pangillan, T.; Bonad

Hum. Mol. Genet. 2, 961-968, 1993

A:Title: Genomic organization of the sequence coding for fibrillin, the defective gene p

A:Reference number: I54355; MUID:93372860; PMID:8364578

A:Accession: 154355
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 132-3002 <PER>
 A:Cross-references: GB:LI3923; NID:G306745; PIDN:AA02036.1; PID:G306746
 R:Maalen, C.L.; Corson, G.M.; Maddox, B.K.; Glanville, R.W.; Sakai, L.Y.
 Nature 352, 334-337, 1991
 A:Title: Partial sequence of a candidate gene for the Marfan syndrome.
 A:Reference number: S17064; MUID:91304568; PMID:1852207
 A:Accession: S17064
 A:Molecule type: mRNA
 A:Residues: 1030-3002 <MAS>
 A:Cross-references: EMBL:X63556
 R:Dietz, H.C.; Valle, D.; Franccomano, C.A.; Kendzior, R.J.
 Science 259, 680-683, 1993
 A:Title: The skipping of constitutive exons in vivo induced by nonsense mutations.
 A:Reference number: 159574; MUID:93157831; PMID:8430317
 A:Accession: 159574
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 2217-2288, '1', 2290-2325 <RES>
 A:Cross-references: GB:S54426; NID:G264860; PIDN:AA02544.1; PID:G264861
 R:Lee, B.; Godfrey, M.; Vitale, E.; Hori, H.; Mattei, M.G.; Sarfarazi, M.; Tsipouras, P.
 Nature 352, 330-334, 1991
 A:Title: Linkage of Marfan syndrome and a phenotypically related disorder to two different
 A:Reference number: S17062; MUID:91304567; PMID:1852206
 A:Accession: S17062
 A:Molecule type: mRNA
 A:Residues: 'VLTVVFIFLSYNNML', 944-1444 <LEE1>
 A:Cross-references: EMBL:X62008; NID:G31398; PIDN:CA556534.1; PID:G5924015
 A:Accession: S62111
 A:Molecule type: protein
 A:Residues: 1166-1176, 'X', 1178-1180, 'D', 1182-1185 <LEE2>
 R:Maddox, B.K.; Sakai, L.Y.; Keene, D.R.; Glanville, R.W.
 J. Biol. Chem. 264, 21381-21385, 1989
 A:Title: Connective tissue microfibrils. Isolation and characterization of three large F
 A:Reference number: A34198; MUID:90078246; PMID:2512293
 A:Accession: A34198
 A:Molecule type: protein
 A:Residues: 565-575, 1890-1892, 'I', 1894-1900 <MAD>
 A:Comment: Fibrillin is a major component of elastin-associated microfibrils.
 C:Genetics:
 A:Gene: GDB:FBN1
 A:Cross-references: GDB:127115; OMIM:134797; OMIM:154700
 A:Map position: 15q21.1-15q21.1
 A:Introns: 2236/1; 2258/1; 2297/1
 C:Superfamily: fibrillin 1; EGF homology
 C:Keywords: alternative splicing; calcium binding; extracellular matrix; glycoprotein; M
 F:1-3002/Product: fibrillin (5'-region exon A splice form) #status predicted <MATC>
 F:1332-3002/Product: fibrillin (5'-region exon C splice form) #status predicted <MATC>
 F:1332-1367/Domain: EGF homology <EGF>
 F:1457-1492/Domain: EGF homology <EGF2>
 F:2262-2295/Domain: EGF homology <EGF1>

Query Match 3.5%; Score 102; DB 2; Length 3002;
 Best Local Similarity 21.9%; Pred. No. 69;
 Matches 114; Conservative 61; Mismatches 212; Indels 134; Gaps 32;

19 PASGLSSSTRSR--ESQTLASTSGNPFQANVEMKTFM--ERENLTHHQSGLYVLDGDD 74
 2196 FEGGCKSSPKSRHNSQEOCCALKGBGWDPCGLCTPEPEARQICPVSSGIIVG-PDD 2254
 75 KEYDGLYREPAQLCPHWGHILOQPD-----RLPYRNFLADVPEKAYKQSGNPLRG 129
 2255 SAVDMECKEP-DVC-----KHGQCINTDGYRCECFGYTLAECVDTECSVGNPCGN 2309
 130 GFULN-----PVTSQGRISPFEMELLEKNINASTDLGCAFAFATVAMDKNATKY 185
 2310 GTCKNVIIGFECTCEGFEFGPMWTC-----DINECAQ-----NPLICAF 2350
 186 RYFVYDSKRLCHILYVSMQLEGGKYCSVKGEPPDLTYCFKPR---KSVTENHLLY 242
 2351 RCNVTGSGYCKCPGVGIV---LAEEDRMCMDEDECEGKKIDCEKQMECNILGTWCIC 2407

243 GSAYVGENPDFAISKCPNALRGYRFGWKKGRCLD-----YT-ELTPTVI-----ERVE 291
 2408 GPGY-QRRPDG--EGCVDENECCQKPGICENGKRLNTRGSTTCCECNDFTASPNODELD 2464
 292 SK-AQCWKTPE--DQVADOPHTYPLTSQASWMDWPLHQSDQPHSGV----- 339
 2465 NREGYCFTEVLQNMCOIGSSNRNPVTSECCCDGARGWP-HCBICPFGQTVARFKLCPR 2523
 340 GRNNGF-----YVDTTGEKCALSDQVDP-----CLVSDAASVYTAAGSL 381
 2524 GR--GFMTNGADIDCKVYHVCNNGEC-----VNDKSYHCICTKYTPDIITGTCVDL 2576
 382 SE-ETP---NFIPSNPSVTPPTPEPTALQCTADK---PPDSFGACVQACKRQKTS-C 431
 2577 NECNAPRPPCFICNT-----ESSYQSCSKRYGLQDGRSGCNLDLCATQNHQ 2628
 432 ----VGG-----QIQSTVSD--CTADEQNEGGS 453
 2629 FLCVNTIGFTCKCPGPGFTGHTSCIDNNECTSD-INLCGS 2668

RESULT 26
 A60643
 antigen 5401 - Elmeria tenella (fragment)
 C:Species: Elmeria tenella
 C:Date: 14-May-1993 #sequence_revision 14-May-1993 #text_change 18-Jun-1993
 C:Accession: A60643
 R:Danthorh, H.D.; Augustine, P.C.; Ruff, M.D.; McCandlish, R.; Strauberg, R.L.; Likel,
 Poult. Sci. 68, 1643-1652, 1989
 A:Title: Genetically engineered antigen confers partial protection against avian coccidi
 A:Reference number: A60643; MUID:90160107; PMID:2622819
 A:Accession: A60643
 A:Status: not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-287 <DAN>
 F:11-120/Region: 22-residue repeats (A-G-X-X-G-G-S-G-G-X-A-E-L-P-G-E-E-G-G-A-G)

Query Match 3.5%; Score 101.5; DB 2; Length 287;
 Best Local Similarity 24.6%; Pred. No. 27;
 Matches 49; Conservative 20; Mismatches 69; Indels 61; Gaps 9;

336 SGGVRNRYFYVVD---TGECKALSDQVDPCLVSDAASVYTAAGSLSEETNFIIPS 392
 135 AGGABEGAGGEGEYVQPEGBGASGEGQV-----ETPEPEPE 174
 393 NPSVTPPEPTALQCTADKFPDSFACVQACKRQKTSVGGQISTVSDCTADQNEGC 452
 175 TPEARPEPEPTETPEAB-PTREGA-----EESKEKG 207
 453 SN--TALLAGLVAGVLLALLGCGCYPAKRLDRNKGVOAHH--EHEFOSDRGARKKPS 509
 208 SGPPTAAVAG-GVGGVLLAAVGGVAAYSGGGGGGGAEEAQQVFEGBESGASAEITPE 266

510 ----DLMOEAEPFWDNA 523
 267 ADTVIDITDED--YWADS 283

RESULT 27
 S07296
 plastocyanin-plastocyanin reductase (EC 1.10.99.1) cytochrome f precursor - wheat chloro
 N:Alternate names: cytochrome b-f complex cytochrome f
 C:Species: chloroplast Triticum aestivum (common wheat)
 C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 03-Jun-2002
 C:Accession: S07296; S27220
 R:Wiley, D.L.; Howe, C.J.; Aufferet, A.D.; Bowman, C.M.; Dyer, T.A.; Gray, J.C.
 Mol. Gen. Genet. 194, 416-422, 1984
 A:Title: Location and nucleotide sequence of the gene for cytochrome f in wheat chloropl
 A:Reference number: S07296
 A:Accession: S07296
 A:Molecule type: DNA
 A:Residues: 1-320 <WIL>

QY 440 SVDCTADEQ-----NEGGSTALIAAGVGLLAL 471
DB 377 VEDSPQRSDRLFAVDQMGSVTSLTAGSGSKLLTT 415

RESULT 30

T99219

translation initiation factor eIF-4 gamma homolog F27H5.30 [similarity] - Arabidopsis thaliana

N:Alternate names: protein F27H5.30

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 20-Jun-2000

C:Accession: T99219

R:Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; Lemcke, R.

submitted to the Protein Sequence Database, April 2000

A:Reference number: Z25018

A:Accession: T99219

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1606 <RIB>

A:Cross-references: EMBL:AL163852; GSPDB:GND00061; ATSP:F27H5.30

A:Experimental source: cultivar Columbia; BAC clone F27H5

C:Genetics:

A:Gene: ATSP:F27H5.30

A:Introns: 455/3; 1370/2; 1435/2; 1523/1; 1529/1; 1558/3; 1586/2

Query Match 3.4%; Score 99.5; DB 2; Length 1606;

Best Local Similarity 20.5%; Pred. No. 44;

Matches 119; Conservative 71; Mismatches 217; Indels 173; Gaps 29;

QY 20 ASGLSSTRSRESQTLASTSGNPRQANTEMKTFMRFLTLHHOSGIYVDLGGDK----- 75
DB 310 SSDSTSSVVARNAQNVMSAL--PVNAKVSVK-----PAGVEKLGSPKDRSH 355
QY 76 -EVDGTLVREPAGLCIPMGKHIETLQOP-----DRLPYRNFLDEVPTKEKXQSG 124
DB 356 GEVNISLSQKNVACGLSSS---QQPKSPVSGVNSAPKSPKSVETVPLAKSVEIV 411
QY 125 NPLPGGFNLFPVTPS-----GQRISFPFMELLEKNKNIKASTDLGCAEP 169
DB 412 PPVKSSEVETAPVTTTIRRAEMVSEISVEDQCTKVEPHNLTEENGQTMPSLVSDPEPT 471
QY 170 APTVAMDKNKAATKTRYPVVDKSKRLCHILVSNQMLEGKKYCVKKEPDLTYCYCK 229
DB 472 A--TVAAKEN-----LSLPATNGFRKQLKV-----STSDAPTSDSVDTS 510
QY 230 PRKSVTEHHLYGSAVYGENPDAPISKPCNALRGVREGVWKKGRCLDYTELDT----- 285
DB 511 IDKSTGSSHA--SSSISGSSPPEKDLCKDNRT-----ASDKLDEKSVISDAKHET 559
QY 286 ---VIERVESKAO-----CMV--KTFENDGVASDQPH--TYPLTQASQWMDWPLHOSDOP 334
DB 560 LSGVLEKQNEVNGATDVCPSSEKLAVTDDTSDLPSTHSTVLSSTV-----PLGHS--ET 612
QY 335 HSGGCGRANGFYVDTTGKCKALSDQVPCVSDAANSYTAAGSLSE--ETPNPFIIP- 391
DB 613 HNSAVETN--TRRNSTGKKKKIKKILQKADAGTSDLYMYKKPPEEKSSNVVHDV 669
QY 392 SNPSVPTPETALQCTADKFP-----DSFGACDVQACKRQKTSQVGGIOSTSYDCTA 445
DB 670 SKONLLPAIPQ-AVEAIVDTPEPKNEBEDMEDADADVSTPLCTETRA-----DNSVNAKR 720
QY 446 DEQNEGCSN-----TALTAGLAV-----GGVLLALLGGCCYPAKR 481
DB 721 GSSDEVDNINCINTEKKYSRDLFLKFDALCTALPEGPDVSPDIALNAILVYMG----- 772
QY 482 LDRNKGVQAAHHHEHQ-----SDR---GAR--KKRPSDL 511
DB 773 -----ASHHEHDSYPTPGKVMRQASGARLDRRPSNV 804

RESULT 31

S44054

genome polyprotein - Marburg virus (strain Popp)

N:Alternate names: structural protein L

N:Contains: RNA-directed RNA polymerase (EC 2.7.7.48)

C:Species: Marburg virus.

A:Variate: strain Popp

C>Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 18-Jun-1999

C:Accession: S44054; S32776

R:Bukreyev, A.A.; Volchok, V.E.; Blinov, V.M.; Dryga, S.A.; Netesov, S.V.

submitted to the EMBL Data Library/January 1994

A:Description: Full-length nucleotide sequence of Marburg virus Popp strain: The compari

A:Reference number: S44049

A:Accession: S44054

A:Molecule type: genomic RNA

A:Residues: 1-2331 <BUK>

A:Cross-references: EMBL:Z29337; NID:g450908; PIDN:CAA82542.1; PID:g450915

A:Experimental source: strain Popp

R:Bukreyev, A.A.; Netesov, S.V.

submitted to the EMBL Data Library/September 1992

A:Description: The partial nucleotide sequence of Marburg virus genome.

A:Reference number: S32775

A:Accession: S32776

A:Molecule type: genomic RNA

A:Residues: 1-2331 <BUW>

A:Cross-references: EMBL:X68494; NID:g296962; PIDN:CAA48508.1; PID:g296963

A:Experimental source: strain Popp

C:Genetics:

A:Gene: L

C:Superfamily: parafluenza virus RNA-directed RNA polymerase

C:Keywords: ATP; nucleotidyltransferase

Query Match 3.4%; Score 99; DB 2; Length 2331;

Best Local Similarity 22.8%; Pred. No. 83;

Matches 68; Conservative 31; Mismatches 101; Indels 98; Gaps 14;

QY 4 VGVQVLVAVDCTIFASGLSSTRSRESQTLASTSG-----NPRQANTEM- 50
DB 176 IGTDLFGLDIADFIIFK--VPVKTIIRNAVSLQASKPGLRWYRQDNTPLYCDDEFTVS 233
QY 51 -----KTFMERFNL-----THHQSGIYVDLQODKEVDGTLVREPAGLCPI 91
DB 234 VASVYECFTIMKQVFERNTWETICARAWLEDSDGADYPL--DVLEBLYNQ----- 282
QY 92 WCKHIELOQDRLPYRNFLDEVPTKEKXQSGNPLPGGFNL-----NFW 136
DB 283 -GDQIIAM-----YLED-----GFLDKILBLEPLCVSCIQTHGF 315
QY 137 TP-----SGORISFPFMELLEKNKNIKASTDLGCAEFAFKTVAMDKNKAATKRYPPVY 191
DB 316 TGGKXWFGSQRIEYSYBELCSLNMKFKISGNKACQNFIKITII--OGKLTPOQYCELF 372
QY 192 DSKKRLCH-ILVSNQMLEGKKYC-SVKGSEPPDLTYCYCKPRK-SVTENHHLYGSA 246
DB 373 SLQKMGHPVLVYIDALDKVKKQASVXILKPKVMFETFCVFKFIVAKNHHSGSWSY 430

RESULT 32

E65203

probable dehydrogenase (EC 1.8.1.-) udha - Escherichia coli (strain K-12)

C:Species: Escherichia coli

C>Date: 12-Sep-1997 #sequence_revision 17-Sep-1997 #text_change 01-Mar-2002

C:Accession: E65203; S21563

R:Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Perna, N.T.; Burland, V.; Riley, M.; Co

A.; Rose, D.J.; Mau, B.; Shao, Y.

Science 277, 1453-1462, 1997

A:Title: The complete genome sequence of Escherichia coli K-12.

A:Reference number: A64720; MUID:97426617; PMID:9278503

A:Accession: E65203

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-444 <BLAT>

A:Cross-references: GB:AE000470; GB:U00096; NID:g2367332; PIDN:AACT6944.1; PID:g1790400;

A:Experimental source: strain K-12, substrain MG1655

R:Gustafsson, C.
 Submitted to the ENBL Data Library, May 1992
 A:Reference number: S21563
 A:Accession: S21563
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-41, 'L', '43-95, 'L', '97-324 <GUS>
 A:Cross-references: EMBL:X66026; NID:943236; PIDN:CAA46822.1; PID:943237
 C:Genetics:
 A:Gene: udhA
 C:Superfamily: dihydrolipoamide dehydrogenase; dihydrolipoamide dehydrogenase homology
 C:Keywords: oxidoreductase

Query Match 3.4%; Score 98; DB 2; Length 444;
 Best Local Similarity 20.3%; Pred. No. 9.3;
 Matches 87; Conservative 53; Mismatches 137; Indels 152; Gaps 21;

```

OY 150 LLEKSNIKASTDLGRCAFAFKTV---AMDKNKATKRRPFYVDSKKRLCHIL----- 201
DB 41 IIEFNQNP-PLVSDHRLRSLSPADILNHADNVINQOTMRQGFY---SRNHCEILQGNAR 96
OY 202 YV-----SMOLMEKKYCSVKGEPP-----DLTWYCFKPKRSVTENHH----- 239
DB 97 FVDHTTLALDCPDGSEVETLAEKFIACGSRPHPTDVFTHPRIYDSDSLMSHEPRH 156
OY 240 -LIYSAAYG-----ENPDAFISKCPNQLRGYRFGWKKGRCLD 278
DB 157 VLIYAGVIGCEYASIFRGMVQKVDLIMTRDLALFLQEMSDSL-SYHF--MNSGVVIR 213
OY 279 YTE-----LDTYIERVES---KAQCWV-----KTFENDGVASDQPHYPL 316
DB 214 HNEEYKEIEGCDGDIYIMHKKSGKLLKADCLLYANGRTGNTSLAQNLLETDSRGLKV 273
OY 317 TSQASWMDWMPLHOSDOPHSGVGGRNNGFYVDYTG--EGKCALSDQVPDCLVSDSAVS 374
DB 274 NS-----MYQAOHPHYAVAGDVIIGPISLASAAYQGR-----IAQALVK 313
OY 375 YTAAGSLSEETPN--FIIPSNPSVTPPTETALQCTADKFPDSFGACDVQACROKTSKV 432
DB 314 GEATNHLLEDIPGTGYITPEISSV--GKTEQQLTANKVPEVGRAPFKHLAR----- 363
OY 433 GGQIOSTVDTCTADEQNEGSGNTALLIAGLVGVL-----ALLGGCCYFAKRLDRNK 486
DB 364 -----AQIVGMNVGTLKILFRERKEILGIHCF----- 391
OY 487 GVQAAHHEH 495
DB 392 GERAAEITH 400

```

RESULT 33

Internalin like protein (LPTKG) [imported] - *Listeria innocua* (strain C1p11262)

C:Species: *Listeria innocua*
 C:Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 27-Nov-2001

C:Accession: AC1525
 R:Glasner, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berche, P.; Bloeker, D.; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian, K.D.; Fsihi, H.

Science 294, 849-852, 2001

A:Authors: Krell, J.; Kuhn, M.; Kuntz, F.; Kurapat, G.; Madueno, E.; Maitournam, A.; Maok, C.; Schlueter, T.; Simoes, N.; Tietzer, A.; Vazquez-Boland, J.A.; Voss, H.; Wehlund, A.; Title: Comparative genome of *Listeria species*.

A:Reference number: AB1077; MUID:21537279; PMID:11679669

A:Accession: AC1525

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-521 <GLA>

A:Cross-references: GB:AL592022; PIDN:CA95971.1; PID:916413191; GSPDB:GN00178

C:Genetics:

A:Experimental source: strain C1p11262

Query Match 3.4%; Score 98; DB 2; Length 521;
 Best Local Similarity 19.7%; Pred. No. 12;
 Matches 78; Conservative 57; Mismatches 133; Indels 128; Gaps 21;

```

OY 67 IYVDGDKKENDGTLREPAALCTPWGHITLQOBDRLPYRNNFLEDV--PFEKEKQSGN 125
DB 196 VYIYLAADKIKD-----ISPLAKSKFO-----QLTLNNEISIDISPKMTLYSED 241
OY 126 PLPGGFNLNFTPSGQRISSPFMELLENKSNIKASTDLGRCAFAFKTVAMDKN--NKAT 183
DB 242 PLADDF---YIDISNNHISDI-----SSLK-NADGKLDYF---FAEDQSIVNPK 285
OY 184 KYRYPFVYDSK-KRLCHILYVSMQMEKKYCSVKGEPPDLTW-----YCFKPRK 232
DB 286 AFSTNFTLENKVNQINGLTVPKNISNGSYSNM-----ILSMQPSFVAMLDYGFSE-- 338
OY 233 SVTENHLLIYGSAYGEPDPAFISCPNQLRGYRFGWKKGRCLDYLDTYIERVES 292
DB 339 -----TTQIGRSTGEFSGKVTQSLVGY-----TV----- 363
OY 293 KAQCWVTFENDGV-----ASDQPHYPLTSQASWMDWMPLHOSDOPHSGVGGRNNGFY 346
DB 364 -----TFDNEGTLSTRTTFASDELVTEPA-----KSKTGFTFT--GWY 399
OY 347 YVDTTGEKCALSDQVPDCLVSDSAVSYTAAGSLSEETPNFIIPSNPSVTPPTETALQ 406
DB 400 DAKTGKKMNPATDKMP-----ANNMTLYAQYEBGTTTPVPDASP-VAPTKPTDPVK 450
OY 407 CTADKFPDSFGACDVQACROKTSVGGQIOSTSYD 442
DB 451 --PDEIVSSSESGDME-IKGQSGTIAASENATSID 483

```

RESULT 34

B95031
 alkaline amylopullulanase, probable [imported] - *Streptococcus pneumoniae* (strain TIGR4)

C:Species: *Streptococcus pneumoniae*
 C:Date: 03-Aug-2001 #sequence_revision 03-Aug-2001 #text_change 03-Aug-2001

C:Accession: B95031
 R:Rettelin, H.; Nelson, K.E.; Paulsen, I.T.; Eisen, J.A.; Read, T.D.; Peterson, S.; Heidon, J.D.; Unayam, L.A.; White, O.; Salzberg, S.L.; Lewis, M.R.; Radune, D.; Holtzapfel, nson, T.; Hickey, E.K.; Holt, I.E.

Science 293, 498-506, 2001

A:Authors: Loftus, B.J.; Yang, F.; Smith, H.O.; Venter, J.C.; Dougherty, B.A.; Morrison, A.; Title: Complete Genome Sequence of a virulent isolate of *Streptococcus pneumoniae*.

A:Reference number: A95000; MUID:21357209; PMID:11463916

A:Accession: B95031

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1280 <KUR>

A:Cross-references: GB:AE005672; PIDN:AAK74446.1; PID:914971739; GSPDB:GN00164; TIGR:SP4

A:Experimental source: strain TIGR4

C:Genetics:

A:Gene: SP0268

Query Match 3.3%; Score 97.5; DB 2; Length 1280;
 Best Local Similarity 18.3%; Pred. No. 46;
 Matches 90; Conservative 68; Mismatches 146; Indels 189; Gaps 24;

```

OY 28 RSRESQTLASSTGSPFOANVEMKTFMERFNLTHRHQSGIYVDLGQDKVDTLYREBAG 87
DB 923 RLRLGINLMLVLAQSTPF-----IHSGQ-----EYGRTKQ-----FRDPAY 957
OY 88 LCPFWGKHIEIQDRLPYRNNFLEDVPTKEVYQSGNPPLBGGNMLNFTVTSQGRISFP 147
DB 958 KTPV-----ABDKVPNKKHLRD-----KDGPFDPYPYFIHDSYSSDAVNF 1001
OY 148 MLEKSNIKASTDLGRCAFAFKTVAMDKNKATKRYRPFVDSKKRLCHILYVSMQL 207
DB 1002 W---TKATDGAAYENNVKSRPYMKGLIALRSTDA--FRKSLDIDIDRV-HLTV----- 1051
OY 208 MEKKYCSVKGEPPDLTWYCFKPKRSVTENHLLIYGSAYGENDPAF-ISKCPNQLRGY 266

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Db 71 ---SKSDTDTQRTIPCKGNTDKIHVLNIYFDLNNLKGMWETSNTDINDYGGKIIKV 127
Oy 144 SPPFELLEKKSNIIKAST-----DGRCAEFAF 171
Db 128 DEIPSTNSNPENIKDSNGENYDVMLOSWSNNSSEGLNATSEAVESPIKSGKVLFGH 187
Oy 172 KTVAMDKNNKATKYRYPFVYDSKKRLCHILYVSMQMEGKCYCYKGEPPDLT----- 224
Db 188 DSINQYNSLNDLVANVAKFPSPDAK-----LYTGAIVGGRITLSPGSTTSLITTKTGL 241
Oy 225 ---WYCKRPK-STENHHLIYGSAVYGENDAFISKCPNOLAGYFGWKKRCCLDY 279
Db 242 VNFPRKIGNNLSVPYTHNSOISYGD-----IWRFTHKSY 276
Oy 280 TELDTVIERVESKAQCWVKPENDINGV-----ASDQP-----HYPLTQAS 321
Db 277 T--ADDMT-----NPNFYLSTNNNGVLTQTHSGOATSDKGLANTLFLYLAQVTDQTS 330
Oy 322 WNDWVPLHQS---DQP-----HSGGVGRNYGF-----YVDTTGB----- 353
Db 331 WDD-----HKGDVDAPSKRPVINSYNDTFKQGISLNTSGSTGYDYVEATGKNDGTX 386
Oy 354 -----GKCALSDQVDPCLVSD---SAVSYT-----AA 378
Db 387 VDSDTKCTVTYTGIAVGIWVDQNSDTIPSNITTTSTNYTLNLSYKNDFYVHIAIDKA 446
Oy 379 GSLSEETNFIIPSNPSTPTPTPEFALQCTADKFPDSGACDVQCKOKTSCVGGQIOS 438
Db 447 GNISVTHQKQSVNDAT-----NIALNKTDTNL--TVGANDTLTATITPDAVDKNVTW 498
Oy 439 TSVDTCTADEQNECGSNTALLAG 460
Db 499 TSSDPSIATVDASGITAVKPG 520

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RESULT 38
A40228
neurexin I-alpha precursor - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 21-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 09-Dec-2002
C:Accession: A40228; S27884
R:Uenikayov, Y.A.; Petrenko, A.G.; Geppert, M.; Suedhof, T.C.
Science 257, 50-56, 1992
A:Title: Neurexins: synaptic cell surface proteins related to the alpha-latrotoxin recep
A:Reference number: A40228; MUID:92320296; PMID:1621094
A:Accession: A40228
A:Status: preliminary; nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-1507 <USH>
A:Cross-references: GB:M6374; NID:9205710; PIDN:AA41704.1; PID:9205711
C:Superfamily: neurexin; EGF homology
C:Keywords: alternative splicing; transmembrane protein
F:1-30/Domain: signal sequence #status predicted <SIG>
F:31-1507/Product: neurexin I-alpha #status predicted <MAT>
F:680-712/Domain: EGF homology <EGF>
F:1087-1119/Domain: EGF homology <EGF1>

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Query Match 3.3%; Score 97; DB 2; Length 1507;
Best Local Similarity 22.3%; Pred. No. 64;
Matches 52; Conservative 38; Mismatches 103; Indels 40; Gaps 11;
Oy 330 QSDPHSGVGRNNGFY-----VDTTGE-----GKCALSDQVDPCLVSDSAVSYT 376
Db 1288 EGGDFPGQOLS---GLYNGKLKVLMAAENDANLAIYGNVRIVGVPSSMTTESTATAMQ 1344
Oy 377 A--AGSLSEETPNFIIPSNPSTPTPTPEFALQCTADKFPDSFGAC-----DVQCKROKT 429
Db 1345 SEMSTSIWETTTTLATSTARBGKPTKPEISGTTDDILVAS--ABCPDDEDIDPEPSS-- 1402
Oy 430 SCVGGQIOISTVY-----DCTADEQNECGSNTALLAGLVGVLALLGGCCFPAKLD 483
Db 1403 ---GGLANPRTVGRGEPYPSAEVIRESSSTTGWVGIVAAALCILILLAMY--KYRN 1457

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```

Oy 484 ENKGVQAAHHEFEQSDRGARKRPPDLMQAEPSFMDEAENIE-ODGETHV 535
Db 1458 RDEG---SYHDESRNYSNSAQSGNAVVEKQFSSAKSANKKNKDKXEYV 1507

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RESULT 39
B86414
hypochemical protein P28N24.14 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Dec-2001
C:Accession: B86414
R:Theologis, A.; Becker, J.R.; Palm, C.J.; Federpiel, N.A.; Kaul, S.; White, O.; Alonso,
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewart, K.;
ansen, N.F.; Hughes, B.; Hutzar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Lueros, J.S.; Maiti, R.; Matzfall,
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: B86414
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1020 <STO>
A:Cross-references: GB:A8005172; NID:9502422; PIDN:AA88121.1; GSPDB:GN00141
C:Genetics:
A:Map position: 1

```

```

Query Match 3.3%; Score 96; DB 2; Length 1020;
Best Local Similarity 20.8%; Pred. No. 44;
Matches 78; Conservative 45; Mismatches 130; Indels 122; Gaps 19;

```

```

Oy 223 LTWYCFRKRKSVTENHHLIYGSAVYGENPDAFISKCPNOLRG-----YRFGWKKGR 275
Db 102 LEWH---PRIPITON-HLIYDDL-----PHIMDPYECRCGPRLHLTDKFDINGPS 150
Oy 276 CLD-YTELDTVIERVES-----KAQCWVTFENDVQVASDQPHYPLTSQMSW 322
Db 151 CLKRYSD--PYFPRASSNLSQGNKKFKQDKKCKMKKKKSSSRDMSRLASLANQVAR 208
Oy 323 NDWVPLHQSDDPHS-----GCVGRNNGFY-----YVDTTGEKCALSDQVDPCLVSDS 370
Db 209 KTPASPSGSGTSTKTSTSDMKRYDFQHNHRSFBSRGSG-----YNECL---S 258
Oy 371 AAVSYTAAGSLSEETPNFIIPSNPSTPTPTPEFETA---LQCTADKFPDSFGACDVQCKRO 427
Db 259 TATSLSKTG---BRPKGVFVSS--SLTPGSCITIASVSECETEDAHDFGSPGCGQAR 313
Oy 428 KTSCY-----GGQIOISTVDCTADEQNECGSNTALLAGLVGVL 468
Db 314 GSSCVSDEKAEIVESLGLQTBASENVANSVVDTTDEKSYDEG----- 359
Oy 469 LALLGGCGYFAPKRLDRNKGVAHHEHFEQSDRGARKRPPDLMQ-----ABPSFW 520
Db 360 ---IGVDVFSKXNDENK-----SESLRKRAIGIDEVREIKNGEIVGEPR-- 402
Oy 521 DEABENIEODGETHV 535
Db 403 -DSEGETESBECEFCV 416

```

```

RESULT 40
G97902
alpha-amylase (EC 3.2.1.1) [imported] - Streptococcus pneumoniae (strain R6)
C:Species: Streptococcus pneumoniae
C>Date: 22-Oct-2001 #sequence_revision 22-Oct-2001 #text_change 02-Nov-2001
C:Accession: G97902
R:Hoskins, J.A.; Albom Jr., W.; Arnold, J.; Blaszcak, L.; Burgett, S.; Dehoff, B.S.; E
e, R.; LeBlanc, D.J.; Lee, L.N.; Lefkowitz, E.J.; Lu, J.; Matsushima, P.; McAhren, S.; M
y, P.; Sun, P.M.; Winkler, M.E.

```

J. Bacteriol. 183, 5709-5717, 2001
 A: Authors: Yang, Y.; Young-Bellido, M.; Zhao, G.; Zook, C.; Baltz, R.H.; Jaekunas, S.R.;
 A: Title: Genome of the Bacterium Streptococcus pneumoniae Strain R6.
 A: Reference number: A97872; MUID: 21429245; PMID: 11544234
 A: Accession: G97902
 A: Status: preliminary
 A: Molecule type: DNA
 A: Residues: 1-1256 <KUR>
 A: Cross-References: GB:AE007317, PIND:AAK99051.1, PID:915457796; GSPDB:GN00174
 C: Genetics:
 A: Gene: Pula
 C: Keywords: glycosidase; hydrolase

Query Match 3.3%; Score 96; DB 2; Length 1256;
 Best Local Similarity 18.5%; Pred. No. 59;
 Matches 91; Conservative 64; Mismatches 140; Indels 198; Gaps 24;

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QY 28 RRSRQTLSTASTGNPFQANVEKTEMERFNLTHHSGIYVDLGQDKEVDGTLVREPAG 87
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 908 RLRLGNLMLVLTAGTFP-----IHSQ-----EYGRTKQ-----FRDPAY 942
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 88 LCPIMGKHLELOQPPRLPYRNPFLEDPTEKEYKSGNPLPGGFNLNFTVPSGORISPP 147
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 943 KTPV-----AEDKVPNKSRLRD-----KDNPFDPYFYFHDSDSSDAVNKPD 986
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 148 MELLEKNSTIKASTDGRCAEFKTVANDKNNKATKRYRYPFYDSEKRLCHILVYSMQL 207
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 987 W---TATGDKAYPENVKSRDYWKGLIALRQSTDA--FRLKSLQDIXDRV-HLTV---- 1036
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 208 MEGKKYCSYKGEPPDLTWYCFPRKSVTENHHLIYSAVGENPDAF-ISKCPNQLRGY 266
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1037 -----PGQNGVEKEDVIGVQITAPRGDIYAVFVNADEKAREF 1074
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 267 REGW-----KKGRCLDYTE-----LTDVIERVESKAQC 296
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1075 NLGTAFAHLRNAEVLADENQAGSVGIANPKG--LEWTEKGLKLNALTATVL-RVSQNGT- 1130
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 297 WYKTFENDGVASDQPTTYPLTSGASWMDWPLHOSDQPHSGVGRNYGFYVDTTGEKC 356
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1131 -----SHESTAEKPPDTPSK-----PEHQDPAPFA-----RPDST----- 1161
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 357 ALSDVPPCLVSDSAVSYTAAGLSSETPNFIIIPNSVTPPTPETALQCTADKFPDSF 416
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1162 -----KPDAKVAD-----AENKPS-----QATDSQAF--- 1184
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 417 GACDVQACKRKQKTSVCGQIQSTSV-----CTADEQNEC-----GSNTALIAGLA 462
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1185 -----QPAQBAQASVKEAVQNESVENSCKNIPATPDRQAELPNTGIRKMENTLFAGIS 1239
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY 463 VGGVLLALLGCG 475
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1240 -----LLALLGLG 1247
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

Search completed: October 2, 2003, 15:52:26
 Job time : 49 secs

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OM protein - protein search, using SW model

Run on: October 2, 2003, 15:39:29 / Search time 25 seconds

(without alignments)
1017.658 Million cell updates/sec

Title: US-10-039-770a-1

Perfect score: 2922
Sequence: 1 MGLGVGVLLVADCTIFA.....EAEENIRDSGETHWVEGDY 541

Scoring table: BLOSUM62
Gapop 10.0, Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database: SwissProt_41.4

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	447	15.3	562	1	AMAI_PLAFR
2	431	14.8	622	1	AMAI_PLAFR
3	431	14.8	622	1	AMAI_PLAFR
4	423.5	14.5	563	1	PK66_PLAFU
5	412	14.1	622	1	AMAI_PLAFR
6	412	14.1	622	1	AMAI_PLAFR
7	410	14.0	622	1	AMAI_PLAFR
8	398.5	13.6	558	1	AMAI_PLAFR
9	127	4.3	2459	1	MAPB_MOUSE
10	120	4.1	2464	1	MAPB_MOUSE
11	118	4.0	2468	1	MAPB_MOUSE
12	117	4.0	697	1	SM2A_SCHGR
13	113	3.9	765	1	DRP4_FELCA
14	111.5	3.8	1592	1	SORL_CHICK
15	107.5	3.7	376	1	CATW_HUMAN
16	107.5	3.7	1104	1	NFX1_HUMAN
17	106	3.6	415	1	LMP2_MOUSE
18	104	3.6	1207	1	RPOC_STRP3
19	104	3.6	1213	1	RPOC_STRP3
20	104	3.6	1255	1	ERB2_HUMAN
21	102	3.5	2871	1	FN1_HUMAN
22	101.5	3.5	1213	1	CYF_WHEAT
23	100	3.4	1213	1	RPOC_STRP8
24	99	3.4	2331	1	RRPL_MABVP
25	98.5	3.4	572	1	SVR_PYRPU
26	98.5	3.4	732	1	ACPH_PIG
27	98	3.4	465	1	STHA_ECOLI
28	98	3.4	2842	1	APC_RAT
29	97.5	3.3	2871	1	FN1_MOUSE
30	97	3.3	468	1	FN1_MOUSE
31	97	3.3	484	1	LEW2_PIG
32	97	3.3	529	1	FN1_MOUSE
33	97	3.3	906	1	AD22_HUMAN

34	97	3.3	1514	1	NX1A_RAT	063372	rattus norv
35	95.5	3.3	320	1	CYF_ATRBE	0888w4	actropa bel1
36	95.5	3.3	320	1	CYF_ORYZA	P07888	oryza sativ
37	95.5	3.3	583	1	C166_MOUSE	061490	mus muscicu
38	95	3.3	357	1	MYCM_HUMAN	P12525	homo sapien
39	95	3.3	2845	1	APC_MOUSE	061315	mus muscicu
40	94.5	3.2	320	1	CYF_SPIOL	P16013	spiniacia ol
41	94.5	3.2	41	1	CYF_TOBAC	P06449	nicotiana t
42	94.5	3.2	468	1	T10A_HUMAN	O00220	homo sapien
43	94.5	3.2	705	1	SM2A_DROME	024323	drosophila
44	94	3.2	982	1	ENV_VITLV	P03379	viena lenti
45	94	3.2	989	1	ENV_VITLV1	P23422	viena lenti

ALIGNMENTS

RESULT 1	AMAI_PLAFR	STANDARD	PRT	562 AA.
AC	P22622:			
DT	01-AUG-1991 (Rel. 19, Created)			
DT	01-AUG-1991 (Rel. 19, Last sequence update)			
DT	16-OCT-2001 (Rel. 40, Last annotation update)			
DE	Apical membrane antigen 1 precursor (Merozoite surface antigen).			
GN	AMA-1, OR AG352.			
OS	Plasmodium fragile.			
OC	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.			
OX	NCBI_TaxId=5857;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=90205978; PubMed=2181309;			
RA	Peterson M.G., Nguyen-Dinh P., Marshall V.M., Elliott J.F.,			
RA	Collins W.E., Anders R.F., Kemp D.J.;			
RT	"Apical membrane antigen of Plasmodium fragile.";			
RL	Mol. Biochem. Parasitol. 39:279-284(1990).			
CC	-1- FUNCTION: INVOLVED IN PARASITE INVASION OF ERYTHROCYTES.			
CC	-1- SUBCELLULAR LOCATION: Type I membrane protein.			
CC	-1- SIMILARITY: STRONG TO AMA-1 FROM P.CHABAUDI AND P.FALCIPARUM, AND			
CC	TO PK66 FROM P.KNOXLEST.			
CC	-----			
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration			
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CC	or send an email to license@isb-sib.ch).			
CC	-----			
DR	EMBL; M29898; AAA29474.1; -;			
DR	PIR; A44944;			
DR	InterPro; IPR003298; Apmem_Agl.			
DR	Pfam; PF02430; AMA-1; 1.			
DR	PRINTS; PRO1361; MEROZOITESA.			
KW	Malaria; Signal; Transmembrane; Antigen; Glycoprotein.			
FT	SIGNAL	1	21	POTENTIAL.
FT	CHAIN	22	562	APICAL MEMBRANE ANTIGEN 1.
FT	DOMAIN	22	484	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	485	507	POTENTIAL.
FT	DOMAIN	508	562	CYTOPLASMIC (POTENTIAL).
FT	CARBOHYD	84	84	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	176	176	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	226	226	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	405	405	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	441	441	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	441	441	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	SEQUENCE	562 AA;	64488 MW;	98AB72D437EA7164 CRC64;
Qy	Query Match	15.3%;	Score 447;	DB 1; Length 562;
	Best Local Similarity	25.9%;	Pred. No. 1.1e-26;	
	Matches 159;	Conservative 91;	Mismatches 231;	Indels 132; Gaps 26;
	6 VQVLVAVADCTIF-----ASGLSSSTRS-----RESQTLASSTSGNPFQANVEMKT 52			

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DB 4 IYCLIFLSAQCLVHMGKCEPNOKPSRLTRSAKNVLLQEOPWVERSTRMSNPW-----KA 57
QY 53 FMERNLTHHOSGIYVDLGODKEVDGTLTYREPAGLCPTMGHIELQOPDRLPYNNFLE 112
DB 58 FMEKDYDKRTSSSGIRVLDGEDAEVGNSSYRIAPACKCPVFGGIYI0NSE-----VSFLT 112
QY 113 DVPT-EKEKQSGNPLPGGFNLNFTVPSGORISPPPM-----ELKSNISIKASTDLGSCA 167
DB 113 PVATNGKLIKDGCGAFPP-----QANDHISPSIKRLRREYENEDMLKNDLALCK 163
QY 168 EFAFTV-AMDKNKKATKYRPPYVYDSKRLCHILYVSMQMEGKKYCSVKGEPPDLTWY 226
DB 164 THAASFVEMEDKN-----SSYRHPAVYDDEDKICMYLTLSPQEWMPGRYCSKDAENKD-AMF 219
QY 227 CFPKPKSTENHLLYGSAYVGEN-PDAFISKCPNOLRGYFGYWKGRCLDYELDT 285
DB 220 CFPKPKNETFPD-----LAYSKNVNDQNKCPKKNLGNSSFGMLVGNCEIPIYVDV 274
QY 286 VIERVESKACQWVTFENDGVASDOPHTYPLTSQASWMDWMPDLHOSDQPHSGV----- 339
DB 275 ---QAKDLRECNRIYFE-ASASDQPTQY-----EELTDYQKIQSGFRNDGMIKSAFL 325
QY 340 -----GNNYGFYVDTTGECK-CALSDQVPCIVSDAASVYTAAG---SLG 382
DB 326 PVGAFNSDNFKSGKGYWNAFDT--ENKVCYLFNAKPTCLINDKNFIATLALSHQEVYD 383
QY 383 EETPFPIIPSN-----PSYTPPFPETALLOCTAKKFPDSRGA 418
DB 384 NEFPISYDEMERERKESRMSLYNDKARIVLPRIFISNDKOSLKCPCAPEHITNST 443
QY 419 CDVQACKROKTSV-GGQIOSTSVDTADE-----QNECGSNTALIALAGVGL 468
DB 444 CNFYVC-----NCEKRAEIKENNEVALEKPKQDYQVAGSSKQMLIIIGITGCV 498
QY 469 IALLGGCGYFAKRLDRNKGVAHHEHEFQSDRGARKRPSDLMOEAEPSEFWEAEENIE 528
DB 499 VA-LASMFYFRKKAHNDK-----YDKMGADQYGGKPTRKDEMLDPEASFWGEER--R 548
QY 529 QDGETHWVWEGDY 541
DB 549 ASHTTPVLMKEY 561

RESULT 2
AAA1_PLA1F STANDARD; PRT; 622 AA.
ID AAA1_PLA1F
AC P22621;
DT 01-AUG-1991 (Rel. 19, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Apical membrane antigen 1 precursor (Mercozote surface antigen).
GN AMA-1 OR P783.
OS Plasmodium falciparum (isolate FC27 / Papua New Guinea).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5837;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=89384584; PubMed=2701947;
RA Peterson M.G., Marshall V.M., Smythe J.A., Crewther P.E., Lew A.,
RA Silva A., Anders R.F., Kemp D.J.;
RT "Integral membrane protein located in the apical complex of
RT Plasmodium falciparum."
RL Mol. Cell. Biol. 9:3151-3154(1989).
CC -1- FUNCTION: INVOLVED IN PARASITE INVASION OF ERYTHROCYTES.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: STRONG TO AMA-1 FROM P.CHABAUDI AND P.FRAGILE, AND TO
CC PK66 FROM P.KOMLESI.
CC -----
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CC -----
DB 53 EMBL; M27133; AAA29475.1; -
DB 58 EMBL; M27957; AAA29476.1; -
DB PIR; A08267; CAA00764.1; -
DB PIR; A32499; A32499.
DB InterPro; IPR003298; Apmem_Ag1.
DB Pfam; PF02430; AMA-1; 1.
DR PRINTS; PR01361; MEROZOITESA.
KW Malaria; Signal; Transmembrane; Antigen; Glycoprotein.
FT SIGNAL 1 24
FT CHAIN 1 25
FT DOMAIN 25 546
FT TRANSMEM 547 567
FT DOMAIN 568 622
FT CARBOHYD 162 162
FT CARBOHYD 286 286
FT CARBOHYD 371 371
FT CARBOHYD 421 421
FT CARBOHYD 422 422
FT CARBOHYD 499 499
FT CARBOHYD 308 308
FT CONFLICT 332 332
FT CONFLICT 407 407
FT CONFLICT 439 439
FT CONFLICT 496 496
FT CONFLICT 503 503
SQ SEQUENCE 622 AA; 72009 MW; 7D41335E249F9A1BF CRC64;

Query Match 14.8%; Score 431; DB 1; Length 622;
Best Local Similarity 26.2%; Pred. No. 2.2e-25;
Matches 149; Conservative 86; Mismatches 212; Indels 122; Gaps 24;

QY 41 GNPQANVEMKTFMERENLTHHOSGIYVDLGODKEVDGTLTYREPAGLCPTMGHIELQ 100
DB 107 GNFW-----TEYMAKYDIEVHSGIRVLDGEDAEVAGTQYRPSGCGVFGGIILEN 160
QY 101 PDRLPYNNFLQEDVTEKEYKQSGNPLPGGFNLNFTVPSGORISPPME-----LLEKSN 156
DB 161 SN-----TTFPLPATNGQYIKD-----GGAPF--PTEPLMSBMTLDERKHFKNKY 207
QY 157 IKASTDLGRCAEFKTYAMDKNKKATKYRPPYVYDSKRLCHILYVSMQMEGKKYCSV 216
DB 208 VKNDELTLGSRHAGNM--PDNDKSNVKKPAYVDDKDKCHILYIAAGNNGRKYCN- 264
QY 217 KGEPPDLTWYCPKPKSTENHLLYGSAYVGEN-PDAFISKCPNOLRGYFGYWKGR 275
DB 265 KDESRENMFQFRPAKDISFQNY-----TYLSKNVVDWMEKVCPRKNLQNAKFFGLMVDGN 319
QY 276 CLDYTELTD-TYIERVESKACQWVTFENDGVASDOPHTYP--LTSQASWMDWMP----- 327
DB 320 CEDIHVNEFSKIDLFE-----CNKLVEFLS--ASDQPKQYCHLTDYKIEKGFGKNRAS 373
QY 328 -----LHOSDQPHSGVGRNYGFYVDTTGECKCALSDQVPCIVSDAASVYTA 377
DB 374 MIKSAFLPTGAFKDRYKSHGKGYWNAFDT--ENKVCYLFNAKPTCLINDKNFIATLALSH 430
QY 378 AGSLSEETPNFIIPSN-----PSYTPPFPETAL 405
DB 431 LSHPIEVEHNF--PCLYKNEIMKEIERESKRILKNDNDGNNKIAPRIFISDQKSL 488
QY 406 OCTADKFPDSRGACVQACKROKTSVCGVQIOSTSVDTA-----DRONEGSGN----- 454
DB 469 KCPDPEIVSSTCNFPYCK-----CVRRAEVTSSNNEVVYKKEKDEYADIPKPKPYD 543
QY 455 --TALIAGAVGVLLALLGGCGYFAKRLDRNKGVAHHEHEFQSDRGARKRPSDL 512
DB 544 KKKIILASAAVAVALITLM--VLYKR-----KMAKAYDMDEPQYKGSNSR-NDNM 595
QY 513 OEAPSEFWEAEENIEQDGETHWVWEGDY 541
DB 596 LDPEASFWGEER--ASHTTPVLMKEY 621

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RESULT 3
AMAL_PLAFLH STANDARD; PRT; 622 AA.
ID AMAL_PLAFLH STANDARD; PRT; 622 AA.
AC PS0491;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Apical membrane antigen 1 precursor (Merozoite surface antigen).
GN AMA-1 OR PF83.
OS Plasmodium falciparum (isolate thn / Thailand).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxId=70151;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91101665; PubMed=2270110;
RA Thomas A.W., Waters A.P., Carr D.;
RT "Analysis of variation in Pf83, an erythrocytic merozoite vaccine candidate antigen of Plasmodium falciparum."
RL Mol. Biochem. Parasitol. 42:285-287(1990).
CC CC - FUNCTION: INVOLVED IN PARASITE INVASION OF ERYTHROCYTES.
CC CC - SUBCELLULAR LOCATION: Type I membrane protein.
CC CC - SIMILARITY: STRONG TO AMA-1 FROM P.CHABAUDI AND P.FRAGILE, AND TO PK66 FROM P.KNOWLESI.
CC CC -----
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CC CC -----
DR EMBL; M58547; AAA29720.1; -.
DR InterPro; IPR003298; Apmem_Ag1.
DR Pfam; PF02430; AMA-1; 1.
DR PRINTS; PR01361; MERZOITPESA.
DR Malattia; Signal; Transmembrane; Antigen; Glycoprotein.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 622 APICAL MEMBRANE ANTIGEN 1.
FT DOMAIN 25 546 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 547 567 POTENTIAL.
FT DOMAIN 568 622 CYTOPLASMIC (POTENTIAL).
FT CARBOHYD 286 286 N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT CARBOHYD 371 371 N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT CARBOHYD 421 421 N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT CARBOHYD 422 422 N-LINKED (GLCNAC. . . ) (POTENTIAL).
FT CARBOHYD 499 499 N-LINKED (GLCNAC. . . ) (POTENTIAL).
SO SEQUENCE 622 AA; 71989 MW; 1DFPA53593C9AC5 CRC64;

Query Match 14.8%; Score 431; DB 1; Length 622;
Best Local Similarity 26.7%; Pred. No. 2,2e-25;
Matches 153; Conservative 81; Mismatches 209; Indels 130; Gaps 25;

OY 41 GNPFQANVEMKTFMERFNLTHNHSGIYVDGODEKVNGTLTYREBAGLCPIIMGKHIEIQ 100
DB 107 GNPF-----TEYMAKYDI EKHGSGIRYVDGEDEAVGTGYRLPSGCKPVFGKIIEN 160
OY 101 PDRLPYRNNPLEDEVTE-KEYYQSQNPLPGGFNLI NFVPSSGORISPPME----LLEIKNS 155
DB 161 S-----KTTPILPTVATENODLKDGFAFP-----PTBELISPMTLDDQRHLKYONE 206
OY 156 NIKASTDIGRCAEFAFKTVAMDKNKKARKTRPPFYDSKKKLCHLLYSVMQLMEKKYC 215
DB 207 YVKNDDELTLSCSRHAQG--NMPEDNKSNYKPAYVYDEDKCKHLLTYLAADENNRPVCN 264
OY 216 VKGBEPDLTWYCFEKRRK-SVTENHLLIYGSAVGEN-PDAFISKCPNALRGYRGVWK 273
DB 265 -KDESKRSMFCFRAXOKLPENT-----TLSKNVVDMNEVEVPRKMLEAKKGVLWD 317
OY 274 GRCLDYELTDLTVERVESKACQCVKTEINDGVASDQHPTP--LTSQAQMWDMWP----- 327

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Db 318 GNCDDIPRVNF-----SANDLECNKLVPELS--ASDQKQYQHQHLLTDYBKIKMGRKNKA 372
Oy 328 -----LHOSDPOHSGCVGRNGFYVDITTBESKCALSDOVPCDLSDAVST 376
Db 373 SMKSAFLPTAPAFADRYKSRGKGYNMGNVNTETQ---KCEIFNVKPTCLINNSSVIAT 429
Oy 377 AAGSLSEETPEFIIPSN-----PSTPTPTPEA 404
Db 430 ALSHPNEVNNP--PCSLYKDEIKKEIERESKRITKLDNDNDEGNKKIAPRIFISDDKOS 487
Oy 405 LQCTADKPEPDSFGACDVQACRKOKTS CVGQIIGST-----VDCTAD--EQNECG 452
Db 488 LKCPCDPEIVSNSTCNFPVCK-----CYEKABATSNNEVVYKEEYKQBYADIPHKPT 542
Oy 453 SNTALI-----AGLAVGVLLTALLAGGCGFYAKRLDRNKGQVAAHHEHESQSDRGARKRP 508
Db 543 DNMKIIIIASSAAVAVLITLV-----YLYKR-----KGNMEKYDKMBEPQYGGKSTR- 591
Oy 509 SDLMQEAEPSPFMDAEENIEDDGGTHVWVEDY 541
Db 592 NDEMLDPDPAEFWGBEK--RASHTPPLVMEKPY 621

RESULT 4
PK66_PLAKU
ID PK66_PLAKU STANDARD, PRT, 563 AA.
AC P21303;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 15-JUN-1999 (Rel. 38, Last annotation update)
DE Merozoite receptor PK66 precursor (66 kDa protective minor surface antigen).
DE PK66.
GN Plasmodium knowlesi (strain nur1).
OS Eukaryota; Alveolata; Apicomplexa; Haemosporidia; Plasmodium.
OX NCBI_Taxid=5852;
RN [1].
RP SEQUENCE FROM N.A.
RC STRAIN=Lane W1;
RX MEDLINE=91009268; PubMed=2211675;
RA Waters A.P., Thomas A.W., Deans J.A., Mitchell G.H., Hudson D.E., Miller L.H., McCutchan T.F., Cohen S.;
RA "A merozoite receptor protein from Plasmodium knowlesi is highly conserved and distributed throughout Plasmodium.";
RT J. Biol. Chem. 265:17974-17979 (1990).
RL [2].
RN RP
RP SEQUENCE FROM N.A.
RC STRAIN=NURI;
RX MEDLINE=91187058; PubMed=2011149;
RA Waters A.P., Thomas A.W., Mitchell G.H., McCutchan T.F.;
RT "Intra-genetic conservation and limited inter-strain variation in a protective minor surface antigen of Plasmodium knowlesi merozoites.";
RL Mol. Biochem. Parasitol. 44:141-144 (1991).
CC -1- FUNCTION: MEROZOITE RECEPTOR PK66 IS A SURFACE ANTIGEN INVOLVED IN PARASITIC INVASION OF ERYTHROCYTES.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN. CONCENTRATED AT THE APICAL END PRIOR TO RUPTURE, FOLLOWING WHICH IT CAN DISTRIBUTE ITSELF ENTIRELY ACROSS THE SURFACE OF THE FREE MEROZOITE. DURING INVASION PK66 IS EXCLUDED FROM THE ERYTHROCYTE AT, AND BEHIND, THE INVASION INTERFACE.
CC -1- MISCELLANEOUS: PK66 EXPRESSED IN MATURE SCHIZONTS IS RAPIDLY PROCESSED AS THE SCHIZON RUPTURES, YIELDING A 42/44 kDa DOUBLET ASSOCIATED WITH THE SURFACE MEROZOITE.
CC -1- SIMILARITY: STRONG TO AMA-1/Pf83 OF P.FALCIPARUM, P.CHABAUDI, AND P.FRAGILE.
CC -----
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CC EMBL: M58317; AAA63444.1; -
DR EMBL: M61057; AAA29728.1; -
DR InterPro: IPR003298; Apmem_Ag1.
DR Pfam: PF02430; AMA-1; 1.
DR PRINTS: PR01361; MEROZOITRESA.
KW Malaria; Signal; Transmembrane; Antigen; Glycoprotein.
FT SIGNAL 1 13
FT CHAIN 1 13
FT DOMAIN 14 563
FT TRANSMEM 14 487
FT DOMAIN 488 508
FT CARBOHYD 509 563
FT CARBOHYD 36 36
FT CARBOHYD 107 107
FT CARBOHYD 176 176
FT CARBOHYD 189 189
FT CARBOHYD 238 238
FT CARBOHYD 441 441
FT VARIANT 228 228
SQ SEQUENCE 563 AA; 64680 MM; 9EF0620264AA5CCF CRC64;
N -> K (IN STRAIN LINE W1).
Query Match 14.5%; Score 423.5; DB 1; Length 563;
Best Local Similarity 24.9%; Pred. No. 7, 2e-25;
Matches 150; Conservative 94; Mismatches 249; Indels 109; Gaps 25;
QY 6 VQVLVLVADCTIFASGL---SSSTRSRSQTLSTSGNPNPQANEM---KTWEREN 58
DB 4 IYIYFLSLQCLVHMGKCRNOKTITLTSANNASLEKPIIERSTRMSPMKAFMEKTD 63
QY 59 LTHHNSGIYVDLGDQKEVDGLTYRBPAGLCPIWGHIELOPDRLLPYENNFLEDPY-E 117
DB 64 LRAHNSGIRIDGDEAEVGSNRYRIPACKCPVFGGIYIENSN-----VSFLTPVATGA 118
QY 118 KEYKSGNPLPGGFNLNFTVPSGQRISSPPM---ELLEKSNITKASTLGRCAEAFKT 173
DB 119 QRLKEGFAFPN-----ADHISPIITIANLKERYEKNADIMLNDIALCKTAAAF 169
QY 174 VAMDKNKATKYRYPVDSKRLCHILYVSMOMEGKCYSCXKGBPLTWCFPRRS 233
DB 170 VIAEDQN--TSYRHPAVYDEKNTCYMLYSAOENMGPRICSPDSQNKD-AMFCFEPDKN 226
QY 234 VTEN--HHLIYGSAYVGENPDPAFISKCPNOLRGYRFGVWKKGRCLDYTELTDVIERVES 292
DB 227 --ENFNLVYLSGNVND---WENKCPKRLGNAGKGLWVDGCEI-----PYNVEVA 276
QY 293 KA--QCWVTFENDVASDQPHTY--PLTSQASMDWMPLHOSDQPHSG----- 337
DB 277 RSLRECNRIYFE--ASASDQPRQYEELTDYEKIOEGFRQNNNDMTKSAFLPYGAFNSDN 334
QY 338 --GVGNNGYFYVDTTGEGKCALSDQVPCIVSDSAVSTAG---SLSEETPNFIIS 392
DB 335 FSKSGGYWMAFDSV--NNKCYIFNFKPFTLINDKNFPATLASHPOEVNNEPFCSTIYD 393
QY 393 N-----PSVTPRPETALQCTADKRPDSFGACDVQACKROK 428
DB 394 EIERETIKKSRNNMLYSVDKERTVLRPISTDKESIKCSEBEHISNSTCNRYVC----- 449
QY 429 TSCV--GGQIQSTS-----VDTADRONECGSN--TALLAGLAVGVLLALIGGCYTA 479
DB 450 -NCVEKRAEIKENNEVILKEEFKEDYENPDGKHKMKLLIITVTAVCVVAASLFYR 508
QY 480 KRLDRKGYQAHAHNEHFEFSDRGARKKRPDLMOEAPRFDMAEENIEDGSETHVMVG 539
DB 509 KKAQDDK---YDKMDQAEAYGKTANTRKDEMLDRBASFWGDK--RASHTTPVLMEX 560
QY 540 DY 541
DB 561 PY 562
RESULT 5
ID AMA1_PLAF8 STANDARD; PRT; 622 AA.

AC P50492;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Apical membrane antigen 1 precursor (Merozoite surface antigen).
GN AMA-1 OR PF83.
OS Plasmodium falciparum (isolate 768).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
NCBI_Taxid=57266;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91101665; PubMed=2270110;
RA Thomas A.W., Waters A.P., Carr D.;
RT "Analysis of variation in PF83, an erythrocytic merozoite vaccine candidate antigen of Plasmodium falciparum."
RL Mol. Biochem. Parasitol. 42:285-287(1990).
CC -1- FUNCTION: INVOLVED IN PARASITE INVASION OF ERYTHROCYTES.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
CC -1- SIMILARITY: STRONG TO AMA-1 FROM P. CHABAUDI AND P. FRAGILE, AND TO PK66 FROM P. KNOWLESI.
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CC
CC EMBL: M58548; AAA29721.1; -
DR InterPro: IPR003298; Apmem_Ag1.
DR Pfam: PF02430; AMA-1; 1.
DR PRINTS: PR01361; MEROZOITRESA.
KW Malaria; Signal; Transmembrane; Antigen; Glycoprotein.
FT SIGNAL 1 24
FT CHAIN 25 622
FT DOMAIN 25 546
FT TRANSMEM 547 567
FT DOMAIN 568 622
FT CARBOHYD 162 162
FT CARBOHYD 286 286
FT CARBOHYD 371 371
FT CARBOHYD 421 421
FT CARBOHYD 422 422
FT CARBOHYD 499 499
SQ SEQUENCE 622 AA; 71990 MM; 1C9C8715DBE2915F CRC64;
Query Match 14.1%; Score 412; DB 1; Length 622;
Best Local Similarity 25.8%; Pred. No. 6, 3e-24;
Matches 147; Conservative 81; Mismatches 219; Indels 122; Gaps 23;
QY 41 GNPFOANVEMKTFMRFLNTHHNSGIYVDLGDQKEVDGLTYRBPAGLCPIWGHIELOQ 100
DB 107 GNPW-----TEYMAKYDIKEVSGGIRVDLGEDEAVAGTQRLPSGKCPVFGKGIILEN 160
QY 101 PRLRLPNRNFLFEDVPT-EKEYKSGNPLPGGFNLNFTVPSGQRISSPPM---ELLEKNS 155
DB 161 SN-----TTFELKPVATGNDLKDGGFAPF-----PTNLLISPMTLDMHRDQYKNE 206
QY 156 NTKASTDLGRCAEPAFKTVAMDKNKATKYRYPFYDSKRLCHILYVSMOMEGKCYSC 215
DB 207 YKNDLDELTLCSRHAGN--MNPDDNKNISYKRAYADVYDKKCHILYLAOENNGPRYCN 264
QY 216 VAGGERPDLTYGFKRKSTENHHLIYGSAYVGEN--PDAFISKCPNOLRGYRFGVWKKG 274
DB 265 -KDESKRNSMFCFRPAKDKSFONY-----TYLSKVVVDWMEKVCPRKNLENKFGIWDG 318
QY 275 RCLDYTELTDVIERVESKAQCVKTFENDVASDQPHTYP--LTSQASMDWMP----- 327
DB 319 NCEDLPHVNEF--SANDLFECKNLVFEIS--ASQPKQYBQHLTDYEKIKGFGKKNKAS 373
QY 328 -----LHQSDFHSGGVGRNRYGYVDTTGEGKCALSDQVPCIVSDSAVSTYA 377

DR EMBL, M58546; AAA29719.1; -
 DR InterPro; IPR003298; Apmem_Ag1.
 DR Pfam; PF02430; AMA-1; 1.
 DR PRINTS; PR01361; MEROZOITESA.
 KM Malaria; Signal; Transmembrane; Antigen; Glycoprotein.
 FT SIGNAL 1 24
 FT CHAIN 25 622
 FT DOMAIN 25 622
 FT TRANSMEM 547 546
 FT DOMAIN 568 622
 FT CARBOHYD 162 162
 FT CARBOHYD 286 286
 FT CARBOHYD 371 371
 FT CARBOHYD 421 421
 FT CARBOHYD 422 422
 FT CARBOHYD 499 499
 SQ SEQUENCE 622 AA; 71967 MW; 089336BE0464695C CRC64;
 Query Match 14.0%; Score 410; DB 1; Length 622;
 Best Local Similarity 26.0%; Pred. No. 8,9e-24;
 Matches 149; Conservative 80; Mismatches 214; Indels 130; Gaps 25;
 Oy 41 GNPQANVEMKTFMERFNLTHHOSGIYVDLGODKEVDGTLREPAGLCPINGKHIELQO 100
 Db 107 GNPW-----TEYMAKYDIEVHAGSIRVDLGBDAVAGTOYRLPSGKCPVFGKIIIE 160
 Oy 101 PRLPLRYNNFLIEDVPT-EKEYKOSGNPLPGGFNLNFTPSGGRISFPFM---ELLEKNS 155
 Db 161 SN-----TFLKPVATAGNODLKDGGFAFP-----PTNPLISPMITNGKRDYKXNE 206
 Oy 156 NIKASTDLGRCAEFKFAKTVAMKNNKATKYRYPFVYDSSKRLCHILYVSMQMEGKKYCS 215
 Db 207 YKKNLDELTLCSHNAH--MNPNDKNSNYKIPAVTDYDKCHILYIAOENNGERYCN 264
 Oy 216 VKGEPPDLTWYCFKPKK-SVTENHHLIYSAYVGEN-PDAFISKCPNALRGYRGVWKK 273
 Db 265 -KDQSRNMFRCRPAKOKLFENY-----TILSKYVVDNWEVCPKRLLENAKFGLAVD 317
 Oy 274 GRCLDYTELTVYIEVESKACQWTFENDGVASQPHTPP--LTSQASNDWMP----- 327
 Db 318 GNCEDIPIVNEF---SANDLFECNKLVPFLS--ASQPKQYEOHLDYERIKIEGFNKKNA 372
 Oy 328 -----LHSDPHSGGVRNYPFYVDVTGEGKCALSDQVDCIVSDSAVAVYT 376
 Db 373 SMIKAFPLTGAFAKADRYKSHKGVMGNVNNETO--KCEIYNVPTCLINNSYIAT 429
 Oy 377 AAGSLSEETPNFIIPSN-----PSVTPPTPETA 404
 Db 430 ALSHPIEVEHNF--PCSLYKDEIKKEIERESKRIKLDNDDEGNKKIAPRIFISDKDS 487
 Oy 405 LOCTADKFPDSFGACVQACROKTCVGGQIOSTS-----VDCIAD--EQNECG 452
 Db 488 LKPCPCPEWVNSNCTCFPVCK-----CVERRAVTSNNEVYVKEBYKDEYADVPEKPT 542
 Oy 453 SNTALI-----AGIAYGVGILLALLGGCYFAKRLDNKGQVQAHNHEFQSDGAKKRP 508
 Db 543 DNNKILTIASSAAVAVALTILMV-----YLYK-----KG-NAEKYKMDQPHYIGKSTSR 591
 Oy 509 SDLMQEAEPSPFMDAEENIEQDETHVWEGDY 541
 Db 592 NDEMUDPEASFWGEER---RASHTTVLMEKPY 621
 RESULT 8
 AMAL PLACH STANDARD; PRT; 558 AA.
 AC P16445;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Apical membrane antigen 1 precursor (Merozoite surface antigen).
 GN AMA-1.
 OS Plasmodium chabaudi.

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_Taxid=5825;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=DS;
 RX MEDLINE=90114335; PubMed=2608101;
 RA Marshall V.M., Peterson M.G., Lew A.M., Kemp D.J.;
 RT "Structure of the apical membrane antigen 1 (AMA-1) of Plasmodium
 RT chabaudi.";
 RL Mol. Biochem. Parasitol. 37:281-284(1989).
 RN [2]
 RP SEQUENCE OF 38-377 FROM N.A.
 RC STRAIN=DK;
 RX MEDLINE=96333375; PubMed=8757669;
 RA Crewether P.E., Matthew M.L., Plegg R.H., Anders R.F.;
 RT "Protective immune responses to apical membrane antigen 1 of
 RT Plasmodium chabaudi involve recognition of strain-specific
 RT epitopes.";
 RL Infect. Immun. 64:3310-3317(1996).
 CC -1- FUNCTION: INVOLVED IN PARASITE INVASION OF ERYTHROCYTES.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: STRONG TO AMA-1/PP83 FROM P.FALCIPARUM, P.FAGILE AND
 CC TO PK66 FROM P.KNOWLEST.
 CC -----
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 CC -----
 DR EMBL, M25248; AAA90929.1; -
 DR EMBL, A08270; CAH00765.1; -
 DR EMBL, U49745; AAB36511.1; -
 DR PIR; A44964; A44964.
 DR InterPro; IPR003298; Apmem_Ag1.
 DR Pfam; PF02430; AMA-1; 1.
 DR PRINTS; PR01361; MEROZOITESA.
 KM Malaria; Signal; Transmembrane; Antigen; Glycoprotein.
 FT SIGNAL 1 21
 FT CHAIN 22 558
 FT DOMAIN 22 480
 FT TRANSMEM 481 503
 FT DOMAIN 504 558
 FT CARBOHYD 20 20
 FT CARBOHYD 189 189
 FT CARBOHYD 231 231
 FT CARBOHYD 249 249
 FT CARBOHYD 276 276
 FT CARBOHYD 288 288
 FT CARBOHYD 412 412
 SQ SEQUENCE 558 AA; 63973 MW; 9773F3E64394972 CRC64;
 Query Match 13.6%; Score 398.5; DB 1; Length 558;
 Best Local Similarity 25.8%; Pred. No. 5,9e-23;
 Matches 147; Conservative 86; Mismatches 202; Indels 135; Gaps 24;
 Oy 42 NFPQANVEMKTFMERFNLTHHOSGIYVDLGODKEVDGTLREPAGLCPINGKHIELQO 101
 Db 53 NFWP-----KMEKYDIEKVGSGIRVDLGBDAVAGNODYRIPSGKCPVWGKGIITONS 106
 Oy 102 DRLPYRNNFLIEDVPT-EKEYKOSGNPLPGGFNLNFTPSGGRISFPFM---ELLEKNS 156
 Db 107 -----KVSFLTRVATAGNODKVGGLAFP-----QTDVNIISPTIDNLKMTKDKHE 152
 Oy 157 IKASTDLGRCAEFKFAKTVAMKNNKATKYRYPFVYDSSKRLCHILYVSMQMEGKKYCSV 216
 Db 153 ILALNDMSLCAGHA--SFVYPTGTNTVTAIRHAYVDKSNKTCYILYVAQENMGPRYCS- 209
 Oy 217 KGEPPDLTWYCFKPKKSVTENHHLIYSAYVGENDAFISKCPNALRGYRGVWKKGRG 276
 Db 210 NEDNENOPFCFTPEKK--DEYKILSYLTKNLRED--WETSCPNSKSIONAKRGVWVDYGC 265

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Cy 277 LDY--TELLDTVIERESKACQWTFENDVASDOPHTY----- 314
Db 266 SEYKKEVHND-----KTLFECNOIVNES--ASQPPQYKEKLEDTAKIRGIVDRNGK 318
Cy 315 -----PLISQASNDWMPHQSDQPHSGGVGRNYGYVDTTGEKCALSDQVDCLV 367
Db 319 LIGBALPITGS-----YRADQVSKSGKGYWANYDKTK--KCYIFNKKPFCL 365
Cy 368 SDSAAVSTAGSLSEETPNFIIPN-----PSVTPPT 400
Db 366 NDKQFVATTAALSSL-EEGPQSESPEDDIYKKIABEIKVMANVRNNGNDTKFPPIFISD 424
Cy 401 PETALQCTADKPPSPFACADVOAC-----KROKTSQVSGQIOSTSVDTADEQNEGCS--- 453
Db 425 DKSELNCEPPTQLTQSTCKFCVNCVKEKQFIS-----ENNEVEIIDEKSEYESPIN 478
Cy 454 --NTALLAGLAVGVLLALLIGGCGYPAKRLDRNKQVAHHEHEFGSDRGARKKRPEDL 511
Db 479 QRMILIIILITATGAILASLLI---FYFPRK---SNK--PGDDYDKMGQADTYGKAQSRKDE 530
Cy 512 MQEAPSPFMDAEENIEDGETHWVVEGDY 541
Db 531 MLDPVSPFWGSDK---RASHTTPVLMEXPY 557

RESULT 9
MAPB_RAT STANDARD: PRT: 2459 AA.
AC P15205; Q62958; Q9ER21; Q9GWR2;
DT 01-APR-1990 (Rel. 14, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Microtubule-associated protein 1B (MAP 1B) (Neuraxin) [Contains: MAP1
DE 1B light chain LC1].
GN MAP1B.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE OF 1-142 FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Testis;
RX MEDLINE=96257242; PubMed=866295;
RA Liu D., Fischer I.;
RT "Isolation and sequencing of the 5' end of the rat microtubule-
RT associated protein (MAP1B)-encoding cDNA.";
RL Gene 172:307-308(1996).
RN [2]
RP SEQUENCE OF 96-2459 FROM N.A., DOMAIN, AND INDUCTION.
RC STRAIN=Sprague-Dawley; TISSUE=Brain, and Glial tumor;
RX MEDLINE=92347374; PubMed=1639092;
RA Zauner W., Kratz J., Staunton J., Feick P., Wiche G.;
RT "Identification of two distinct microtubule binding domains on
RT recombinant rat MAP 1B.";
RL Eur. J. Cell Biol. 57:66-74(1992).
RN [3]
RP SEQUENCE OF 1541-2459 FROM N.A., AND TISSUE SPECIFICITY.
RC TISSUE=Spinal cord;
RX MEDLINE=90059871; PubMed=2555150;
RA Rientz A., Gremmling J., Hermans-Borgmeyer I., Kirsch J.,
RA Litzner U.Z., Prior P., Gundelfinger B.D., Schmitt B., Betz H.;
RT "Neuraxin, a novel putative structural protein of the rat central
RT nervous system that is immunologically related to microtubule-
RT associated protein 5.";
RL EMBO J. 8:2879-2888(1989).
RN [4]
RP DEVELOPMENTAL STAGE, AND PHOSPHORYLATION.
RX MEDLINE=97405699; PubMed=9260743;
RA Ma D., Nothias F., Boyne L.J., Fischer I.;
RT "Differential regulation of microtubule-associated protein 1B (MAP1B)
RT in rat CNS and PNS during development.";
RL J. Neurosci. Res. 49:319-332(1997).

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CC -1- FUNCTION: The function of brain MAPs is essentially unknown.
CC phosphorylated MAP1B may play a role in the cytoskeletal changes
CC that accompany neurite extension. Possibly MAP1B binds to at least
CC two tubulin subunits in the polymer, and this bridging of subunits
CC might be involved in nucleating microtubule polymerization and in
CC stabilizing microtubules.
CC -1- SUBUNIT: 3 different light chains, LC1, LC2 and LC3, can associate
CC with MAP1A and MAP1B proteins.
CC -1- TISSUE SPECIFICITY: Nervous system (spinal cord, brain stem,
CC cerebellum and cerebrum). Not expressed in liver, spleen, kidney,
CC heart or muscle.
CC -1- DEVELOPMENTAL STAGE: In cerebral cortex, spinal cord and sciatic
CC nerve levels are high early in development but decrease during
CC postnatal development and are low in adults. In dorsal root
CC ganglia levels remain high throughout development.
CC -1- INDUCTION: By nerve growth factor.
CC -1- DOMAIN: Has a highly basic region with many copies of the sequence
CC KEE and KKEI/V, repeated but not at fixed intervals, which is
CC responsible for the binding of MAP1B to microtubules.
CC -1- PTM: LC1 is coexpressed with MAP1B. It is a polypeptide generated
CC from MAP1B by proteolytic processing. It is free to associate with
CC both MAP1A and MAP1B. It interacts with the amino-terminal region
CC of MAP1B (by similarity).
CC -1- PTM: Phosphorylated.
CC -1- SIMILARITY: TO MAP1A.
CC -1- CAUTION: A C-terminal fragment of this protein (residues 1597 to
CC 2459) was originally described as neuraxin in Ref.3.
CC -----
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CC or send an email to license@isb-eb.ch).
CC -----
CC EMBL; U52950; AAB17068.1; -
CC EMBL; X60370; CAC16462.1; -
CC DR EMBL; X16623; CAA34567.1; ALT_SEQ.
CC DR PIR; A56577; A56577.
CC DR InterPro; IPR00102; MAP1B_neuraxin.
CC DR Pfam; PF00414; MAP1B_neuraxin; 10.
CC DR PROSITE; PS00230; MAP1B_NEURAXIN; 8.
CC KW Microtubules; Repeat; Phosphorylation.
CC FT ? 2459
CC REPEAT 1869 1885 MAP1B 1.
CC FT REPEAT 1886 1902 MAP1B 2.
CC FT REPEAT 1903 1919 MAP1B 3.
CC FT REPEAT 1920 1936 MAP1B 4.
CC FT REPEAT 1937 1953 MAP1B 5.
CC FT REPEAT 1954 1970 MAP1B 6.
CC FT REPEAT 1988 2004 MAP1B 7.
CC FT REPEAT 2005 2021 MAP1B 8.
CC FT REPEAT 2022 2038 MAP1B 9.
CC FT REPEAT 2039 2055 MAP1B 10.
CC FT DOMAIN 559 1035 GLU-RICH.
CC FT DOMAIN 588 786 LYS-RICH (HIGHLY BASIC, CONTAINS MANY
CC KEE AND KKEI/V REPEATS).
CC FT LYS-RICH.
CC FT DOMAIN 2224 2312 LYS-RICH.
CC FT CONFLICT 127 127 M -> V (IN REF. 1).
CC FT CONFLICT 140 140 T -> S (IN REF. 1).
CC FT CONFLICT 2112 2112 R -> K (IN REF. 3).
CC FT CONFLICT 2169 2169 L -> I (IN REF. 3).
CC SO SEQUENCE 2459 AA; 269497 MW; 283F6872DDB8BA2 CRC64;
Query Match 4.3%; Score 127; DB 1; Length 2459;
Best Local Similarity 19.4%; Pred. No. 0.27;
Matches 97; Conservative 55; Mismatches 101; Indels 168; Gaps 21;
Cy 15 DCTIFAGGLSSRTSRSSQTLASSTSGNPQANVEMTFPERF--NLTHHGQSIYVDLG 72
Db 1749 DMSLYASLASEKQVSLGEGKLSPKSDISPLTPRESSPTYPGFSDSGAKESTPAAYQTS 1808

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QY 73 QDKEVDGTLVREPAQ-----LCPIWGHIELOQDPRLPYRNNLEDPTEKEKQSGNPL 127
DB 1809 SSSPIDAAA-ABEYGRSSMLPDTMOHIALSR-----DLTSSVEKONGAKT 1855
QY 128 PGGFNLFNFTPSGORISP-----DITSSVEKONGAKT 149
DB 1856 PGDFVAVQKPESTTESPEEDYDYESHEKTIQADHVGYYEYKERTIKSPCDSGYSYE 1915
QY 150 LLEKSNIKASTDLGRCAEFAFTV-----AMDKNNKATK-----YRPFYDYSK 195
DB 1916 TLEKTT--KTPEDGGVSCETIKTRTPREGGYSEISEKTRTPESGYTEKTERSR 1973
QY 196 RL-----CHILYVSMQL-----EGKY-----CSVKGEPDLTWYCF 228
DB 1974 LLDLSNGYDTEDEGHTLGDOSYETTEKTSPESESYETTTKTRPDTSAICY 2033
QY 229 KERKSVTENHLLYGSAYVGENPDAFISKCPNALRGVRFGWKKGRCIDYELDTYIE 288
DB 2034 ETMEKITTPQ--ASTVSEYTS-----RC--YTPERKSPSE 2066
QY 289 RVESRAQCVKTFENDGVASDOPHYPLTSQASMN--DWM-----PLHOSDOP--HSGVY 340
DB 2067 ARQDYLCLVSSCE-----FKHPKTELSPSFINPNPLEWFAGEEPTESERPLTOSGGAP 2121
QY 341 RNYGFYVDTTGEKCALSDOVPDCLVSDA-----AVSYTAAGSLSEETP 386
DB 2122 PPSG-----GKQGRQCDERTPTPSVSASQSDSDVPPETEBPSITADANDSEDE 2174
QY 387 NFIIPSNPST-----PPTP 401
DB 2175 SETIPTDKVTYKHMPPAP 2195

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RESULT 10
MAPB MOUSE STANDARD; PRT; 2464 AA.

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ID MAPB MOUSE STANDARD; PRT; 2464 AA.
AC P14873;
DT 01-APR-1990 (rel. 14, Last sequence update)
DT 28-FEB-2003 (rel. 41, Last annotation update)
DE Microtubule-associated protein 1B (MAP 1B) (MAP1.2) (MAP1(X))
DE (Contains: MAP1 light chain LC1).
DE GN MAP1B OR MTAP1B OR MTAP5.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OC NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A., AND DOMAIN.
RC STRAIN=Swiss Webster; TISSUE=Brain;
RX MEDLINE=90094539; PubMed=2480963;
RA Noble M., Lewis S.A., Cowan N.U.;
RT "The microtubule binding domain of microtubule-associated protein
RT MAP1B contains a repeated sequence motif unrelated to that of MAP2
RT and tau."
RT J. Cell Biol. 109:3367-3376(1989).
CC -I- FUNCTION: THE FUNCTION OF BRAIN MAPS IS ESSENTIALLY UNKNOWN.
CC PHOSPHORYLATED MAP1B MAY PLAY A ROLE IN THE CYTOSKELETAL CHANGES
CC THAT ACCOMPANY NEURITE EXTENSION. POSSIBLY MAP1B BINDS TO AT LEAST
CC TWO TUBULIN SUBUNITS IN THE POLYMER, AND THIS BRIDING OF SUBUNITS
CC MIGHT BE INVOLVED IN NUCLEATING MICROTUBULE POLYMERIZATION AND IN
CC STABILIZING MICROTUBULES.
CC -I- SUBUNIT: 3 DIFFERENT LIGHT CHAINS, LC1, LC2 AND LC3, CAN ASSOCIATE
CC WITH MAP1A AND MAP1B PROTEINS.
CC -I- DOMAIN: Has a highly basic region with many copies of the sequence
CC KKEE and KKEIV, repeated but not at fixed intervals, which is
CC responsible for the binding of MAP1B to microtubules.
CC -I- PTM: LC1 IS COEXPRESSED WITH MAP1B. IT IS A POLYPEPTIDE GENERATED
CC FROM MAP1B BY PROTEOLYTIC PROCESSING. IT IS FREE TO ASSOCIATE WITH
CC BOTH MAP1A AND MAP1B. IT INTERACTS WITH THE AMINO-TERMINAL REGION
CC OF MAP1B.
CC -I- SIMILARITY: TO MAP1A.

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DR EMBL, X51396; CA35761.1; -.
DR PIR, S07549; QRMSP1.
DR MGD; MGI:1306778; Map1b.
DR GO; GO:0016358; P: dendrite morphogenesis; IMP.
DR GO; GO:0001578; P: microtubule bundling; IMP.
DR InterPro; IPR000102; MAP1B neuraxin.
DR Pfam; PF00414; MAP1B neuraxin; 10.
DR PROSITE; PS00230; MAP1B_NURAXIN; 7.
KW Microtubules; Repeat; Phosphorylation.
FT CHAIN ? 2464 MAP1 LIGHT CHAIN LC1.
FT REPEAT 1874 1890 MAP1B 1.
FT REPEAT 1891 1907 MAP1B 2.
FT REPEAT 1908 1924 MAP1B 3.
FT REPEAT 1925 1941 MAP1B 4.
FT REPEAT 1942 1958 MAP1B 5.
FT REPEAT 1959 1975 MAP1B 6.
FT REPEAT 1993 2009 MAP1B 7.
FT REPEAT 2010 2026 MAP1B 8.
FT REPEAT 2027 2043 MAP1B 9.
FT REPEAT 2044 2060 MAP1B 10.
FT DOMAIN 589 787 MAP1B 10. (HIGHLY BASIC, CONTAINS MANY
FT LYS-RICH AND KKEIV REPEATS).
SQ SEQUENCE 2464 AA; 270408 MW; FBD3DD99CFBDA87 CRC64;

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Query Match 4.1%; Score 120; DB 1; Length 2464;

Best Local Similarity 19.3%; Pred. No. 0.92; Indels 184; Gaps 22;

Matches 98; Conservative 53; Mismatches 174;

```

QY 15 DCTIFASGLSSSTRESQTLASTSGNPFQANVEMKTFMERFN-----LTHNQ 64
DB 1754 EMSLYASLASLSEKRYLSEKXLSPKSDISPLRPRESSPLYSFGFSSTAAKETAHQAAS 1813
QY 65 SGIYVDLQDYEVDGTLVREPAQ-----LCPIWGHIELOQDPRLPYRNNLEDPTEKE 119
DB 1814 SSSPIDAAT-----ABEYGRSSMLPDTMOHIALNR-----DLTSSV 1852
QY 120 YKQSGNPLPGGFNLFNFTPSGORISP-----AMDKNNKATK-----YRY 187
DB 1853 EKDSGKTPGDENAVQKPENAAGSPDEEDYDYESQETKTRTHDVVRYTEKERTISP 1912
QY 146 ----FPMELLEKSNIKASTDLGRCAEFAFTV-----AMDKNNKATK-----YRY 187
DB 1913 CDSGYSEYTIETKT--KTPEDGGVYCEITEKTRTPREGGYSEISEKTRTPESGYTY 1970
QY 188 PFVYDSKRL-----CHILYVSMQL-----EGKY-----CSYK--GEP 220
DB 1971 EKTERRSRLLDLSNGYDTEDEGHTLGDOSYETTEKTSPESESYETSTYKTRS 2030
QY 221 PDLTWYCKPKRSVENHLLYGSAYVGENPDAFISKCPNALRGVRFGWKKGRCIDYT 280
DB 2031 PPTSVCYETMEKITTPQ--ASTVSEYTS-----RC--YT 2063
QY 281 ELTDVIRVRSKQACWKTFENDGVASDOPHYPLTSQASMN--DWM-----PLHOSDOP 334
DB 2064 TEKSPSEARQVDVCLVSSCE-----FKHPKTELSPSFINPNPLEWFAGEEPTESERK 2118
QY 335 --HSGVGRNNGFYVDTTGEKCALSDOVPDCLVSDA-----AVSYTAAGSLSEETP 378
DB 2119 LTQSGGAPPSG-----GKQGRQCDERTPTPSVSASQSDSDVPPETEBPSITAD 2171
QY 379 GSLSEETNFIIPSNPST-----PPTP 401
DB 2172 ANIDSEDESETIPTDKVTYKHMPPAP 2200

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RESULT 11
 MAPB_HUMAN STANDARD; PRT; 2468 AA.
 ID MAPB_HUMAN
 AC P46821;
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Microtubule-associated protein 1B (MAP1B) [Contains: MAP1 light chain LC1].
 GN MAP1B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Petal brain;
 RX MEDLINE=95104835; PubMed=7806212;
 RA Lien L.V., Feener C., Fischbach N., Kunkel L.M.;
 RT "Cloning of human microtubule-associated protein 1B and the identification of a related gene on chromosome 15.";
 RL Genomics 22:273-280(1994).
 CC -1- FUNCTION: THE FUNCTION OF BRAIN MAPS IS ESSENTIALLY UNKNOWN.
 CC PHOSPHORYLATED MAP1B MAY PLAY A ROLE IN THE CYTOSKELETAL CHANGES THAT ACCOMPANY NEURITE EXTENSION. POSSIBLY MAP1B BINDS TO AT LEAST TWO TUBULIN SUBUNITS IN THE POLYMER, AND THIS BRIDGING OF SUBUNITS MIGHT BE INVOLVED IN NUCLEATING MICROTUBULE POLYMERIZATION AND IN STABILIZING MICROTUBULES.
 CC -1- SUBUNIT: 3 DIFFERENT LIGHT CHAINS, LC1, LC2 AND LC3, CAN ASSOCIATE WITH MAP1A AND MAP1B PROTEINS.
 CC -1- DOMAIN: Has a highly basic region with many copies of the sequence KKEE and KKEI/V, repeated but not at fixed intervals, which is responsible for the binding of MAP1B to microtubules.
 CC -1- PTM: LC1 is coexpressed with MAP1B. It is a polypeptide generated from MAP1B by proteolytic processing. It is free to associate with both MAP1A and MAP1B. It interacts with the amino-terminal region of MAP1B (by similarity).
 CC -1- SIMILARITY: TO MAP1A.
 CC -----
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 CC -----
 CC EMBL; L06237; AAA18904.1; -
 CC Genew; HGNC:6836; MAP1B.
 DR DR MIM; 157129; -
 DR DR GO; GO:0005875; C:Microtubule associated complex; TAS.
 DR DR InterPro; IPR001012; MAP1B_neuraxin.
 DR DR Pfam; PF00414; MAP1B_NEURAXIN; 10.
 DR DR PROSITE; PS00230; MAP1B_NEURAXIN; 6.
 KW Microtubules; Repeat; Phosphorylation.
 FT CHAIN ? 2468 MAP1 LIGHT CHAIN LC1.
 FT REPEAT 1878 1894 MAP1B 1.
 FT REPEAT 1895 1911 MAP1B 2.
 FT REPEAT 1912 1928 MAP1B 3.
 FT REPEAT 1929 1945 MAP1B 4.
 FT REPEAT 1946 1962 MAP1B 5.
 FT REPEAT 1963 1979 MAP1B 6.
 FT REPEAT 1997 2013 MAP1B 7.
 FT REPEAT 2014 2030 MAP1B 8.
 FT REPEAT 2031 2047 MAP1B 9.
 FT REPEAT 2048 2064 MAP1B 10.
 FT DOMAIN 589 790
 SO SEQUENCE 2468 AA; 270618 MW; 540839CDBF09D461 CRC64;
 Query Match 4.0%; Score 118; DB 1; Length 2468;
 Best Local Similarity 19.4%; Pred. No. 1.3;
 Matches 129; Conservative 66; Mismatches 222; Indels 248; Gaps 28;

QY 15 DCTTFASGLSSSTRSRESQTLASSTSGNPFQANVEMKTFMERFNLTHHSGIYVDLGD 74
 DB 1758 DMSLYASLTSKVKQSLBEEKSLSPKSDISP-----LTPRESSPLVSPETSD 1802
 QY 75 -----KEYDGLY-----REPAG-----LCPIWGHILEQPDRLPYRNFLPD 113
 DB 1803 STSAVKEKATACHSSSSPPIDAASAEYGFASVLFDMQHLALNR-----D 1850
 QY 114 VPTKEVYQSGNPLPGGFNLNPTPSGORISP-----FMELLEKNS----- 155
 DB 1851 LSTPELEDSGAKTPGDSYAYQKEETTRSPDEEDYSEYEKTRTSVGYEYKIE 1910
 QY 156 -NIKASDLCRCAEFAFTV-----AMDKNKATK----- 184
 DB 1911 RTTSPSDSGSYETIGTITTPEDGDYSYIEIKTTTPREGGSYVISEKTSPPEVS 1970
 QY 185 -YRPPFV-----YDSKRRLCHIL-----YVSQMLEGKY-CSVK 217
 DB 1971 GYSYEKTERSHRLLDISNGYDSEDDGHTLGDPSYETTEKITSPESEGSYETSTK 2030
 QY 218 -GEPPDLTWGCFPKRKSTYENHHLIYGAYVGENPDATISCPNALRGYRFGWKKGR 276
 DB 2031 TTRTPDSTGYCYETAETKTRTPQ--ASTYSYETSD----- 2063
 QY 277 LDYTELDTVIERVESKACQWKTFFENDGVASDQPHYPLT--SQASWN-----DMW----- 326
 DB 2064 LCTYRAKSPBEAODVCLVSSCE-----YKPKTELSPSFNPPLFVFASEE 2114
 QY 327 PLHOSDOP--HSGVGRNRYFYVDTEGKCALSDQVDCLVSDA----- 371
 DB 2115 PTESEKRLTSGGAPPPG-----GKQGRCDDETPTSVSBSAQSDVDVPEPTE 2167
 QY 372 -AVSTTAAGSSETPNPIISNPSVT-----PPPEPALQCTADKFPDSCGACDVQC- 424
 DB 2168 ECPSTTADANIDSESEETITPTDVTYKMDPPAPVQDPSPSRRHD-VSMVPEALA 2226
 QY 425 -----KROKTCVGGIOISTVDTADEQNEGCSNTALJAGLAVGVLILA 470
 DB 2227 IEQNLGKALKKDLKENTTKTKPKTKTKSSSVYKSSD-----GKSPFLAASRKPAGL----- 2277
 QY 471 LLGGCYFAKRLDRNKGVQAHHHEHFEQSDRGARKRPSDLMQEAEPFWDE--AEENIE 528
 DB 2278 -----KSSDPKSVSVASPKKESYEKAKPPTTPEVKARGBE 2315
 QY 529 QDGET 533
 DB 2316 KDKET 2320
 RESULT 12
 SW2A_SCHGR STANDARD; PRT; 697 AA.
 ID SW2A_SCHGR
 AC Q9XZC8;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Semaphorin 2A precursor (Sema 2A) (Sema II).
 GN SEMA-2A.
 OS Schistocerca gregaria (Desert locust).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Orthoptera; Orthoptera; Acrididae; Acridomorpha; Acridoidae; Acrididae; Cyrtacanthacridinae; Schistocerca.
 OX NCBI_TaxID=7010;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=99203450; PubMed=10101134;
 RA Iabister C.M., Tsai A., Wong S.T., Kolodkin A.L., O'Connor T.P.;
 RT "Discrete roles for secreted and transmembrane semaphorins in neuronal growth cone guidance in vivo.";
 RL Development 126:2007-2019(1999).
 CC -1- FUNCTION: ACTS AS CHEMOREPULSIVE GUIDANCE MOLECULE CRITICAL FOR

	CC	AXON FASCICULATION AND FOR DETERMINING BOTH THE INITIAL DIRECTION
CC	AND SUBSEQUENT PATHFINDING EVENTS OF THE TI AXON PROJECTION.	
CC	- SUBCELLULAR LOCATION: Secreted (potential).	
CC	- TISSUE SPECIFICITY: EXPRESSED IN A GRADIENT IN THE DEVELOPING LIMB	
CC	BUD EPITHELIAL DURING TI PRONEURON AXON OUTGROWTH.	
CC	- SIMILARITY: BELONGS TO THE SEMAPHORIN FAMILY.	
CC	- SIMILARITY: Contains 1 Sema domain.	
CC	- SIMILARITY: Contains 1 immunoglobulin-like C2-type domain.	
CC	-----	
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CC	-----	
DR	EMBL; AF134904; AAD30114.1; .-	
DR	InterPro; IPR007110; IG-like.	
DR	InterPro; IPR003599; IG.	
DR	InterPro; IPR001627; Sema.	
DR	Pfam; PF01403; Sema; 1.	
DR	SMART; SM00409; IG; 1.	
DR	SMART; SM00630; Sema; 1.	
DR	PROSITE; PSS00835; IG-LIKE; 1.	
KW	Signal; Immunoglobulin domain; Neurogenesis; Developmental protein;	
KM	Glycoprotein.	
FT	SIGNAL 1 20 POTENTIAL.	
FT	CHAIN 21 697 SEMAPHORIN 2A.	
FT	DOMAIN 231 515 Sema.	
FT	DISULFID 526 634 IG-LIKE C2-TYPE.	
FT	BY SIMILARITY.	
FT	CARBOHYD 618 654 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD 63 633 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD 66 66 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD 132 132 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD 198 198 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD 283 283 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD 369 369 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD 534 534 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD 629 629 N-LINKED (GLCNAC. . .) (POTENTIAL).	
FT	CARBOHYD 679 679 N-LINKED (GLCNAC. . .) (POTENTIAL).	
SQ	SEQUENCE 697 AA; 78673 MW; 7FB5AB4A965E1B4 CRC64;	
	Query Match 4.0%; Score 117; DB 1; Length 697;	
	Best Local Similarity 19.6%; Pred. No. 0.29; Indels 184; Gaps 26	
	Matches 106; Conservative 63; Mismatches 187;	
Oy	21 SGLSSSTRSEQTSASTSGNPFOANVEMKTFMERFNLTNHHOSGIYVDLGODKEVDST 80	
Dd	65 TMSISDCRSDSLTEPTNI-----ANCYSKKRSADFCDKNHIRVIOPMGDSRLYIGCT 119	
Oy	81 LYREPAGLCPIWGKHIELQOPLRPYRNFLLEDVPEKE-----YKSGNP-LPG-- 129	
Dd	120 NAHSPEQDWV-VYSNLTLQRHEHVPIGVIGIAKCPDPEDSDSTAWEANGEGDIPGLYS 178	
Oy	130 GFNLMPV-----TSGQGISPFMEELLE-----KNSNIKASTDLGRCAEPAF 171	
Dd	179 GTNAETTKADTVIPTDLYNLTGTREKREYSFKTKLYKDSFMLDNPNFVSFDVEGYLVFF 238	
Oy	172 KIVAADKNNKATRYRFYVDSKKRLC-----HLIYVS-MQLMEGGKYCSVKGEPPDL 223	
Dd	239 RETAYEYINCGKS-----YISRVARCKKDVGSKNLSQNMWTFPKARLNGSIPEGFP-- 291	
Oy	224 TWYCKRKPSV-----TENHMLIYGSAVVG-----ENPAFAFSKPNOALREY 266	
Dd	292 --FYNEILOGVYKMPTDKRFVGFFSYSTVLGSAISCFTLLNDIOEVFGSKREQDTS-- 348	
Oy	267 RFQGV-----KKGRCLDYTB-LTDVYLIERVESKAQCWKTFENDGVAADPHTY 314	
Dd	349 --SAMLPLVPKSVPRDPRPECVNDDLELLDTVLNFIKSH----- 385	
Oy	315 PLTQSASNDMWPLHQSDQPHSGG-----VGRN--YGFYYVD 349	

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Dh 386 -----PLMGDAVSHGGKPFYFRDVLFTQLVVDLKLVLVGNMXYIYYAG 433
Oy 350 TTGGKCALSDQYDPDCLVSDSAVSYTAAGSLSEETPNFIIPNSPSTPTPTALQCTA 409
Db 434 TS-----TGOV-----YKVVQWDSGSL-----FQSLVLDIFDVTPEPVOALHLK 475
Oy 410 DKPDSFGACD-----VOACKRKQKSCYGGGQIQSTSVDCAD-----EQNEGCSNT 455
Db 476 E-YASLYAASDNVYRQLELMWCHRYSNC-----LOCADDPYCGMRDSDNSCSY 525

RESULT 13
DPP4_FELCA
ID _DPP4_FELCA STANDARD; PRT; 765 AA.
AC OSN217;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Dipeptidyl peptidase IV (EC.3.4.14.5) (DPP IV) (T-cell activation
  antigen CD26).
GN DPP4 OR CD26.
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Cranialta; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
XN (1)
RN SEQUENCE FROM N.A.
RP TISSUE=Periphereal blood;
RC MEDLINE=20094000; Pubmed=10630304;
RX Nishimura Y., Miyazawa T., Ikeda Y., Isumi Y., Nakamura K., Sato E.,
  Mikami T., Takahashi E.;
RA "Molecular cloning and sequencing of a cDNA encoding the feline T-cell
  activation antigen CD26 homologue."
RL Immunogenetics 50:366-368(1999).
CC -1- FUNCTION: Removes N-terminal dipeptides sequentially from
  polypeptides having unsubstituted N-termini provided that the
  penultimate residue is proline (By similarity).
CC -1- CATALYTIC ACTIVITY: Release of an N-terminal dipeptide, Xaa-Xbb-|-
  Xcc, from a polypeptide, preferentially when Xbb is Pro, provided
  Xcc is neither Pro nor hydroxyproline.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Type II membrane protein. Also exists in
  a soluble form (By similarity).
CC -1- PTM: The soluble form (SDP) derives from the membrane form (MDPP)
  by proteolytic processing (By similarity).
CC -1- SIMILARITY: Belongs to peptidase family S9B.
CC -----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC or send an email to license@isb.sib.ch).
CC -----
CC EMBL; AB023952; BAA92344.1; -.
DR MEROPS; S09.003; -.
DR InterPro; IPR002469; DPPIV_N term.
DR InterPro; IPR001375; Peptidase_S9.
DR InterPro; IPR002471; Prol_endopep_ser.
DR InterPro; IPR000379; Ser_serfs_site.
DR Pfam; PF00930; DPPIV_N_term; 1.
DR Pfam; PF00326; Peptidase_S9; 1.
DR PROSITE; PS00708; PRO_ENDOPEP_SER; 1.
KW Hydrolase; Aminopeptidase; Dipeptidase; Serine protease;
  Transmembrane; Glycoprotein; Signal-anchor
  Dipeptidyl peptidase IV MEMBRANE FORM
  (MDPP).
FT CHAIN 38 765 DIPEPTIDYL PEPTIDASE IV SOLUBLE FORM
FT FT (SDP) (BY SIMILARITY).
FT DOMAIN 1 6 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 7 29 SIGNAL-ANCHOR (TYPE-II MEMBRANE PROTEIN)
  (POTENTIAL).

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FT DOMAIN 30 765 EXTRACELLULAR (POTENTIAL).
FT ACT SITE 629 629 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT SITE 707 707 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT SITE 739 739 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT CARBOHYD 84 84 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 91 91 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 149 149 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 178 178 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 228 228 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 280 280 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 320 320 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 330 330 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 331 331 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 519 519 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 684 684 N-LINKED (GLCNAC. . .) (POTENTIAL).
SO SEQUENCE 765 AA; 88213 MW; 38CB98A22B175D9 CRC64;

Query Match 3.9%; Score 113; DB 1; Length 765;
Best Local Similarity 18.2%; Pred. No. 0.66;
Matches 105; Conservative 66; Mismatches 161; Indels 246; Gaps 27;

QY 1 MGIVGVVLL-VIVADCTIFASGLSSSTRRESQTLASSTGNPQAVNEMKTEPERNL 59
DB 9 LGLGLALLITITVPPVLLKNGDAADSRRTYLTLYL-KNFR---VKFSLRWVS 63
QY 60 THHSGGIYVDLGDQKEVDGTLREPAGLCPWGHIELQPDRLPYNN--FLSDVPT 117
DB 64 DHDY-----LYKQDNILF-----NAEYNSSTFLEN-STF 94
QY 118 KEYKQSNPLDQGFENLFTVTSQGISFPFMELEKSNINAKSTDLGRCAFAKTVAMD 177
DB 95 DEFESINDVS-----VSPDQGIT-----LLE----- 116
QY 178 KKKATKRYRF-----VYDSKRLCHILYVSMQMEKGYCSVKGEPPDLTWYCFKPK 232
DB 117 -YNYVKKQRHSYTSYSDIYDLNKR-----QLITEKI-----PNTQWITWSP-- 158
QY 233 SVTENHLLYGSAYVGENPDAFISKPN-----QALGY 266
DB 159 ---EGHKL---AYWKW-DYVVKRPPSSSRITWGEENALYNGIADWYEEIFRAT 210
QY 267 RFGVWK-KGRCLDYELTDTVIERYESHAQCVKTFENDVASDQPHYPLTQASWMDW 325
DB 211 SALWMSPKGTFLAAYQFNDTQVPLEY-----SFYSDSLQYPTMR----- 252
QY 326 WPLMSQDPHSGGVRNGFYVDTGSGKALSQVDCIIVSDSANSYTAAGSLSET 385
DB 253 -----IPYKAGANPTV 265
QY 386 PNFIIPNSVTPPTPTALQCT--ADKFPDSFGACDVQACKROKTSVCG--GOIGSTVD 442
DB 266 KLFVYIKTD-NLNPNTNATSEITPPHMLTGDYILCDVTANBERISLQMLRRLONYSVM 324
QY 443 CTADQNECGSNTALIALAGVGLLALLGGCGYFAKRLDRNKGVAAHHEHFEQSDRG 502
DB 325 DIRDYNNGTG-----KWISSAQEHIMSTGTG 351
QY 503 -ARKKRPEDLMQEAEPFWDAAENIE---QDEGTHV 535
DB 352 WVGRRFP-----ABPHFTSDGRNFFYKLIISNEDGKHI 383

RESULT 14
SORL_CHICK STANDARD; PRT; 1592 AA.
AC Q98930;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Sortilin-related receptor (Sorting protein-related receptor containing
LDR class A repeats) (SortLA) (SortLA-1) (Low-density lipoprotein
receptor relative with 11 ligand-binding repeats) (LDR relative with
11 ligand-binding repeats) (LR11) (Fragment).

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OS Gallus gallus (chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A. .
RC TISSUE=Brain;
RX MEDLINE=97301565; PubMed=9157966;
RA Moriwaki S., Yamazaki H., Bujo H., Kusunoki J., Kanaki T., Seimiya K.,
RT Moriwaki N., Nimz J., Schneider W.J., Saito Y.;
RT "A novel mosaic protein containing LDL receptor elements is highly
RT conserved in humans and chickens."
RL Arterioscler. Thromb. Vasc. Biol. 17:996-1002(1997).
CC -1- FUNCTION: LIKELY TO BE A MULTIFUNCTIONAL ENDOCYTIC RECEPTOR, THAT
CC MAY BE IMPLICATED IN THE UPTAKE OF LIPOPROTEINS AND OF PROTEASES.
CC BINDS LDL, THE MAJOR CHOLESTEROL-CARRYING LIPOPROTEIN OF PLASMA,
CC AND TRANSPORTS IT INTO CELLS BY ENOCYTOSIS. BINDS THE RECEPTOR-
CC ASSOCIATED PROTEIN (RAP). COULD PLAY A ROLE IN CELL-CELL
CC INTERACTION. BOTH ESTROGEN STATUS AND CHOLESTEROL LEVELS LACK
CC REGULATORY EFFECTS ON THIS RECEPTOR.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (potential).
CC -1- TISSUE SPECIFICITY: EXPRESSED ABUNDANTLY IN BRAIN. PRESENT IN THE
CC TESTES, ADRENAL GLANDS AND DETECTABLE IN THE LUNG.
CC -1- SIMILARITY: Contains 5 BNR repeats.
CC -1- SIMILARITY: Contains 1 EGF-like domain.
CC -1- SIMILARITY: Contains 11 LDL-receptor class A domains.
CC -1- SIMILARITY: Contains 2 fibronectin type III domains.
CC -----
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CC -----
DR EMBL; Y08109; CA69324.1; -.
DR HSSP; P01130; 1A1T.
DR InterPro; IPR006209; EGF_like.
DR InterPro; IPR003961; FN_III.
DR InterPro; IPR002860; GH_BNR.
DR InterPro; IPR006210; IEGF.
DR InterPro; IPR002172; LDL_receptor_A.
DR InterPro; IPR000033; LDL_receptor_rep.
DR InterPro; IPR006581; VPS10.
DR Pfam; PF02012; BNR; 5.
DR Pfam; PF00041; fn3; 1.
DR Pfam; PF00057; ldl_recept_a; 11.
DR Pfam; PF00058; ldl_recept_b; 5.
DR PRINTS; PR00261; LDLRECEPTOR.
DR SMART; SM0181; EGF; 1.
DR SMART; SM00060; FN3; 1.
DR SMART; SM00192; LDLA; 11.
DR SMART; SM00135; LY; 5.
DR SMART; SM00602; VPS10; 1.
DR PROSITE; PS01186; EGF_2; 1.
DR PROSITE; PS01209; LDLR_1; 11.
DR PROSITE; PS50068; LDLR_2; 11.
DR Endocytosis; Cholepor; EGF-like domain; Repeat; Glycoprotein; LDL;
KW Lipid transport; Cholesterol metabolism.
FT NON TER 1 1
FT REPEAT 43 54 BNR 1.
FT REPEAT 139 150 BNR 2.
FT REPEAT 348 359 BNR 3.
FT REPEAT 428 439 BNR 4.
FT REPEAT 469 480 BNR 5.
FT DOMAIN 710 884 5 X APPROXIMATE YWTD REPEATS.
FT REPEAT 710 713 1.
FT REPEAT 754 757 2.
FT REPEAT 798 801 3.
FT REPEAT 841 844 4.
FT REPEAT 881 884 5.

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FT	DOMAIN	933	979	EGF-LIKE.
FT	DOMAIN	983	1021	LDL-RECEPTOR CLASS A 1.
FT	DOMAIN	1022	1062	LDL-RECEPTOR CLASS A 2.
FT	DOMAIN	1063	1100	LDL-RECEPTOR CLASS A 3.
FT	DOMAIN	1103	1143	LDL-RECEPTOR CLASS A 4.
FT	DOMAIN	1143	1180	LDL-RECEPTOR CLASS A 5.
FT	DOMAIN	1180	1224	LDL-RECEPTOR CLASS A 6.
FT	DOMAIN	1230	1268	LDL-RECEPTOR CLASS A 7.
FT	DOMAIN	1273	1312	LDL-RECEPTOR CLASS A 8.
FT	DOMAIN	1324	1362	LDL-RECEPTOR CLASS A 9.
FT	DOMAIN	1376	1415	LDL-RECEPTOR CLASS A 10.
FT	DOMAIN	1419	1457	LDL-RECEPTOR CLASS A 11.
FT	DOMAIN	1462	1551	FIBRONECTIN TYPE-III 1.
FT	DOMAIN	1559	>1592	FIBRONECTIN TYPE-III 2.
FT	DISULFID	985	997	BY SIMILARITY.
FT	DISULFID	992	1010	BY SIMILARITY.
FT	DISULFID	1004	1019	BY SIMILARITY.
FT	DISULFID	1024	1038	BY SIMILARITY.
FT	DISULFID	1032	1051	BY SIMILARITY.
FT	DISULFID	1045	1060	BY SIMILARITY.
FT	DISULFID	1065	1077	BY SIMILARITY.
FT	DISULFID	1072	1090	BY SIMILARITY.
FT	DISULFID	1084	1099	BY SIMILARITY.
FT	DISULFID	1105	1117	BY SIMILARITY.
FT	DISULFID	1112	1130	BY SIMILARITY.
FT	DISULFID	1124	1141	BY SIMILARITY.
FT	DISULFID	1145	1155	BY SIMILARITY.
FT	DISULFID	1150	1168	BY SIMILARITY.
FT	DISULFID	1162	1222	BY SIMILARITY.
FT	DISULFID	1232	1244	BY SIMILARITY.
FT	DISULFID	1239	1257	BY SIMILARITY.
FT	DISULFID	1251	1266	BY SIMILARITY.
FT	DISULFID	1275	1288	BY SIMILARITY.
FT	DISULFID	1283	1301	BY SIMILARITY.
FT	DISULFID	1295	1310	BY SIMILARITY.
FT	DISULFID	1333	1351	BY SIMILARITY.
FT	DISULFID	1345	1360	BY SIMILARITY.
FT	CARBOHYD	6	6	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	65	65	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	275	275	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	337	337	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	523	523	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	581	581	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	725	725	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	778	778	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	975	975	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1098	1098	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1152	1152	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1366	1366	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1454	1454	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1514	1514	N-LINKED (GLCNAC. . .) (POTENTIAL).
FT	CARBOHYD	1592	1592	N-LINKED (GLCNAC. . .) (POTENTIAL).
SEQ	SEQUENCE	1592	1592	AA; 178409 MW; 24EDANA5BA231B203 CRC64;

```

Query Match 3.8%; Score 111.5; DB 1, Length 1592;
Beet Local Similarity 22.2%; Pred. No. 2.3;
Matches 46; Conservative 24; Mismatches 88; Indels 49; Gaps 9

Qy 271 WKGRCLD-----YTSLDTVLIERESKAQCKWTFENDVASDOPHTPLT--SQASW 322
Db 829 WPNGISVDHWTMYTTEAYMDRIERIVDFNG-----LQFSVILDSLPHPAIVAFKNEIYW 882

Qy 323 NDWWPLHSDQPHSG-----VGRNYG-----FYVDTEEGCALSDQYPPDLVS 370
Db 883 NDMWSQSLIFRASKNSGSRMELTVGRYLYGIMDKIFRGKTTQGNALHPCLCLPMSN 942

Qy 371 AAVSYTAGSLSEETPNFIIPSNPSTVPTPEATALOCTADKPPDSFACDVOACKOKTS 430
Db 943 NRSRCKCPGVS-----STVLDSGEVKDC-----PHGSMGN-NTCVSEBNT 984

Qy 431 CVGGQIGQSTSVDC-----TADENNEG 452
Db 985 CLPNQYRCFENGNCINSIWQCDNNNDG 1011

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ID	CATW	HUMAN	STANDARD	PRT	376	AA
AC	PS6202	01-NOV-1997	(Rel. 35, Created)			
DT	01-NOV-1997	(Rel. 35, Last sequence update)				
DT	28-FEB-2003	(Rel. 41, Last annotation update)				
DE	Cathepsin W precursor	(EC 3.4.22.-) (Lymphopain)				
GN	CTSM					
OS	Homo sapiens (Human)					
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.					
OX	NCBI_TaxID=9606;					
RN	[1]					
RP	SEQUENCE FROM N.A.					
FX	MEDLINE=99039559; PubMed=9823953;					
RA	Brown J., Matutes E., Singleton A., Price C., Molgaard H., Buttle D.,					
RA	Ever T.;					
RT	"Lymphoblast, a cytotoxic T and natural killer cell-associated					
RL	cytotoxic proteinase.";					
RL	Leukemia 12:1771-1781(1998).					
RN	[2]					
RP	SEQUENCE FROM N.A.					
FX	MEDLINE=97261885; PubMed=9108299;					
RA	Limewers C., Smeekens S.P., Broemme D.;					
RT	"Human cathepsin W, a putative cysteine protease predominantly					
RT	expressed in CD8+ T-lymphocytes.";					
RL	FEBS Lett. 405:253-259(1997).					
RN	[3]					
RP	SEQUENCE FROM N.A.					
FX	MEDLINE=98342076; PubMed=9675123;					
RA	Wex T., Levy B., Smeekens S.P., Ansgore S., Deenick R.J., Broome D.;					
RT	"Genomic structure, chromosomal localization, and expression of human					
RT	cathepsin W.";					
RL	Biochem. Biophys. Res. Commun. 248:255-261(1998).					
CC	-1- FUNCTION: MAY HAVE A SPECIFIC FUNCTION IN THE MECHANISM OR					
CC	REGULATION OF T-CELL CYTOLYTIC ACTIVITY.					
CC	-1- TISSUE SPECIFICITY: EXPRESSED IN NATURAL KILLER AND CYTOTOXIC T					
CC	CELLS.					
CC	-1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C1.					
CC	-----					
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CC	-----					
DR	EMBL, AF013611; AAB82449.1; -					
DR	EMBL, AF015954; AAB82457.1; -					
DR	EMBL, AF055903; AAC32181.1; -					
DR	HSSP, P14080; IYAL.					
DR	MEROPS, C01.037; -					
DR	GeneW, HGNC:2546; CTSM.					
DR	MIM, 602364; -					
DR	GO, GO:0008234; F:cysteine-type peptidase activity; TAS.					
DR	GO, GO:0006955; P:immune response; TAS.					
DR	InterPro, IPR000668; Peptidase C1.					
DR	InterPro, IPR000169; SHProt_acsite.					
DR	Pfam, PF00112; Peptidase_C1; 1.					
DR	PRINTS, PR00705; PAPA1N.					
DR	ProDom, PD000158; Peptidase_C1; 1.					
DR	SMART, SM00645; Pept_C1_1					
DR	PROSITE, PS00139; THIOL_PROTEASE_CYS; FALSE_NEG.					
DR	PROSITE, PS00639; THIOL_PROTEASE_HIS; 1.					
DR	PROSITE, PS00640; THIOL_PROTEASE_ASN; 1.					
KW	Hydrolase; Thiol protease; Glycoprotein; Signal; Zymogen.					
FT	SIGNAL	1	21	POTENTIAL.		
FT	PROPEP	22	127	POTENTIAL.		
FT	CHAIN	128	376	CATHEPSIN W.		

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FT ACT SITE 153 153 BY SIMILARITY.
FT ACT_SITE 231 231 BY SIMILARITY.
FT ACT_SITE 331 331 BY SIMILARITY.
FT DISULFID 150 191 BY SIMILARITY.
FT DISULFID 184 226 BY SIMILARITY.
FT DISULFID 284 352 BY SIMILARITY.
FT CAROHXD 50 50 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CAROHXD 205 205 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 376 AA; 42099 MW; 718DB8478916FB0 CRC64;

Query Match
Best Local Similarity 21.7%; Score 107.5; DB 1; Length 376;
Matches 92; Conservative 50; Mismatches 150; Indels 131; Gaps 23;

8 VLVVLVADCTTFASGLSTRSRESQTLASTSGNPFQNMVMTKFMERFNTL-----H 61
10 LLALLVAG---LAQGRGLRAQD-----LGPDLLEKAFKLFQIQFNSTVSPREH 59
QY 62 HHQSGIYV-----DLGQ-----DKEVDGTL--YREPAGLCPWGXKH 96
DB 60 AHRLDIFAHNLAAQARLOBEDLGTAEFGVTPSPDLTEEFQQLYGRRAAGVPMGRBI 119
QY 97 ELQGPDRLPYRNPLFEDVPTKEKYQSG---NPLGCGFNLN---FVTSGGQKISFPME 150
DB 120 RSEBPE-----ESVPSGCDWRKVAAGALSIPIDOKKNCMMAMAAAGN-----IET 164
QY 151 LEKNS-----NINASTDLGRCAE-----FAFKTVAMDKNNKATRYRPFYVSK 195
DB 165 LMRISFMDPVDSVHLLDCCGCGGCGHGFWDAFITV--LNSGLASEKDYPPGKRYA 223
QY 196 RLCHILYVSMQMEKRYCSYKGEPPDLTWYCFERKRSVTENHLI-----YGSAYVE 249
DB 224 HRCH-----PKYQKV-----AM--IQFIMQNNHRIAGLATYGPITVTI 264
QY 250 NPDAISKCPNQAALRGYRFGWKKRCIDYTLTDTVI-----EKVESACQWVTFEND 304
DB 265 N-----MKPLDLYRKGIVKATPTTCDPLVHVSILVGFSGVKEBEGIMATVSSQ 315
QY 305 GVASDQPTVPL--TSQASWMDWMPHOSDQPSGVGNRYVDYDTGEGKCALSDOV-- 362
DB 316 S-QPPPHPTPYWILKNSGMAQMGKGYFRLHRS-----NTGCIITYPLTARVQ 364
QY 363 -PD 364
DB 365 KPD 367

RESULT 16
NF_X1_HUMAN STANDARD; PRT; 1104 AA.
AC Q12986;
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Transcriptional repressor NF-X1 (EC 6.3.2.-) (Nuclear transcription
factor, X box-binding, 1).
GN NF_X1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RS SEQUENCE FROM N.A.
RX MEDLINE=95053707; PubMed=7964459;
RA Song Z., Krishna S., Thanos D., Strominger J.L., Ono S.J.;
RT "A novel cysteine-rich sequence-specific DNA-binding protein
RT interacts with the conserved X-box motif of the human major
RT histocompatibility complex class II genes via a repeated Cys-His
RT domain and functions as a transcriptional repressor."
RL J. Exp. Med. 180:1763-1774(1994).
RP FUNCTION AS A E2-DEPENDENT UBIQUITIN LIGASE.
RX MEDLINE=99432238; PubMed=10500182;

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RA Lortick K.L., Jensen J.P., Fang S., Ong A.M., Hatakeyama S.,
RA Weisman A.M.;
RA "RING fingers mediate ubiquitin-conjugating enzyme (E2)-dependent
RT ubiquitination."
RL Proc. Natl. Acad. Sci. U.S.A. 96:11364-11369(1999).
CC -1- FUNCTION: Repressor of HLA-DRA transcription. Binds to the X-box
CC motif of MHC class II genes. May play an important role in
CC regulating the duration of an inflammatory response by limiting
CC the period in which MHC class II molecules are induced by
CC interferon gamma. Mediates E2-dependent ubiquitination.
CC -1- SUBCELLULAR LOCATION: Nuclear.
CC -1- INDUCTION: By interferon gamma.
CC -1- DOMAIN: The RING-type zinc finger domain interacts with an
CC ubiquitin-conjugating enzyme (E2) and facilitates ubiquitination.
CC -1- SIMILARITY: Contains 1 RING-type zinc finger.
CC -1- SIMILARITY: Contains 1 R3H domain.
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CC EMBL: U15306; AAA69517.1; -.
CC PIR: I38869; I38869.
CC TRANSPAC: T01694; -.
CC Genew; HGNC:7803; NF_X1.
DR MIM: 603255; -.
DR GO: GO:0003700; P:transcription factor activity; TAS.
DR GO: GO:0006954; P:inflammatory response; TAS.
DR GO: GO:0001022; P:negative regulation of transcription from P. . .; TAS.
DR GO: GO:0006366; P:transcription from pol II promoter; TAS.
DR InterPro: IPR001374; R3H.
DR InterPro: IPR000967; Znf_NFX1.
DR InterPro: IPR001965; Znf_PHD.
DR InterPro: IPR001841; Znf_ring.
DR Pfam: PF01424; R3H; 1.
DR Pfam: PF00097; ZF-C3HC4; 1.
DR Pfam: PF01422; ZF-NFX1; 8.
DR SMART; SM00393; R3H; 1.
DR SMART; SM00438; ZNF_NFX; 9.
DR SMART; SM00184; RING; 1.
DR PROSITE; PS00518; ZF_RING_1; FALSE_NEG.
DR PROSITE; PS50089; ZF_RING_2; 1.
KW Ub1 conjugation pathway; ligase; Transcription regulation; Repressor;
KW DNA-binding; Nuclear protein; Repeat; Zinc-finger.
FT ZN FING 342 393
FT DOMAIN 424 876
FT REPEAT 424 463
FT REPEAT 480 517
FT REPEAT 541 580
FT REPEAT 606 647
FT REPEAT 695 734
FT REPEAT 806 842
FT REPEAT 843 876
FT DOMAIN 992 1041
FT DOMAIN 1068 1073
SQ SEQUENCE 1104 AA; 123149 MW; 36FECA4292F78130C CRC64;

Query Match
Best Local Similarity 19.7%; Score 107.5; DB 1; Length 1104;
Matches 103; Conservative 61; Mismatches 159; Indels 199; Gaps 29;

85 PAGLCPIWKGKIEHQDPRLPYRNPLFEDVPTKEKYQSGNPLPGFNLFVTPSGORIS 144
DB 579 PCGGTPL-SQLBELGSSS-----RTKMDPVPSG--KVCGKPLPG--SLDFIHCEKLC 630
QY 145 PFMELLEKNSNINASTDLGRCAEFAPKTYAMD---KANKATYRYPFYVD---SKRL 197
DB 631 EGDGPGVSRSTVISC-----RC---SPRTKELPCTSLKSDAT-----FMCDKRCNKRRL 677

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Query Match 3.6%; Score 106; DB 1; Length 415;
 Best Local Similarity 21.1%; Pred. No. 1;
 Matches 71; Conservative 24; Mismatches 91; Indels 150; Gaps 15;

277 LDYELDTVIERVESKACQWKTENGVASD-----QHTYPLTQASMNWMPRLHQ 330
 Db 112 LSYTSDSTVPPGAVAKGVHTVKPENEKVPDLVIFKCNVLTNLTPLVV--QKRWGHL 169
 Qy 331 SDQHSQGVGNHNGFYVDTTGECKALSDQVPCDCLVSDSAVSTAAGSLEETPNFI 390
 Db 170 QAFVONGVSVK-----EVCYCE-EDQTPPTV---APIHTTPS-----TTTLT 210
 Qy 391 P-SNPSVTP-PYPETA-----LQCTADKFPDSF-----GAC 419
 Db 211 PTSTPTPTPTPTPTVGNYSINGNTTCLATWGLQNLITEKVPPIFINPATNFTGSC 270
 Qy 420 DVQA----- 423
 Db 271 QPQSAQLRLNNSQIKYLDLIFAVKNEKRFYKENVVNYLANSAFNISNKLSPWAPL 330
 Qy 424 -----CKRQKTSVCGQIQ-----STVDCATDEQNEGSGNTALJAG 460
 Db 331 GSSYWCNKEQVLSRAFOINTFNKLPQFVNTKQVSTAQDCSADBNFL--VPIAVG 387
 Qy 461 LAVGVLLALLGGGCFYFAKRLDENKGVQAAHHEH 496
 Db 388 AALGGVLLVLL--AYFI-----GLKRRHTGYE 413

RESULT 18
 RPOC_STRP3 STANDARD; PRT; 1207 AA.

AC 08K6W2;
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE DNA-directed RNA polymerase beta' chain (EC 2.7.7.6) (Transcriptase
 beta' chain) (RNA polymerase beta' subunit).
 GN RPOC OR SPY3 0076 OR SPS0077.
 OS Streptococcus pyogenes (serotype M3).
 OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
 CC Streptococcus;
 OX NCBI_TaxID=198466;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=MGAS315 / Serotype M3;
 RX MEDLINE=22133808; PubMed=12122206;
 RA Betes S.B., Sylva G.L., Barbican K.D., Lei B., Hoff J.S.,
 RA Mammarella N.D., Liu M.-Y., Smoot J.C., Porcella S.F., Parkins L.D.,
 RA Campbell D.S., Smith T.M., McCormick J.K., Leung D.Y.M.,
 RA Schlievert P.M., Mueser J.M.;
 RT "Genome sequence of a serotype M3 strain of group A Streptococcus:
 RT phage-encoded toxins, the high-virulence phenotype, and clone
 RT emergence.";
 RT Emerg. Natl. Acad. Sci. U.S.A. 99:10078-10083(2002).
 RL (12)
 RN SEQUENCE FROM N.A.
 RC STRAIN=SSI-1 / Serotype M3;
 RA Nakagawa I., Kurikawa K., Nakata M., Tomiyasu Y., Yamashita A.,
 RA Yamazaki K., Okahashi N., Kawabata S., Yasunaga T., Hattori M.,
 RA Hayashi H., Hamada S.;
 RT "The genome of invasive Streptococcus pyogenes; a comparative analysis
 RT of S. pyogenes SSI-1, SP370 and MGAS315.";
 RT Submitted (May-2002) to the EMBL/Genbank/DBPst databases.
 RL (1)
 CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
 CC SUBSTRATES.
 CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
 CC [RNA] (N).
 CC -1- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
 CC ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
 CC BETA' CHAIN.
 CC -1- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.

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DR EMBL; AB014137; AAM78683.1;
 DR EMBL; AP005141; BAC63172.1; ALT_INIT.
 DR InterPro; IPR00722; RNA_pol_A.
 DR InterPro; IPR006592; RNA_pol_A.
 DR Pfam; PF04997; RNA_pol_Rp1_1; 1.
 DR Pfam; PF00623; RNA_pol_Rp1_2; 1.
 DR Pfam; PF04983; RNA_pol_Rp1_3; 1.
 DR Pfam; PF05000; RNA_pol_Rp1_4; 1.
 DR Pfam; PF04998; RNA_pol_Rp1_5; 1.
 DR SMART; SM00663; RPOA_N; 1.
 KW Transferase; DNA-directed RNA polymerase; Transcription;
 KW Complete proteome.
 FT CONFLICT 602 D -> N (IN REF. 2).
 SO SEQUENCE 1207 AA; 134695 MW; 9672B98E0AA8745 CRC64;

Query Match 3.6%; Score 104; DB 1; Length 1207;
 Best Local Similarity 19.3%; Pred. No. 6;
 Matches 91; Conservative 54; Mismatches 166; Indels 160; Gaps 22;

Qy 115 PTEKEYQSGNPLBGGNLFVTPSGORISPEFM-ELLEKN-SNIA----- 159
 Db 349 PTLKMY-QCGVPRMAIEL-----FRFVREIYAEVAGNVAAKRWVGERI 398
 Qy 160 -----STDLRCAEFAPKTVAMDKNKATKYRVPV-----YDSKK 195
 Db 399 WDLIEVYIKENPVLLNAPTLHRGLQAFEVLD--GKALRL-HPLVCEAYNADPBGDQ 455
 Qy 196 RLCHILVSNQLMGKKYCSVKGPPDLTWYCFKPKRS--VTENHLLYGSAYV---- 247
 Db 456 MAIHV-PLSEBAQAEARLLMAAE-----HILNPKDGKRPVTPSQMVLCNYYLTWEDA 508
 Qy 248 GENDATATSKCPNALGYPFGVKKGRCLDTLTPTVIERVESKACQWKTENDGVA 307
 Db 509 GREGEGMIFPKDKAEAVNAYRNG-----YALHSRV-----GIA 541
 Qy 308 SDQHTVPLTQASMNWMPRLHQSDPHSGGVGNHNGFYVDTTGECKALSDQVPCDCLV 367
 Db 542 VDSMPNKP-----WKD-----SQNHK-----IMVTYKILPNDIMP----- 573
 Qy 368 SDSAAVSYTAAGSLSEETPNFIIPSNPSVTPPEETAQCTADKFPDSFGACDVQACKRQ 427
 Db 574 -----EDLPYQEBNNANLTGDTDFLEKQDQIQEVIDGLDINVFKK 618
 Qy 428 KTSVCG-----QISTVSDCTADQNEGSGNTALJAGLVGVLALLGGGCFYFAK 480
 Db 619 KN--LGIINIAETFRFRTTETSAFLDKLDGYHSHLAGITVGIADIPV----- 667
 Qy 481 RLDRNKG--VOAAHHEHFDSDRGARKKRPDSLMOBAEPPSPWDAEENIEQ 529
 Db 668 ---DNKAEIIDAHHRYEINIKAFRRGLMTDDDRYVAVTTTWRAKALEK 715

RESULT 19
 RPOC_STRP3 STANDARD; PRT; 1213 AA.

AC P95816;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DE DNA-directed RNA polymerase beta' chain (EC 2.7.7.6) (Transcriptase
 beta' chain) (RNA polymerase beta' subunit).
 GN RPOC OR SPY0099.
 OS Streptococcus pyogenes.
 CC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;

Query Match	Best Local Similarity	3.6%;	Score 104;	DB 1;	Length 1213;
Matches	91;	Conservative	55;	Mismatches	165;
				Indels	160;
				Gaps	22;
OC	Streptococcus.				
OC	NCBI_TaxID=1314;				
OC	[1]				
RP	SEQUENCE FROM N.A.				
RP	STRAIN=SF370 / ATCC 700294 / Serotype M1;				
RC	MEDLINE=97016803; PubMed=8863429;				
RC	MEDLINE=21192684; PubMed=11296296;				
RA	Ferrecci J.J., Moshan W.M., Ajdic D.J., Savic D.J., Savic G., Lyon K.,				
RA	Pirmeaux C., Seize S., Suvorov A.N., Kenton S., Lai H.S., Lin S.P.,				
RA	Qian Y., Jia H.G., Najjar F.Z., Ren O., Zhu H., Song L., White J.,				
RA	Xuan X., Clifton S.W., Roe B.A., McLaughlin R.;				
RT	"complete genome sequence of an M1 strain of Streptococcus				
RT	pyogenes.";				
RL	Proc. Natl. Acad. Sci. U.S.A. 98:4658-4663(2001).				
RN	[2]				
RP	SEQUENCE OF 67-1056 FROM N.A.				
RC	STRAIN=NCDO 923;				
RC	MEDLINE=97016803; PubMed=8863429;				
RA	Morse R., Collins M.D., O'Hanton K., Wallbanks S., Richardson P.T.;				
RA	"Analysis of the beta' subunit of DNA-dependent RNA polymerase does				
RT	not support the hypothesis inferred from 16S rRNA analysis that				
RT	Oenococcus oeni (formerly Leuconostoc oenos) is a facultative				
RT	(fast-evolving) bacterium.";				
RL	Int. J. Syst. Bacteriol. 46:1004-1009(1996).				
CC	1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION				
CC	OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS				
CC	SUBSTRATES.				
CC	1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +				
CC	{RNA}(N).				
CC	1- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE				
CC	ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1				
CC	BETA' CHAIN.				
CC	1- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.				
CC	-----				
CC	This SWISS-PROT entry is copyright. It is produced through a collaboration				
CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -				
CC	the European Bioinformatics Institute. There are no restrictions on its				
CC	use by non-profit institutions as long as its content is in no way				
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CC	entities requires a license agreement. See http://www.isb-sib.ch/announce/				
CC	or send an email to license@isb-sib.ch .				
CC	-----				
DR	EMBL; AE006480; AAK33217.1; --				
DR	EMBL; X96385; CAA65249.1; --				
DR	HSSP; Q9KWU6; 1HQM.				
DR	InterPro; IPR000722; RNA pol A.				
DR	InterPro; IPR007080; RNA_pol_Rpb1_1.				
DR	InterPro; IPR007066; RNA_pol_Rpb1_3.				
DR	InterPro; IPR007083; RNA_pol_Rpb1_4.				
DR	InterPro; IPR007081; RNA_pol_Rpb1_5.				
DR	InterPro; IPR006592; RNA polA N.				
DR	Pfam; PF04997; RNA_pol_Rpb1_1; 1.				
DR	Pfam; PF00623; RNA_pol_Rpb1_2; 1.				
DR	Pfam; PF04983; RNA_pol_Rpb1_3; 1.				
DR	Pfam; PF05000; RNA_pol_Rpb1_4; 1.				
DR	Pfam; PF04998; RNA_pol_Rpb1_5; 1.				
DR	SMART; SMO0663; RPOLA N; 1.				
KW	Transferase; DNA-directed RNA polymerase; Transcription;				
KW	Complete proteome.				
FT	Complete	435	KA -> NL (IN REF. 2).		
FT	CONFLICT	447	Y -> G (IN REF. 2).		
FT	CONFLICT	454	MISSING (IN REF. 2).		
FT	CONFLICT	553	N -> S (IN REF. 2).		
FT	CONFLICT	609	R -> G (IN REF. 2).		
FT	CONFLICT	727	I -> F (IN REF. 2).		
FT	CONFLICT	783	G -> S (IN REF. 2).		
FT	CONFLICT	842	E -> V (IN REF. 2).		
FT	CONFLICT	1007	I -> V (IN REF. 2).		
SO	SEQUENCE	1213 AA;	135484 MW;	DA4AE7C9E0F6ACD CRC64;	

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OY      115 PTEKEKOSGNLPGGFNFNFTEPGQRISFPFM-ELLEKN--SNIRA----- 159
Db      349 PTLKMY-QCGVREMAIEL-----FKFVWEIYAEVAGNVAAARWBERGDERI 398

OY      160 -----STDJGRCAEFPAKTVAMDKNKKATKTRYPV-----YDSK 195
Db      399 WDILEVEIKHEHVLINRA-PTLHRLGIOAFEBVLID--GKALRL--HPLVCAYNADPFQDQ 455

OY      196 RLCHILYVSMOLMEGKKCSVKGEPPDLTWPCFKPRKS---VTENHHLIYSAYV----- 247
Db      456 MAIHV-PLSEEAQAEKRLMLAAE-----HILNPKGKRPVYTPSQDMVLGNLYLTMEDA 508

OY      248 GENPDPAFISCKPNOALRGYRFGWKKRGCLDYTELTTVTIERVESKAQCWVKTFENDGVA 307
Db      509 GREGEGMI-FKDXDEAVMAYRNG-----YAHLSRV-----GIA 541

OY      308 SDQPHYPLTSSQSNWDMWPLHQSPHSGVGANNGYVYVDTTGBCKALSDOVPDCLV 367
Db      542 VDSMPKP-----WKD-----NQRK-----IMVTYVKILFNIDMP--- 573

OY      368 SDSAAVYTAAGSLSEETNPFIIPSPNPVTEPTEALQCTADKPDPSFGACDVQACRQ 427
Db      574 -----EDLPYLOEPPNNAULTGTGDKFLBEGQOIQEVIDRLDINVPFK 618

OY      428 KTSVCGS-----QIQTSTVDCTADEONEGCSNTALIGLAVGCVLLALLGGGCTFAK 480
Db      619 KN--LNNIIAETFKKFRRTETSAFLDRKLGDYVHSTAGLTVGIADIPIV----- 667

OY      481 RLDRNKG--VOAAHHEHFQSGRGARKKURPSDLMQOEAPSPFWDAENIRQ 529
Db      668 ---DNAEELIDAAHHEVEINKAFRGRLMTDDDKRYAVATTWRRAKKALEK 715

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ID	ERB2_HUMAN	STANDARD;	PRT; 1255 AA.
AC	P04626;		
DT	13-AUG-1987 (Rel. 05, Created)		
DT	13-AUG-1987 (Rel. 05, Last sequence update)		
DT	15-SEP-2003 (Rel. 42, Last annotation update)		
DE	Receptor protein-tyrosine kinase erbB-2 precursor (EC 2.7.1.112)		
DE	(p185erbB2) (NEU proto-oncogene) (C-erbB-2) (Tyrosine kinase-type cell		
DE	surface receptor HER2) (MNL 19).		
GN	ERBB2 OR HER2 OR NGL OR NEU.		
OS	Homo sapiens (Human).		
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
OX	NCBI_TaxID=9606;		
RN	[1]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=66118663; PubMed=3003577;		
RA	Yamamoto T., Ikwa S., Akiyama T., Semba K., Nomura N., Miyajima N.,		
RA	Saito T., Toyoshima K.;		
RT	"Similarity of protein encoded by the human c-erb-B-2 gene to		
RT	epidermal growth factor receptor.";		
RL	Nature 319:230-234(1986).		
RN	[2]		
RP	SEQUENCE FROM N.A.		
RX	MEDLINE=66070181; PubMed=2999974;		
RA	Coussens L., Yang-Feng T.L., Liao Y.C., Chen E., Gray A.,		
RA	McGrath J., Seeburg P.H., Libermann T.A., Schlessinger J.,		
RA	Francie U., Levinson A., Ullrich A.;		
RT	"Tyrosine kinase receptor with extensive homology to EGF receptor		
RT	shares chromosomal location with neu oncogene.";		
RL	Science 230:1133-1139(1985).		
RN	[3]		
RP	SEQUENCE OF 737-1031 FROM N.A.		
RX	MEDLINE=66016729; PubMed=2995967;		
RA	Semba K., Kamata N., Toyoshima K., Yamamoto T.;		
RT	"A v-erbB-related protooncogene, c-erbB-2, is distinct from the		
RT	c-erbB-1/epidermal growth factor-receptor gene and is amplified in a		
RL	human salivary gland adenocarcinoma.";		
	Proc. Natl. Acad. Sci. U.S.A. 82:6497-6501(1985).		

[4]
 RP VARIANTS VAL-654 AND VAL-655.
 RX MEDLINE=93194196; PubMed=8095488;
 RA Ehsani A., Low J., Wallace R.B., Wu A.M.;
 RT "Characterization of a new allele of the human ERBB2 gene by allele-
 specific competition hybridization.";
 RL Genomics 15:426-429(1993).
 CC -1- FUNCTION: Essential component of a neuoregulin-receptor complex,
 although neuregulins do not interact with it alone. GP30 is a
 potential ligand for this receptor. Not activated by EGF, TGF-
 alpha and amphiregulin.
 CC -1- CATALYTIC ACTIVITY: ATP + a protein tyrosine = ADP + protein
 tyrosine phosphate.
 CC -1- SUBUNIT: Heterodimer with each of the other ERBB receptors
 (Potential). Interacts with PRKCAP (By similarity).
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- PTM: Ligand-binding increases phosphorylation on tyrosine
 residues (By similarity).
 CC -1- POLYMORPHISM: There are four alleles due to the variations in
 positions 654 and 655. Allele B1 (654-Ile-Ile-655) has a frequency
 of 0.782; allele B2 (654-Ile-Val-655) has a frequency of 0.206;
 allele B3 (654-Val-Val-655) has a frequency of 0.012.
 CC -1- SIMILARITY: BELONGS TO THE EGF RECEPTOR FAMILY.
 CC -----
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 or send an email to license@ebi.ac.uk).
 CC -----
 DR EMBL, M11767; AAA35808.1; JOINED.
 DR EMBL, M11761; AAA35808.1; JOINED.
 DR EMBL, M11763; AAA35808.1; JOINED.
 DR EMBL, M11764; AAA35808.1; JOINED.
 DR EMBL, M11765; AAA35808.1; JOINED.
 DR EMBL, M11766; AAA35808.1; JOINED.
 DR EMBL, M11730; AAA35493.1; JOINED.
 DR EMBL, M12036; AAA35978.1; JOINED.
 DR EMBL, X03363; CAA27060.1; JOINED.
 DR PIR, A24571; A24571.
 DR PDB, 1N82; 18-FEB-03.
 DR PDB, 1QR1; 01-JAN-00.
 DR Gene: HGNC:3430; ERBB2.
 DR MIM, 164870; ERBB2.
 DR GO, GO:0005012; F:Neu/ErbB-2 receptor activity; TAS.
 DR GO, GO:0004716; F:receptor signaling protein tyrosine kinase . .; TAS.
 DR GO, GO:0008283; P:cell proliferation; TAS.
 DR GO, GO:0007048; P:oncogenesis; TAS.
 DR GO, GO:0006470; P:protein amino acid dephosphorylation; TAS.
 DR GO, GO:0006466; P:protein amino acid phosphorylation; TAS.
 DR InterPro: IPR000494; EGFR_L_domain.
 DR InterPro: IPR006211; Furin-like.
 DR InterPro: IPR006212; Furin repeat.
 DR InterPro: IPR000719; Prot_Kinase.
 DR InterPro: IPR001245; Tyr_Kinase.
 DR InterPro: IPR004019; YLP_motif.
 DR Pfam, PF00757; Furin-like; 1.
 DR Pfam, PF00669; pkinase; 1.
 DR Pfam, PF01030; Recep_L_domain; 2.
 DR Pfam, PF02757; YLP; 2.
 DR PRINTS: PR00109; TYRKINASE.
 DR PRODOM: PD000001; Prot_Kinase; 1.
 DR SMART, SM00261; FU; 4.
 DR SMART, SM00219; TYRKIN; 1.
 DR PROSITE, PS00107; PROTEIN KINASE ATP; 1.
 DR PROSITE, PS00109; PROTEIN KINASE TYR; 1.
 DR PROSITE, PS00011; PROTEIN KINASE_DOM; 1.
 KW Transmembrane, Glycoprotein, Multigene family, Receptor, Signal,
 Transferrin, Tyrosine-protein kinase, ATP-binding, Phosphorylation,
 Polymorphism, 3D-structure.

FT	SIGNAL	1	21	POTENTIAL.
FT	CHAIN	22	1255	RECEPTOR PROTEIN-TYROSINE KINASE ERBB-2.
FT	DOMAIN	22	1255	EXTRACELLULAR (POTENTIAL).
FT	TRANSMEM	653	675	POTENTIAL.
FT	DOMAIN	676	1255	CYTOPLASMIC (POTENTIAL).
FT	DOMAIN	720	987	PROTEIN KINASE.
FT	NP_BIND	726	734	ATP (BY SIMILARITY).
FT	BINDING	753	753	ATP (BY SIMILARITY).
FT	ACT_SITE	845	845	BY SIMILARITY.
FT	DISULFID	195	204	BY SIMILARITY.
FT	DISULFID	199	212	BY SIMILARITY.
FT	DISULFID	220	227	BY SIMILARITY.
FT	DISULFID	224	235	BY SIMILARITY.
FT	DISULFID	236	244	BY SIMILARITY.
FT	DISULFID	240	252	BY SIMILARITY.
FT	DISULFID	255	264	BY SIMILARITY.
FT	DISULFID	268	295	BY SIMILARITY.
FT	DISULFID	299	311	BY SIMILARITY.
FT	DISULFID	315	331	BY SIMILARITY.
FT	DISULFID	334	338	BY SIMILARITY.
FT	DISULFID	511	520	BY SIMILARITY.
FT	DISULFID	515	528	BY SIMILARITY.
FT	DISULFID	531	540	BY SIMILARITY.
FT	DISULFID	544	560	BY SIMILARITY.
FT	DISULFID	563	576	BY SIMILARITY.
FT	DISULFID	567	584	BY SIMILARITY.
FT	DISULFID	587	596	BY SIMILARITY.
FT	DISULFID	600	623	BY SIMILARITY.
FT	DISULFID	626	634	BY SIMILARITY.
FT	DISULFID	630	642	BY SIMILARITY.
FT	MOD_RES	1139	1139	PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT	MOD_RES	1248	1248	PHOSPHORYLATION (AUTO-) (BY SIMILARITY).
FT	CARBOHYD	68	68	N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHYD	124	124	N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHYD	187	187	N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHYD	259	259	N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHYD	530	530	N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHYD	571	571	N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	CARBOHYD	629	629	N-LINKED (GLCNAC . . .) (POTENTIAL).
FT	VARIANT	654	654	I -> V (IN DBSNP:1801201).
FT	VARIANT	655	655	/FTID=VAR_004077.
FT	VARIANT	655	655	I -> V (IN DBSNP:1801200).
FT	CONFLICT	1170	1170	/FTID=VAR_004078.
FT	CONFLICT	1170	1170	P -> A (IN REF. 2).
FT	SEQUENCE	1255 AA; 137909 MW; 39E9DPA04DC962 CRC64;		

Query Match 3.64; Score 104; DB 1; Length 1255;
 Best Local Similarity 22.5%; Pred. No. 6.3;
 Matches 108; Conservative 43; Mismatches 174; Indels 156; Gaps 27;

QY	81	LYRPPAGLCPIWKGHIEIQDRLPYRNNFIEDVPTKEYQSGNPJLPG--FNINPVT	137
DB	256	LHFNHSGIC-----ELHCPALVTYNTDFESMPN-----PEGYTFGASCVT	297
QY	138	PSGORISPPFPMELKSNINIKASTDLGRCAEFA---FKTVAMDKNKATKYRYPFYVDS	193
DB	298	AC-----PKNYL-----STVGSCTLVGLLHNQGVYAEAGTCRCEKSCSPCA---	339
QY	194	KKRLCH-----ILVSKQLMEKKYC-----SYKEBPDLTWYCFKPRK	232
DB	340	--RVCYGLGMEHLREVRVAVTSANIOEFAGCKIKFGSLAFLPESGDPASNTAALOPEQL	397
QY	233	SVTENHHLIYGSAVVGNSPDAF--ISKCPN-QALRG-----YRQGV-WKKGRC	276
DB	398	QVFETLEITGYLYTISMPDLSPLSVQNLQVIRGILHNQAVSLTLOGLGSLWGLRS	457
QY	277	LDVTELDVTVIERVESKACQVKTFFENDGVAADQ---PHTYPLTSQASWMDWMLPHQSD	332
DB	458	L--RELQGLALIHNNHLCFVH-----VPWDDLFPNPH-----QAL-----LITAN	498
QY	333	QPHSGGVGRNVGYFYVDTEE-----GKCALSDQ-----VPDCLVSSAASVYPAAG	379
DB	499	RFDECEVGEGLACHQLCARGHGCHGPGPTCCVNCQFLRGQCEVCECHVLQGLPREYVNAR	558

QY 380 SLSETPNFITPSNPSTPPTETALQCTAD-----KF 412
 DB 559 HCLPCHPE-COPFONSGVTCFGE-ADQCACAHYKDPFCVAPCSGVKPDLSYMPWKF 616
 QY 413 PDSFGACVQACKCKRKTSCVGGQIGSTSVDCPADSEONGSNTALAGLAVGVLLALL 472
 DB 617 PDEBAC--QPC---PINCTHSCVDLDDKXCPAEOR--ASPLTSLIS--AVGILLVVL 667
 QY 473 G 473
 DB 668 G 668
 RESULT 21
 FBN1_HUMAN STANDARD; PRT; 2871 AA.
 AC P35555;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Fibrillin 1 precursor.
 GN FBN1 OR FBN..
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RX MEDLINE=93372860; PubMed=8364578;
 RA Pereira L.V., D'Alessio M., Ramirez F., Lynch J.R., Sykes B.,
 RA Pangilinan T., Bonadio J.;
 RT "Genomic organization of the sequence coding for fibrillin, the
 RT defective gene product in Marfan syndrome."; Hum. Mol. Genet. 2:961-968(1993).
 RN (2)
 RP SEQUENCE OF 1-932 FROM N.A.
 RC TISSUE=Fibroblast, and Placenta;
 RX MEDLINE=94010947; PubMed=7691719;
 RA Corson G.M., Chalberg S.C., Dietz H.C., Charbonneau N.L., Sakai L.Y.;
 RT "Fibrillin binds calcium and is coded by CDNA that reveal a
 RT multidomain structure and alternatively spliced exons at the 5'
 RT end."; Genomics 17:476-484(1993).
 RN (3)
 RP SEQUENCE OF 899-2871 FROM N.A.
 RX MEDLINE=91304568; PubMed=1852207;
 RA Maslen C.L., Corson G.M., Maddox B.K., Glanville R.W., Sakai L.Y.;
 RT "Partial sequence of a candidate gene for the Marfan syndrome."; Nature 352:334-337(1991).
 RN (4)
 RP SEQUENCE OF 813-1313 FROM N.A.
 RX MEDLINE=91304567; PubMed=1852206;
 RA Lee B., Godfrey M., Vitale E., Hori H., Mattei M.-G., Sarfarazi M.,
 RA Tsipouras P., Ramirez F., Hollister D.W.;
 RT "Linkage of Marfan syndrome and a phenotypically related disorder to
 RT two different fibrillin genes."; Nature 352:330-334(1991).
 RN (5)
 RP CHARACTERIZATION.
 RX MEDLINE=91317849; PubMed=1860873;
 RA Sakai L.Y., Keene D.R., Glanville R.W., Bachinger H.P.;
 RT "Purification and partial characterization of fibrillin, a cysteine-
 RT rich structural component of connective tissue microfibrils."; J. Biol. Chem. 266:14763-14770(1991).
 RN (6)
 RP STRUCTURE BY NMR OF 2054-2125.
 RX MEDLINE=98031893; PubMed=9362480;
 RA Yuan X., Downing A.K., Knott V., Handford P.A.;
 RT "Solution structure of the transforming growth factor beta-binding
 RT protein-like module, a domain associated with matrix fibrils."; EMBO J. 16:6659-6666(1997).

RN (7)
 RP STRUCTURE BY NMR OF 2124-2205.
 RX MEDLINE=96144829; PubMed=856869;
 RA Knott V., Downing A.K., Cardy C.M., Handford P.A.;
 RT "Calcium binding properties of an epidermal growth factor-like domain
 RT pair from human fibrillin-1."; J. Mol. Biol. 255:22-27(1996).
 RN (8)
 RP STRUCTURE BY NMR OF 2124-2205.
 RX MEDLINE=96222301; PubMed=8653794;
 RA Downing A.K., Knott V., Werner J.M., Cardy C.M., Campbell I.D.,
 RA Handford P.A.;
 RT "Solution structure of a pair of calcium-binding epidermal growth
 RT factor-like domains: implications for the Marfan syndrome and other
 RT genetic disorders."; Cell 85:597-605(1996).
 RN (9)
 RP REVIEW ON MPS VARIANTS.
 RX MEDLINE=96174615; PubMed=8594563;
 RA Colod G., Beroud C., Soussi T., Junten C., Boileau C.;
 RT "Software and database for the analysis of mutations in the human
 RT FBN1 gene."; Nucleic Acids Res. 24:137-141(1996).
 RN (10)
 RP REVIEW ON MPS VARIANTS.
 RX MEDLINE=97169383; PubMed=9016526;
 RA Colod-Beroud G., Beroud C., Ades L., Black C., Boxer M., Brock D.J.,
 RA Godfrey M., Hayward C., Karttunen L., Milewicz D., Peltonen L.,
 RA Richards R.I., Wang W., Junten C., Boileau C.;
 RT "Marfan Database (second edition): software and database for the
 RT analysis of mutations in the human FBN1 gene."; Nucleic Acids Res. 25:147-150(1997).
 RN (11)
 RP REVIEW ON VARIANTS.
 RX MEDLINE=96062175; PubMed=9401003;
 RA Hayward C., Brock D.J.H.;
 RT "Fibrillin-1 mutations in Marfan syndrome and other type-1
 RT fibrillinopathies."; Hum. Mutat. 10:415-423(1997).
 RN (12)
 RP VARIANT MPS PRO-1137.
 RX MEDLINE=91304569; PubMed=1852208;
 RA Dietz H.C., Cutting G.R., Pyeritz R.E., Maslen C.L., Sakai L.Y.,
 RA Corson G.M., Puffenberger E.G., Hamosh A., Nanthakumar E.J.,
 RA Christin S.M., Stetten G., Meyers D.A., Francomano C.A.;
 RT "Marfan syndrome caused by a recurrent de novo missense mutation in
 RT the fibrillin gene."; Nature 352:337-339(1991).
 RN (13)
 RP VARIANTS MPS SER-1249; ARG-1663; SER-2221 AND SER-2307.
 RX MEDLINE=93250834; PubMed=1301946;
 RA Dietz H.C., Saraiva J.M., Pyeritz R.E., Cutting G.R., Francomano C.A.;
 RT "Clustering of fibrillin (FBN1) missense mutations in Marfan syndrome
 RT patients at cysteine residues in EGF-like domains."; Hum. Mutat. 1:366-374(1992).
 RN (14)
 RP VARIANT MPS SER-2307.
 RX MEDLINE=92235290; PubMed=1569206;
 RA Dietz H.C., Pyeritz R.E., Puffenberger E.G., Kendzior R.J. Jr.,
 RA Corson G.M., Maslen C.L., Sakai L.Y., Francomano C.A., Cutting G.R.;
 RT "Marfan phenotype variability in a family segregating a missense
 RT mutation in the epidermal growth factor-like motif of the fibrillin
 RT gene."; J. Clin. Invest. 89:1674-1680(1992).
 RN (15)
 RP VARIANTS MPS ILE-548 AND ALA-723.
 RX MEDLINE=94010946; PubMed=8406497;
 RA Dietz H.C., McIntosh I., Sakai L.Y., Corson G.M., Chalberg S.C.,
 RA Pyeritz R.E., Francomano C.A.;
 RT "Four novel FBN1 mutations: significance for mutant transcript level
 RT and EGF-like domain calcium binding in the pathogenesis of Marfan
 RT syndrome."; Genomics 17:468-475(1993).

RN [16]
 RP VARIANTS MFS SER-2144.
 RX MEDLINE=93278402; PubMed=8504310;
 RA Hewett D.R., Lynch J.R., Smith R., Sykes B.C.;
 RT "A novel fibrillin mutation in the Marfan syndrome which could
 RT disrupt calcium binding of the epidermal growth factor-like module."
 RL Hum. Mol. Genet. 2:475-477(1993).
 RN [17]
 RP VARIANTS MFS ARG-862; TYR-1117; PRO-1137 AND PHE-1589, AND VARIANT
 RP ALA-1148.
 RX MEDLINE=94108431; PubMed=8281141;
 RA Tyman K., Comau K., Pearson M., Milgenbus P., Levitt D., Gasner C.,
 RA Berg M.A., Miller D.C., Francke U.;
 RT "Mutation screening of complete fibrillin-1 coding sequence: report
 RT of five new mutations, including two in 8-cysteine domains."
 RL Hum. Mol. Genet. 2:1813-1821(1993).
 RN [18]
 RP VARIANTS MFS GLY-217 AND ARG-2627.
 RX MEDLINE=95067970; PubMed=7977366;
 RA Karttunen L., Raghunath M., Loengqvist L., Peltonen L.;
 RT "A compound-heterozygous Marfan patient: two defective fibrillin
 RT alleles result in a lethal phenotype."
 RL Am. J. Hum. Genet. 55:1083-1091(1994).
 RN [19]
 RP VARIANT EL LYS-2447.
 RX MEDLINE=94245249; PubMed=8188302;
 RA Longqvist L., Child A., Kainulainen K., Davidson R., Puhakka L.,
 RA Peltonen L.;
 RT "A novel mutation of the fibrillin gene causing ectopia lentis."
 RL Genomics 19:573-576(1994).
 RN [20]
 RP VARIANT MFS CYS-627.
 RX MEDLINE=94272487; PubMed=8004112;
 RA Hayward C., Rae A.L., Porteous M.E.M., Logie L.J., Brock L.J.;
 RT "Two novel mutations and a neutral polymorphism in EGR-1-like domains
 RT of the fibrillin gene (FBN1): SSCP screening of exons 15-21 in Marfan
 RT syndrome patients."
 RL Hum. Mol. Genet. 3:373-375(1994).
 RN [21]
 RP VARIANT MFS CYS-122.
 RX MEDLINE=94314977; PubMed=8040326;
 RA Stahl-Hallengren C., Ukkonen T., Kainulainen K., Kristofersson U.,
 RA Saxne T., Tornqvist K., Peltonen L.;
 RT "An extra cysteine in one of the non-calcium-binding epidermal growth
 RT factor-like motifs of the FBN1 polypeptide is connected to a novel
 RT variant of Marfan syndrome."
 RL J. Clin. Invest. 94:709-713(1994).
 RN [22]
 RP VARIANT MFS TYR-1223.
 RX MEDLINE=94351682; PubMed=8071963;
 RA Hewett D.R., Lynch J.R., Child A., Sykes B.C.;
 RT "A new missense mutation of fibrillin in a patient with Marfan
 RT syndrome."
 RL J. Med. Genet. 31:338-339(1994).
 RN [23]
 RP VARIANT MFS HIS-1170.
 RX MEDLINE=95174777; PubMed=7870075;
 RA Hayward C., Porteous M.E.M., Brock D.J.H.;
 RT "A novel mutation in the fibrillin gene (FBN1) in familial
 RT arachnodactyly."
 RL Mol. Cell. Probes 8:325-327(1994).
 RN [24]
 RP VARIANTS MFS GLY-217, ASN-1023, ARG-1074; TYR-1242; ARG-1513;
 RP GLU-2127; TRP-2151; LYS-2447 AND ARG-2511.
 RX MEDLINE=94184368; PubMed=8136837;
 RA Kainulainen K., Karttunen L., Puhakka L., Sakai L., Peltonen L.;
 RT "Mutations in the fibrillin gene responsible for dominant ectopia
 RT lentis and neonatal Marfan syndrome."
 RL Nat. Genet. 6:64-69(1994).
 RN [25]

Query Match 3.5%; Score 102; DB 1; Length 2871;
 Best Local Similarity 21.9%; Pred. No. 27;

Matches 114; Conservative 61; Mismatches 212; Indels 134; Gaps 32;
 QY 19 PASGLSSSTR--ESOTLASTSGNPFQAVNEMKTFM--ERFNLTHHSGIYVDLQD 74
 DB 2065 FEGGKCSSPKRRNSKQKCCALKEGMDPCLECPTEPDDAFROICRYGGIIVG-PDD 2123
 QY 75 KEVDGTLVREPAGLCPIWKHIELOQPD----RLPYNNFLVDVPEKEYKQSGNPLPG 129
 DB 2124 SAVDMECKEP-DVC---KHQCCINTDGSYRCPEFVYTLAGNECVDTDECSVGNPCGN 2178
 QY 130 GPNNL---FVTPSGQRISPPFMELLEKNISIKASTDGRCAEFKTVAMDKNKATKY 185
 DB 219 GTCRNVIGSFECTCEGEPBPMTCE-----DINECAQ-----NPLCAF 2219
 QY 186 RYFPYDSEKRLCHILVYSMQMEKKYCKYKGEPPDITWCFKPR--KSTENHILY 242
 DB 2220 RCVNTYSYECPCVGYV---LREDRRCKDEDECEBKADCTEKQMECKNLIGTYMCIC 2276
 QY 243 GSAYVENPDAFISKPNQALRGYRFGWKKGRCLD---YT-ELTDTVI-----ERVE 291
 DB 2277 GPGY-QRRPDG-BGVNDENECQTKPGICENGRCLNTRGSYTCEGNDGFASPNQDECLD 2333
 QY 292 SK-AQCWVKTEN--DGVASDQHTYPLTSQASNMWPLHSDQPHSGV----- 339
 DB 2334 NREGYCFTEVLQNMCOIGSSNRNRYTKSECCDGGRGWP-HCEICPQGTVAFAKCLCPH 2392
 QY 340 GRNRF-----YVDTGEGKCALSDQYD-----CLVDSAAVSYTAAGSL 381
 DB 2393 GR-GFMTNGADIDCKYIHVCNNGEC---VNDGSHYICICTGYTPDITGSCVDL 2445
 QY 382 SE-ETP--NFILPSNPSVTPPTETALQCTADK---PPDSFGACDVQACKRQKTS- 431
 DB 2446 NECNAQAPRCNCFICNT-----EGSYQSCSKGYILQDGRSCKLDLCATKQNHQ 2497
 QY 432 ----VGG-----QIQTSTVD---CTABEQNEGS 453
 DB 2498 FLCVNTIGFTCKCPGFTQHTSCIDNNECTSD-INLCSG 2537
 RESULT 22
 CYP_WHEAT STANDARD; PRT; 320 AA.
 AC P05151;
 DT 13-AUG-1987 (Rel. 05, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Apocytochrome f precursor.
 GN PRTA.
 OS Triticum aestivum (wheat).
 OC Chloroplast.
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooidae;
 OC Triticeae; Triticum.
 OX NCBI_TaxID=4565;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Willey D.L., Howe C.J., Aufret A.D., Bowman C.M., Dyer T.A.,
 RA Gray J.C.;
 RT "Location and nucleotide sequence of the gene for cytochrome f in
 RT wheat chloroplast DNA."
 RL Mol. Gen. Genet. 194:416-422(1984).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cn. Chinese Spring;
 RA Ogihara Y., Isono K., Kojima T., Endo A., Hanaoka M., Shina T.,
 RA Terachi T., Utsugi S., Murata M., Mori N., Takumi S., Ikeo K.,
 RA Gotohori T., Murai R., Murai K., Matsuo Y., Ohnishi Y., Tajiri H.,
 RA Tannewski K.;
 RT "Chinese spring wheat (Triticum aestivum L.) chloroplast genome:
 RT complete sequence and contig clones."
 RL Plant Mol. Biol. Rep. 18:243-253(2000).
 CC -1- FUNCTION: Translocates protons across the thylakoid membrane and
 CC transfers electrons from photosystem II to photosystem I. It

```

CC receives electrons from the Rieske iron-sulfur protein and passes
CC them to plastocyanin.
CC -1- SUBUNIT: Interacts with plastocyanin and Rieske iron-sulfur
CC protein (by similarity).
CC -1- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane. Membrane-
CC anchored (by similarity).
CC -1- SIMILARITY: Belongs to the cytochrome c family.
CC -----
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CC -----
CC EMBL, X00538; CA25213.1; -.
CC PIR, S07296; S07296.
CC HSRF, P36438; 1HCZ.
CC HAMAP, MF_00610; -.
CC InterPro: IPR002325; Apocyt_F.
CC InterPro: IPR000345; Cyt c heme bind.
CC Pfam: PF01333; Apocytochrome F; 1.
CC PRINTS: PR00610; CYTOCHROME_F.
CC PROSITE: PS00190; CYTOCHROME_C; 1.
CC Electrophoretic transfer; Heme; Chloroplast; Thylakoid; Photosynthesis;
CC Photosystem I; Photosystem II; Transmembrane; Signal.
CC SIGNAL 1 35
CC FT CHAIN 36 320 APOCYTOCHROME F.
CC FT TRANSMEM 286 305 POTENTIAL.
CC FT METAL 36 36 IRON (HEME AXIAL LIGAND) (VIA AMINO
CC BINDING 56 56 NITROGEN) (BY SIMILARITY).
CC FT BINDING 59 59 HEME (COVALENT) (BY SIMILARITY).
CC FT METAL 60 60 HEME (COVALENT) (BY SIMILARITY).
CC FT CONFLICT 291 294 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
CC FT CONFLICT 303 307 FFPA -> NVLE (IN REF. 2).
CC FT CONFLICT 303 307 LVKK -> MFSST (IN REF. 2).
CC SQ SEQUENCE 320 AA; 35363 MW; 721D2B3188552289 CRC64;

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Query Match 3.5%; Score 101.5; DB 1; Length 320;
 Best Local Similarity 21.8%; Pred. No. 1.6;
 Matches 69; Conservative 37; Mismatches 91; Indels 119; Gaps 19;

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QY 83 REPAGL-----CPWGHHELEQDPDLPRNNPLED-----VTEKEYKO-SGNPLP 128
DB 48 REATGRIVCANCHASKRPVIEVPOAV-----LPDVEAVLRIPYDQKQVLANKKK 101
QY 129 GGNLNL--FVTPSG-----QRISEPMELLEKNINIKASTDGRCAEFKFTVANDKNN 180
DB 102 GGLNVAVALLPFGFELAPPRDRISP---ELKEKIGNL-----AFQSYRFDKKN 146
QY 181 KATRYRPFVYDSKRLCHILYVSMOLMEGKYSVKGEPDPLTWYCFKPKRSVTENHH 240
DB 147 -----ILVIGP---VPGKTV-----SEIVFPLSDPRTKDDAHP 178
QY 241 IYGSAYVEN-----PDAFISKCPNOALRGYRFGWKK-----GRCLDTELTLD-- 284
DB 179 LKRPPIVGGNRRGQIYPPDG--SKSNNTVYATSTGIVRKILKEKGVEISITVDASDR 236
QY 285 TVIERVESKQKQWKPFPENDGVASDOPHTYPLTSSQSMNDMWFLHSDOPHSGGVGRNG 344
DB 237 QVTDIIPPEPELLVS--EGESIKLDO---PLTS-----NNVGGFQD--- 273
QY 345 FYVVDTTGEGCALSD 360
DB 274 -----GDAEIVLQD 282

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RESULT 23
 RPOC_STRP8
 ID RPOC_STRP8 STANDARD; PRT; 1213 AA.
 AC Q8P2T2;

```

DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE DNA-directed RNA polymerase beta' chain (EC 2.7.7.6) (Transcriptase
DE beta' chain) (RNA polymerase beta' subunit).
GN RPOC OR SPY18 0100.
OS Streptococcus pyogenes (serotype M18).
OC Bacteria; Firmicutes; Lactobacillales; Streptococcaceae;
OC Streptococcus
OC NCBI_TaxID=186103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MCA58232 / Serotype M18;
RC MEDLINE=21927593; PubMed=11917108;
RA Smoot J.C., Barbican K.D., Van Gompel J.J., Smoot L.M., Chaussee M.S.,
RA Sylva G.L., Sturdevant D.E., Rickielfe S.M., Porcella S.F.,
RA Parkins L.D., Beres S.B., Campbell D.S., Smith T.M., Zhang Q.,
RA Kapur V., Daly J.A., Yeasty L.G., Musser J.M.;
RT "Genome sequence and comparative microarray analysis of serotype M18
RT group A streptococcus strains associated with acute rheumatic fever
RT outbreaks."
RT Proc. Natl. Acad. Sci. U.S.A. 99:4668-4673(2002).
CC -1- FUNCTION: DNA-DEPENDENT RNA POLYMERASE CATALYZES THE TRANSCRIPTION
CC OF DNA INTO RNA USING THE FOUR RIBONUCLEOSIDE TRIPHOSPHATES AS
CC SUBSTRATES.
CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
CC (RNA) (N).
CC -1- SUBUNIT: THE ENZYME CONSISTS OF THE SIGMA CHAIN AND THE CORE
CC ENZYME WHICH IS COMPOSED OF 2 ALPHA CHAINS, 1 BETA CHAIN, AND 1
CC BETA' CHAIN.
CC -1- SIMILARITY: BELONGS TO THE RNA POLYMERASE BETA' CHAIN FAMILY.
CC -----
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CC -----
CC EMBL, AE009961; AAL96913.1; -.
CC InterPro: IPR000722; RNA_pol_A.
CC InterPro: IPR007080; RNA_pol_Rpb1_1.
CC InterPro: IPR007066; RNA_pol_Rpb1_3.
CC InterPro: IPR007083; RNA_pol_Rpb1_4.
CC InterPro: IPR007081; RNA_pol_Rpb1_5.
CC Pfam, PF04997; RNA_pol_Rpb1_1; 1.
CC Pfam, PF04997; RNA_pol_Rpb1_1; 1.
CC Pfam, PF04997; RNA_pol_Rpb1_2; 1.
CC Pfam, PF04983; RNA_pol_Rpb1_3; 1.
CC Pfam, PF05000; RNA_pol_Rpb1_4; 1.
CC Pfam, PF04998; RNA_pol_Rpb1_5; 1.
CC Transferrase; DNA-directed RNA polymerase; Transcription;
CC Complete proteome.
CC SQ SEQUENCE 1213 AA; 135305 MW; 0A9462ACA37E5DA CRC64;

```

Query Match 3.4%; Score 100; DB 1; Length 1213;
 Best Local Similarity 19.1%; Pred. No. 12;
 Matches 90; Conservative 55; Mismatches 166; Indels 160; Gaps 22;

```

QY 115 PTEKEYKSGNPLPGFNLNFTVPSGRIISPPM-ELLEKN--SNKA----- 159
DB 349 PTLKNV--QCGVREMAIEL-----FKPVMKEIYAKVAGNWKAKAKRVERGDERI 398
QY 160 -----STDGRCAEFKFTVAMKNNKATYRPFV-----YDSKK 195
DB 399 WDLEBEVIEKHPVLLNRAPTLARIQIOAFEPVLID--GALRL--HPLVCEAYNADPFDDQ 455
QY 196 RLCHILYVSMOLMEGKYSVKGEPDPLTWYCFKPKRS---VTENHHIYGSAYV----- 247
DB 456 MAIHV-PLISEAQAEARLMLAAE-----HILNPKDGKPVYTPSQDNLVLSGYIYLTMDA 508
QY 248 GENPDAFISKCPNOALRGYRFGWKKGRCLDYTELTDTVIERVESKQKQWTFPNDGVA 307

```

Db 509 GREGGMI.FKODKDEAVMAVRNG-----YAHLSRV-----GIA 541
 Qy 308 SDOPHTYPLTQASWMDWMLHQSDQPHSGVGRVYVDTTGGKCALSDOVPDCLV 367
 Db 542 VDSMWNK-----WKD-----SQRHK-----IMVTVGKILFNDIMP----- 573
 Qy 368 SDSAAVSYTAGSLSEETPNFIIPENPSVTPPTPTALQCTADKPPDSFGACVQACKRQ 427
 Db 574 -----EDLPYLQEPNNANULTGCTPDKXFLPEPQDIQEVIDGLEINVPFKK 618
 Qy 428 KTCSCVGS-----QIOSTSDCTADEQNEGCSNTALLAGLAVGVLLALLGGCCYPAK 480
 Db 619 KN--LGNIIATFKKFRFTETSAFLDRKLDGYHSTLAGLVGADIPIV----- 667
 Qy 481 RLDRNKG--VOAAHHEHEFOSDGRGARKRPSDLMGAEPSFMDAENNEIQ 529
 Db 668 ---DNKAEIIDAHHHVEINKAFRRGLMTDDDRVAVATTTWREAKEALEK 715

RESULT 24
 ID RRPL_MABVP STANDARD; PRT; 2331 AA.
 AC P15252;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE RNA-directed RNA polymerase (EC 2.7.7.46) (large structural protein)
 DE (L protein).
 GN Marburg virus (strain Popp).
 OS Viruses; ssRNA negative-strand viruses; Mononegavirales; Filoviridae;
 OC Marburg-like viruses.
 OX NCBI_TaxID=333728;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE=96028047; Pubmed=7487490;
 RA Butreyev A.A., Volichkov V.E., Blinov V.M., Dryga S.A., Netesov S.V.;
 RT "The complete nucleotide sequence of the Popp (1967) strain of Marburg
 virus: a comparison with the Musoke (1980) strain.";
 RL Arch. Virol. 140:1589-1600(1995)
 CC -1- FUNCTION: THIS PROTEIN IS PROBABLY A COMPONENT OF THE ACTIVE
 CC POLYMERASE. IT MAY FUNCTION IN RNA SYNTHESIS, CAPING, AS WELL AS
 CC METHYLATION OF CAPS, AND POLY(R) SYNTHESIS.
 CC -1- CATALYTIC ACTIVITY: N nucleoside triphosphate = N diphosphate +
 CC (RNA) (N).
 CC -1- SIMILARITY: PRIMARILY WITH THE N-TERMINAL HALF OF THE L PROTEINS
 CC OF RHABDOVIRUSES AND PARAMYXOVIRUSES.
 CC -----
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 CC -----
 DR EMBL: X68494; CA448508.1; -
 DR EMBL: Z29337; CA482542.1; -
 DR PIR: S44054; S44054.
 DR InterPro: IPR007098; RNA_pol_monon.
 DR InterPro: IPR001016; Viral_RNA_pol_L.
 DR Pfam: PF00946; Paramyx_RNA_pol_1.
 KW Transferase; RNA-directed RNA polymerase.
 SO SEQUENCE 2331 AA; 26635 MW; 7ED1D61D0E9F98B CRC64;

Query Match 3.4%; Score 99; DB 1; Length 2331;
 Best Local Similarity 22.8%; Pred. No. 35;
 Matches 68; Conservative 31; Mismatches 101; Indels 98; Gaps 14;
 Qy 4 VGVGVLLVAVDCITFASGLSSSTRSRSQTLASTSG-----NPGQANVEM--- 50
 Db 176 IGTDLTFLGDIADFTIFK--VEVKTIIRNAVSLQASKPGLRVVYRDONLTPLYLCDEPIVS 233

Qy 51 -----KTIMERFNL-----THHSGIYVDLQGDKEVDGTLREBPAGLCPI 91
 Db 234 VASVECFIMIDVIERNTMEICARAMLBSDDADYIPL-----DIVGELYNQ----- 282
 Qy 92 WKHIEIQDPRLPYRNFLLEDVPTKEKYKOSGNPLPGFNL-----NFV 136
 Db 283 -GDQIIM------YLED-----GFKLIGHLEPLCVSCIQTHGIF 315
 Qy 137 TP-----SGQRISPFMELLEKNINIKASTDLGCAEFAFTVAMDKNNKATKRYPRVY 191
 Db 316 TPGRYFQSORIESYBELCSLNWKFKISGKACDAQFITITL---QGKLTPOQYCELF 372
 Qy 192 DSKRLCH-ILYVSMQMEKKYC-SVKGEPDPLTWYCFKPRK-SYENHHLIYGSAY 246
 Db 373 SLQGHGHPVLYIYVDALDKYKGHQSXKILKPKMFEFFCYFKFIVAKNHHSGGSWY 430

RESULT 25
 ID SYE_PYRFU STANDARD; PRT; 572 AA.
 AC Q8U064;
 DT 15-SEP-2003 (Rel. 42, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Glutamy1-tRNA synthetase (EC 6.1.1.17) (Glutamate--tRNA ligase)
 DE (GluRS).
 GN GLTX OR P1753.
 OS Pyrococcus furiosus.
 OC Archaea; Euryarchaeota; Thermococci; Thermococcales; Thermococcaceae;
 OC Pyrococcus.
 OX NCBI_TaxID=2261;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Vc1 / DSM 3638 / ATCC 43587 / JCM 8422;
 RA Weiss R.B., Dunn D.M., Robb F.T., Brown J.R.;
 RT "The complete sequence of the Pyrococcus furiosus genome.";
 RL Submitted (FEB-2002) to the EMBL/Genbank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: ATP + L-glutamate + tRNA(Glu) = AMP +
 CC diphosphate + L-glutamy1-tRNA(Glu).
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: Belongs to class-I aminoacyl-tRNA synthetase family.
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 CC -----
 DR EMBL: AB010273; AAL81877.1; ALT_INTT.
 DR HANAP; MF_00022; -; 1.
 DR InterPro: IPR004526; GluX_arch.
 DR InterPro: IPR000924; Glu_tRNA-synt_1c.
 DR Pfam: PF00749; tRNA-synt_1c; 1.
 DR Pfam: PF03950; tRNA-synt_1c; 1.
 DR PRINTS: PR00987; TRNASYNTGLU.
 DR TIGRFAMs: TIGR00463; gltx_arch; 1.
 DR PROSITE: PS00178; AA_TRNA_LIGASE_1; FALSE NEG.
 KW Aminoacyl-tRNA synthetase; Protein biosynthesis; Ligase; ATP-binding;
 KW Complete proteome.
 FT SITE 107 "HIGH" REGION
 SO SEQUENCE 572 AA; 66562 MW; 5057509BC4FE9FC6 CRC64;

Query Match 3.4%; Score 98.5; DB 1; Length 572;
 Best Local Similarity 21.8%; Pred. No. 5.8;
 Matches 67; Conservative 32; Mismatches 113; Indels 95; Gaps 15;
 Qy 71 LGQDKYVDGTLXREPACLCPIWGNIF-----LQDPDLR--YRNKPLEDVTEKEK 121
 Db 32 LGENPE---LRKKARIVPIVKNVIEVNTLSLEQKGLLEIYEPYFMEGTKEKEK 87
 Qy 122 QSGNPLRGFNLFNVTPSGQRISPFMELLEKNINIKASTDLGCAEFAFTVAMDKNNK 181

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Db      88 KQLPFLPKKRGKQVVT-----RFAPNP-----DGAFLHG-----NMR 119
Qy      182 AF-KRRYFVYDSEK-----KELCHILYVSMQMGKKYCSVKGEPPDLTWYC 227
Db      120 AAILSEYVAKMYDGFILRFDDTPDKVKR-PELIFYDMII-----EDLEWLG 165
Qy      228 FPRRSVTEHHLLIYGSAYVGE---NPDAFISKCPNQAALRGVRFVWKKGRCLDYTELTD 284
Db      166 ITPDELIVASDRLEIYYKAAEELIKMGKAYCTCPDEFKLR---DGIACPHRD--- 218
Qy      285 TVIERVESKACQCVKTFEND-----GVASDPHTYPLTQASWMDWPLHOSDQPHS 336
Db      219 ---EPVEVGLERMKWMLNGEYREGSAVVRIKTDLHNPNPV-----RDMPALRIYDEPNH 270
Qy      337 GGVGNRY 343
Db      271 PRGNRY 277

RESULT 26
ACPH_PIG STANDARD; PRT; 732 AA.
ID ACPH_PIG 19305;
AC 01-NOV-1990 (Rel. 16, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DE 28-FEB-2003 (Rel. 41, Last annotation update)
DE Acylamino-acid-releasing enzyme (EC 3.4.19.1) (acyl-peptide hydrolase)
DE (APH) (acylaminoacyl-peptidase).
GN APEH.
OS Sus scrofa (pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxId=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=90110044; PubMed=2691504;
RA Mitter M., Aesada K., Uchimura Y., Kimizuka F., Kato I., Sakiyama F.,
RA Tsunawawa S.;
RT "The primary structure of porcine liver acylamino acid-releasing
RT enzyme deduced from cDNA sequences."
RL J. Biochem. 106:548-551(1989).
CC -1- FUNCTION: THIS ENZYME CATALYZES THE HYDROLYSIS OF THE AMINO-
CC TERMINAL PEPTIDE BOND OF AN N-ACETYLATED PEPTIDE TO GENERATE
CC AN N-ACETYLATED AA AND A PEPTIDE WITH A FREE AMINO-TERMINUS.
CC IT PREFERENTIALLY CLEAVES OFF AC-ALA, AC-MET AND AC-SER.
CC -1- CATALYTIC ACTIVITY: Acylaminoacyl-peptide + H(2)O = acylamino acid
CC + peptide.
CC -1- SUBUNIT: Homotrimer.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S9C.
CC
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CC
CC EMBL; D00524; BAA00411.1; -
CC DR MEROPS; S09.004; -
CC DR InterPro; IPR001375; Peptidase_S9.
CC DR InterPro; IPR002471; Pro_endopep_ser.
CC DR InterPro; IPR00379; Ser_ester_site.
CC DR Pfam; PF00326; Peptidase_S9; 1.
CC DR PROSITE; PS00708; PRO_ENDOPEP_SER; 1.
CC DR Hydrolase; Acetylation.
CC
CC MOD_RES 1 1
CC FT ACT_SITE 587 587 ACETYLATION.
CC FT ACT_SITE 675 675 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC FT ACT_SITE 707 707 CHARGE RELAY SYSTEM (BY SIMILARITY).
CC SQ SEQUENCE 732 AA; 81243 MW; 017BD40E049A604C CRC64;

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Query Match      3.4%; Score 98.5; DB 1; Length 732;
Best Local Similarity 20.9%; Pred. No. 8.1;
Matches 96; Conservative 56; Mismatches 176; Indels 131; Gaps 25;

Qy      81 LYREBAGLCPIWKGKIELQOPDRLEPYRNNPLEDVEPTEKEYQSGN-----PLPGGFN 132
Db      20 LSRQALSAACGLPEVTTQYQGR--YRTVHT--WTQADLRREMRIRFCROYLVPHDGS 75
Qy      133 LNFVTPSGQRISPFMEELLEKNSN-----IKASTDGRCAEPFAFKVANDKNNKARKY 185
Db      76 VFAGAPNNSVET-REGELLSRESPEGTWKAVALRAGGTGTAEKQFLV-WEKNNKLSF 133
Qy      186 -----RYPFTYDSEKRLC-----HILYVSMQMGKKYCSVKGEPPDLTWYCFKPR 231
Db      134 NLSALEKIGPYVEDDCFGCLSKSHETHLVYA-----DKK-----RPK 172
Qy      232 KSVTEHHLLIYGSAYVGNPDPAFISKCPNQAALRGVRFVWKKGRCLDYTELTVIER-- 289
Db      173 ---ASFQTKALDVTGSDDEWARTKKPDQAIKGPQF-----LFYEDGNNVSKST 221
Qy      290 -----VESKACQCVKTFEN--DGVASDQHTYPLTQASWMDWPLHOSDQPHSGV- 339
Db      222 PVLCLVDIESGN---ISVLEGVPESVSPGQAFWAGDTGVFVGW---HEPRLDGR 273
Qy      340 ---GRNYGFYVDTTGEKCALSDQVPCDLSAAYGTAGSLSETPNFIIPSNPSV 396
Db      274 PCTNRKSLIYVDLTG-GKCEL-----LDSEVAIV---SPRLSPQOCRIVILRFPSL 322
Qy      397 TPTPTETALQC-----TADKPPDSFGACDVQA--CKRQKTCVSGGQIOST 439
Db      323 VPHQ-----QCGQLCLDYMTYRTVSVDVIVPRQGE--DFSGIYSLPLGCMWSADSORV 376
Qy      440 SVDCTADEQ-----NECGSTVIALAGLAVGVLLAL 471
Db      377 VFDSPQSRQDLFAVDTQMGSVTSLTAGSGGSKWLLTI 415

RESULT 27
STHA_ECOLI
ID STHA_ECOLI STANDARD; PRT; 465 AA.
AC P27306;
DT 01-AUG-1992 (Rel. 23, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Soluble pyridine nucleotide transhydrogenase (BC 1.6.1.1) (STH)
DE (NAD(P) (+) transhydrogenase [B-specific]).
GN STHA OR STH OR UDHA OR B3962.
OS Escherichia coli.
OC Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
OC Enterobacteriaceae; Escherichia.
OX NCBI_TaxId=562;
RN [1]
RP SEQUENCE FROM N.A., SEQUENCE OF 1-26, AND CHARACTERIZATION.
RC MEDLINE=99121046; PubMed=9922271;
RA Boonstra B., French C.E., Wainwright I., Bruce N.C.;
RT "The udha gene of Escherichia coli encodes a soluble pyridine
RT nucleotide transhydrogenase."
RL J. Bacteriol. 181:1030-1034(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=K12 / MG1655;
RX MEDLINE=94089392; PubMed=8265357;
RA Blattner F.R., Burland V.D., Plunkett G. III, Sofia H.J.,
RA Daniels D.U.;
RT "Analysis of the Escherichia coli genome. IV. DNA sequence of the
RT region from 89.2 to 92.8 minutes."
RL Nucleic Acids Res. 21:5408-5417(1993).
RN [3]
RP REVISIONS.
RC STRAIN=K12 / MG1655;
RX MEDLINE=97426617; PubMed=9278503;
RA Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,

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RA Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
 RA Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
 RA Mau B., Shao Y.,
 RT "The complete genome sequence of *Escherichia coli* K-12.";
 RL Science 277:1453-1474 (1997).
 RN [4]
 RP SEQUENCE OF 1-345 FROM N.A.
 RC STRAIN=K12;
 RC MEDLINE=93077482; PubMed=1447162;
 RA Guatafason C., Marne S.R.;
 RA "Physical map of the oxyR-lrma region (minute 89.3) of the
 RT *Escherichia coli* chromosome";
 RL J. Bacteriol. 174:7878-7879(1992).
 RN [5]
 RP SEQUENCE OF 346-465 FROM N.A.
 RX MEDLINE=90066338; PubMed=2511419;
 RA Tao K., Makino K., Yonei S., Nakara A., Shinagawa H.,
 RT "Molecular cloning and nucleotide sequencing of oxyR, the positive
 RT regulatory gene of a regulon for an adaptive response to oxidative
 RT stress in *Escherichia coli*: homologies between OxyR protein and a
 RT family of bacterial activator proteins.";
 RL Mol. Gen. Genet. 218:371-376(1989).
 CC -1- FUNCTION: Conversion of NADPH, generated by peripheral catabolic
 CC pathways, to NADH, which can enter the respiratory chain for
 CC energy generation.
 CC -1- CATALYTIC ACTIVITY: NADPH + NAD(+) = NADP(+) + NADH.
 CC -1- COFACTOR: Binds 1 FAD per subunit.
 CC -1- SUBUNIT: HOMODIGOMER; PROBABLE HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: Cytoplasmic.
 CC -1- SIMILARITY: BELONGS TO THE PYRIDINE NUCLEOTIDE-DISULFIDE
 CC OXIDOREDUCTASES CLASS-I.
 CC -1- CAUTION: REF.4 SEQUENCE DIFFERS FROM THAT SHOWN DUE TO A
 CC FRAMESHIFT IN POSITION 14.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL; U00006; AAC43068.1; ALT_FRAME.
 DR EMBL; AE000470; AAC76944.1; ALT_INIT.
 DR EMBL; X65026; CAA46822.1; ALT_FRAME.
 DR EMBL; X16531; -; NOT_ANNOTATED_CDS.
 DR HSSP; P14218; ILPF.
 DR EcGene; EG1428; setA.
 DR HAMAP; MF_00247; -; 1.
 DR InterPro; IPR000759; Adnrxn_reductase.
 DR InterPro; IPR001327; FAD pyr redox.
 DR InterPro; IPR000815; Hg_reductase.
 DR InterPro; IPR000205; NAD_binding.
 DR InterPro; IPR001100; Pyr_redox.
 DR InterPro; IPR004099; Pyr_redox_dim.
 DR Pfam; PF00070; pyr_redox; 1.
 DR Pfam; PF02852; pyr_redox; 1.
 DR PRINTS; PR004419; ADXRDTASE.
 DR PRINTS; PR00368; FADPNR.
 DR PRINTS; PR00945; HGRDTASE.
 DR PRINTS; PR00411; PNRDRTASE.
 DR ProDom; PD000139; FAD pyr redox; 1.
 KW Oxidoreductase; Flavoprotein; FAD; NADP; NAD; Complete proteome.
 FT INT_MPT 0
 FT NP_BIND 7 37 FAD (ADP PART) (BY SIMILARITY).
 FT NP_BIND 300 310 FAD (FLAVIN PART) (BY SIMILARITY).
 FT CONFLICT 63 63 I -> L (IN REF. 4).
 FT CONFLICT 117 117 R -> L (IN REF. 4).
 SO SEQUENCE 465 AA; 51429 MW; 18EF2770B60D3C56 CRC64;
 Query Match 3.4%; Score 98; DB 1; Length 465;
 Best Local Similarity 20.3%; Pred. No. 4.8;
 Matches 87; Conservative 53; Mismatches 137; Indels 152; Gaps 21;

QY 150 LLEKNSNIKASTDGLRCAEFAKTV---AMDKNKATKRYPFVYDSKRLCHIL----- 201
 DB 62 IIFRNQ-PLVSDSRLLRSFADILNADVINOQTRMGGF---ERNHCILQGNAR 117
 QY 202 YV-----SMQMEGKCYCVKGEPP-----DLTWCFKPKSVTENH----- 239
 DB 118 FVDEHTLALDPPDSVETLTAEKEFVIACGSRPHYPPTVDFTPHRIYDSDSLMSHHEPRH 177
 QY 240 -LIYGAAYG-----ENPAFISKCPNOLRGYRFGWKKGRCLD 278
 DB 178 VLIYAGVIGGEYASIFRGMDVKVDLINTRRLLAFIDQEMSDSL-SYHF--MNSGVIR 234
 QY 279 YTE-----LTDVIERVES---KAQCWV-----KTFENDGVASDOPHTYPL 316
 DB 235 HNEVEKIEGGDDGVIMHLNKSCKRLKADCLLYANGRTGNTSLALQNLGLETDSGQGLV 294
 QY 317 TSQASMDWMPHLQSDPHSGVGRNFGFYVDTTG--EGKCALSDQVDPCLVSDSAVS 374
 DB 295 NS-----MYOTAQHVAVAGVDVIGPISLAAYDQGR-----IAQALVK 334
 QY 375 YTAGSLSEERN--FIIPSNPSTPTPTPTALQCTADKFPDSGACDVOACKQKTSV 432
 DB 335 GEATRAHLIEDPTGIYITPEISV---GKTEQLTAKVPEYVGRQFKLAR----- 384
 QY 433 GGOIGSTSVDCDADEQNECGSNTALLIAGVGLL-----ALLGGCYFAKRLDRNK 486
 DB 385 -----AOYGMNVGTLKILFHRTKEILGHC----- 412
 QY 487 GVQAHHHEH 495
 DB 413 GERAAEIIH 421
 RESULT 28
 ID APC RAT STANDARD; PRT; 2842 AA.
 AC P70478;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Adenomatous polyposis coli protein (APC protein).
 GN APC.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Fischer 344/N; TISSUE=Brain;
 RX MEDLINE=96116966; PubMed=8563176;
 RA Toyota M., Ushijima T., Kakiuchi H., Watanabe M., Imai K., Yachi A.,
 RA Sugimura T., Nagao M.;
 RT "cDNA cloning of the rat APC gene and assignment to chromosome 18.";
 RL Mamm. Genome 6:746-748(1995).
 RN [2]
 RP MUTAGENESIS.
 RC STRAIN=Sprague-Dawley, and Fischer 344/N;
 RX MEDLINE=95148647; PubMed=7846077;
 RA Kakiuchi H., Watanabe M., Ushijima T., Toyota M., Imai K.,
 RA Weisburger J.H., Sugimura T., Nagao M.;
 RT "Specific 5'-GGGA-3'-->5'-GGA-3' mutation of the APC gene in rat colon
 RT tumors induced by 2-amino-1-methyl-6-phenylimidazo[4,5-b]pyridine.";
 RL Proc. Natl. Acad. Sci. U.S.A. 92:910-914(1995).
 CC -1- FUNCTION: Tumor suppressor. Promotes rapid degradation of CTNNB1
 CC and participates in Wnt signaling. APC activity is correlated with
 CC its phosphorylation state (By similarity).
 CC -1- SUBUNIT: Forms homooligomers. Associates with catenins. Binds
 CC actin (By similarity).
 CC -1- PTM: PHOSPHORYLATED BY GSK-3B (BY SIMILARITY).
 CC -1- SIMILARITY: Contains 7 ARM repeats.
 CC -----
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DR EMBL: D38629; BAA07609.1; -
 DR HSP: Q02248; 3BCT.
 DR InterPro: IPR000225; Armadillo.
 DR Pfam: PF00514; Armadillo_seg. 4.
 DR SMART: SM00185; ARM; 5.
 DR PROSITE: PS00176; ARM_REPEAT; 1.
 KW Mut signaling pathway; Anti-oncogene; Phosphorylation; Coiled coil;
 KM Repeat.
 FT DOMAIN 1 728 LEU-RICH.
 FT DOMAIN 1 62 COILED COIL (POTENTIAL).
 FT DOMAIN 125 260 COILED COIL (POTENTIAL).
 FT REPEAT 451 493 ARM 1.
 FT REPEAT 503 545 ARM 2.
 FT REPEAT 546 589 ARM 3.
 FT REPEAT 590 636 ARM 4.
 FT REPEAT 637 681 ARM 5.
 FT REPEAT 682 723 ARM 6.
 FT REPEAT 724 765 ARM 7.
 FT DOMAIN 739 2831 SER-RICH.
 FT DOMAIN 1130 1155 ASP/GLU-RICH (ACIDIC).
 FT DOMAIN 1556 1575 ASP/GLU-RICH (ACIDIC).
 FT DOMAIN 1864 1891 HIGHLY CHARGED.
 FT MUTAGEN 523 C->R: IN AN IQ-INDUCED COLON TUMOR.
 SQ SEQUENCE 2842 AA; 310530 MW; 3CB3E8A8A34E8F47 CRC64;

Query Match 3.4%; Score 98; DB 1; Length 2842;
 Best Local Similarity 19.4%; Pred. No. 54;

Match 110; Conservative 68; Mismatches 212; Indels 178; Gaps 25;

QY 20 ASGLSSSTRSRSQTLASTSGNPFQANVEMKTFMERFNL-----THHQSG-----LY 68
 DB 1652 AHSLSLUTIESPNEIAA---GDGVASVOSGEFEKRDITPIEGRTDAQNGKSSIAI 1708
 QY 69 VDLGQDKEVDGTLVRE---PAGLCPTWGHIELOQDRLPYRNPFIEDVPTKEKYQ 122
 DB 1709 PLLDGSKAEEGDILAEICINSALPKG-----RSHKFFRYKIMDQVQASMTS 1755
 QY 123 SGNPLPGFNLPVVTSGQR---ISPFMEL-----LEKNSIKAS-----TDLGR 166
 DB 1756 SGT-----NKQIDTKKKKPKPSVPRKMPQNTETRTVRKNTDSKVNVTEETFSNKKDS 1809
 QY 167 AERAFKTVAMDKNKK---ATKYRYPVYVDSKRLCHILVYSQMLGKKYCSVKCEPD 222
 DB 1810 KKGSLKNNKRDNDKLPDNEDRARGFTDPSPHH-----YAPIETGP-- 1851
 QY 223 LTMVCKPKRSVTEHHLYGSAVYGENPDATISKENQALRGYRGWKKGRCLDYTEL 282
 DB 1852 ---YCSFNRDSTL-----SLIDPDDDDVDLSR-EKALEKRGKSKDSEAVTCHTBP 1898
 QY 283 TDIVIRVSKQKQCMWTFENOS---VASDQHTPLTSQAQWNNMWPLHQSDOPHSG 338
 DB 1899 SSS--OQSAKKAQASTHPRNRPSPKPLQEP--TPQSK-----DVDRG-- 1942
 QY 339 VGRNYPFYVDTTGEGKCALSDQVPCLVSDSAVSTAAGLS-----EET-- 385
 DB 1943 -----AATDKLQNFALIENTPVCFSSNSSLSLSLDVQENNNNEEFG 1984
 QY 386 -PNFIIIPSPSVTPPETALQCTADKFPDSFACVQAKCKQKTSVGGQISTVDC 444
 DB 1985 PVKDAEPANAQCGPKRPQ---ASGYAPKSFVIEDTPVCFSHNS-----LSLSIDSE 2034
 QY 445 ADEQNECGSNTALNAGLAVGVLLALLGGCCFAKRLDRNKGQVAHHEHESQDRGAR 504
 DB 2035 DDLIRRC-----ISSAMFKKRRPSRLKG-----EGEQSPKRYG 2068
 QY 505 KKRPSDLMQEAEPSPWDEAENIEQDGE 532

DB 2069 SVLAEDTLDDKDIQRPSEHGLSPDSE 2096

RESULT 29
 ID FBN1_MOUSE STANDARD; PRT; 2871 AA.
 AC 061554; 060826;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE Fibrillin 1 precursor.
 GN FBN1 OR FBN-1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95130561; PubMed=7829516;
 RA Yin W., Germiller J., Sanguinetti C., Smiley E., Panglinnan T.,
 RA Pereira L., Ramirez F., Bonadio J.;
 RT "Primary structure and developmental expression of Fbn-1, the mouse
 RT fibrillin gene.";
 RL J. Biol. Chem. 270:1798-1806(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CD-1; TISSUE=Kidney;
 RA Ota K., Kumar A., Wada J., Liu Z., Kanwar Y.S.;
 RL Submitted (Apr-1995) to the EMBL/Genbank/DBJ databases.
 CC -1- FUNCTION: STRUCTURAL COMPONENT OF CONNECTIVE TISSUE MICROFIBRILS
 CC THAT BINDS CALCIUM. FIBRILLIN-1-CONTAINING MICROFIBRILS PROVIDE
 CC -1- LONG-TERM FORCE BEARING STRUCTURAL SUPPORT.
 CC -1- PTM: FORMS INTERMOLECULAR DISULFIDE BONDS EITHER WITH OTHER
 CC FIBRILLIN-1 MOLECULES OR WITH OTHER COMPONENTS OF THE
 CC MICROFIBRILS (BY SIMILARITY).
 CC -1- SIMILARITY: Contains 47 EGF-like domains.
 CC -1- SIMILARITY: Contains 7 TGF-beta binding protein (TGFBP) domains.
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DR EMBL: U29454; AAA56840.1; -
 DR EMBL: U22493; AAA64217.1; -
 DR PIR: A55624; A55624.
 DR HSP: P35555; IABJ.
 DR MGI: MGI:95489; Fbn1.
 DR InterPro: IPR000152; Asx hydroxyl.
 DR InterPro: IPR001881; EGF_Ca.
 DR InterPro: IPR006209; EGF_Like.
 DR InterPro: IPR002212; Fibril1-aseoc.
 DR Pfam: PF00608; EGF; 46.
 DR Pfam: PF00683; TB; 9.
 DR SMART: SM00179; EGF_CA; 42.
 DR PROSITE: PS00010; ASX_HYDROXYL; 43.
 DR PROSITE: PS00022; EGF_1; 2.
 DR PROSITE: PS01186; EGF_2; 38.
 DR PROSITE: PS01187; EGF_CA; 43.
 KW Extracellular matrix; Calcium-binding; Glycoprotein; EGF-like domain;
 KW Repeat; Signal; Multigene family.
 FT SIGNAL 1 27 POTENTIAL.
 FT CHAIN 28 2871 FIBRILLIN 1.
 FT DOMAIN 81 112 EGF-LIKE 1.
 FT DOMAIN 115 146 EGF-LIKE 2.
 FT DOMAIN 147 178 EGF-LIKE 3.
 FT DOMAIN 246 287 EGF-LIKE 4.
 FT DOMAIN 288 329 EGF-LIKE 5, CALCIUM-BINDING.
 FT DOMAIN 330 401 TGFBP 1.

FT	DOMAIN	402	446	PRO-RICH.
FT	DOMAIN	449	489	EGF-LIKE 6.
FT	DOMAIN	490	529	EGF-LIKE 7, CALCIUM-BINDING.
FT	DOMAIN	530	571	EGF-LIKE 8, CALCIUM-BINDING.
FT	DOMAIN	572	612	EGF-LIKE 9, CALCIUM-BINDING.
FT	DOMAIN	613	653	EGF-LIKE 10, CALCIUM-BINDING.
FT	DOMAIN	656	721	TGFBP 2.
FT	DOMAIN	723	764	EGF-LIKE 11, CALCIUM-BINDING.
FT	DOMAIN	765	806	EGF-LIKE 12, CALCIUM-BINDING.
FT	DOMAIN	807	846	EGF-LIKE 13, CALCIUM-BINDING.
FT	DOMAIN	910	951	EGF-LIKE 14, CALCIUM-BINDING.
FT	DOMAIN	952	1018	TGFBP 3.
FT	DOMAIN	1028	1069	EGF-LIKE 15, CALCIUM-BINDING.
FT	DOMAIN	1107	1112	EGF-LIKE 16, CALCIUM-BINDING.
FT	DOMAIN	1113	1154	EGF-LIKE 17, CALCIUM-BINDING.
FT	DOMAIN	1155	1196	EGF-LIKE 18, CALCIUM-BINDING.
FT	DOMAIN	1197	1237	EGF-LIKE 19, CALCIUM-BINDING.
FT	DOMAIN	1228	1279	EGF-LIKE 20, CALCIUM-BINDING.
FT	DOMAIN	1280	1321	EGF-LIKE 21, CALCIUM-BINDING.
FT	DOMAIN	1322	1362	EGF-LIKE 22, CALCIUM-BINDING.
FT	DOMAIN	1363	1403	EGF-LIKE 23, CALCIUM-BINDING.
FT	DOMAIN	1404	1445	EGF-LIKE 24, CALCIUM-BINDING.
FT	DOMAIN	1446	1486	EGF-LIKE 25, CALCIUM-BINDING.
FT	DOMAIN	1487	1527	EGF-LIKE 26, CALCIUM-BINDING.
FT	DOMAIN	1528	1569	TGFBP 4.
FT	DOMAIN	1606	1647	EGF-LIKE 27, CALCIUM-BINDING.
FT	DOMAIN	1648	1688	EGF-LIKE 28, CALCIUM-BINDING.
FT	DOMAIN	1689	1758	TGFBP 5.
FT	DOMAIN	1766	1807	EGF-LIKE 29, CALCIUM-BINDING.
FT	DOMAIN	1808	1848	EGF-LIKE 30, CALCIUM-BINDING.
FT	DOMAIN	1849	1890	EGF-LIKE 31, CALCIUM-BINDING.
FT	DOMAIN	1891	1929	EGF-LIKE 32, CALCIUM-BINDING.
FT	DOMAIN	1930	1972	EGF-LIKE 33, CALCIUM-BINDING.
FT	DOMAIN	1973	2012	EGF-LIKE 34, CALCIUM-BINDING.
FT	DOMAIN	2013	2054	EGF-LIKE 35, CALCIUM-BINDING.
FT	DOMAIN	2055	2121	TGFBP 6.
FT	DOMAIN	2127	2165	EGF-LIKE 36, CALCIUM-BINDING.
FT	DOMAIN	2166	2205	EGF-LIKE 37, CALCIUM-BINDING.
FT	DOMAIN	2206	2246	EGF-LIKE 38, CALCIUM-BINDING.
FT	DOMAIN	2247	2290	EGF-LIKE 39, CALCIUM-BINDING.
FT	DOMAIN	2291	2332	EGF-LIKE 40, CALCIUM-BINDING.
FT	DOMAIN	2333	2400	TGFBP 7.
FT	DOMAIN	2402	2443	EGF-LIKE 41, CALCIUM-BINDING.
FT	DOMAIN	2444	2484	EGF-LIKE 42, CALCIUM-BINDING.
FT	DOMAIN	2485	2523	EGF-LIKE 43, CALCIUM-BINDING.
FT	DOMAIN	2524	2566	EGF-LIKE 44, CALCIUM-BINDING.
FT	DOMAIN	2567	2606	EGF-LIKE 45, CALCIUM-BINDING.
FT	DOMAIN	2607	2647	EGF-LIKE 46, CALCIUM-BINDING.
FT	DOMAIN	2648	2687	EGF-LIKE 47, CALCIUM-BINDING.
FT	DISULFID	85	94	BY SIMILARITY.
FT	DISULFID	89	100	BY SIMILARITY.
FT	DISULFID	102	111	BY SIMILARITY.
FT	DISULFID	119	129	BY SIMILARITY.
FT	DISULFID	123	134	BY SIMILARITY.
FT	DISULFID	136	145	BY SIMILARITY.
FT	DISULFID	150	160	BY SIMILARITY.
FT	DISULFID	154	166	BY SIMILARITY.
FT	DISULFID	168	177	BY SIMILARITY.
FT	DISULFID	250	262	BY SIMILARITY.
FT	DISULFID	257	271	BY SIMILARITY.
FT	DISULFID	273	286	BY SIMILARITY.
FT	DISULFID	292	304	BY SIMILARITY.
FT	DISULFID	299	313	BY SIMILARITY.
FT	DISULFID	315	328	BY SIMILARITY.
FT	DISULFID	453	465	BY SIMILARITY.
FT	DISULFID	460	474	BY SIMILARITY.
FT	DISULFID	476	488	BY SIMILARITY.
FT	DISULFID	494	504	BY SIMILARITY.
FT	DISULFID	499	513	BY SIMILARITY.
FT	DISULFID	515	528	BY SIMILARITY.
FT	DISULFID	534	546	BY SIMILARITY.
FT	DISULFID	541	555	BY SIMILARITY.
FT	DISULFID	557	570	BY SIMILARITY.

FT	DISULFID	576	587	BY SIMILARITY.
FT	DISULFID	582	596	BY SIMILARITY.
FT	DISULFID	598	611	BY SIMILARITY.
FT	DISULFID	617	628	BY SIMILARITY.
FT	DISULFID	623	637	BY SIMILARITY.
FT	DISULFID	639	652	BY SIMILARITY.
FT	DISULFID	727	739	BY SIMILARITY.
FT	DISULFID	734	748	BY SIMILARITY.
FT	DISULFID	750	763	BY SIMILARITY.
FT	DISULFID	769	781	BY SIMILARITY.
FT	DISULFID	776	790	BY SIMILARITY.
FT	DISULFID	792	805	BY SIMILARITY.
FT	DISULFID	811	821	BY SIMILARITY.
FT	DISULFID	816	830	BY SIMILARITY.
FT	DISULFID	832	845	BY SIMILARITY.
FT	DISULFID	914	926	BY SIMILARITY.
FT	DISULFID	921	935	BY SIMILARITY.
FT	DISULFID	937	950	BY SIMILARITY.
FT	DISULFID	1032	1044	BY SIMILARITY.
FT	DISULFID	1039	1053	BY SIMILARITY.
FT	DISULFID	1055	1068	BY SIMILARITY.
FT	DISULFID	1074	1086	BY SIMILARITY.
FT	DISULFID	1081	1095	BY SIMILARITY.
FT	DISULFID	1097	1111	BY SIMILARITY.
FT	DISULFID	1117	1129	BY SIMILARITY.
FT	DISULFID	1124	1138	BY SIMILARITY.
FT	DISULFID	1140	1153	BY SIMILARITY.
FT	DISULFID	1159	1171	BY SIMILARITY.
FT	DISULFID	1166	1180	BY SIMILARITY.
FT	DISULFID	1182	1195	BY SIMILARITY.
FT	DISULFID	1201	1212	BY SIMILARITY.
FT	DISULFID	1208	1221	BY SIMILARITY.
FT	DISULFID	1223	1236	BY SIMILARITY.
FT	DISULFID	1242	1254	BY SIMILARITY.
FT	DISULFID	1249	1263	BY SIMILARITY.
FT	DISULFID	1265	1278	BY SIMILARITY.
FT	DISULFID	1284	1296	BY SIMILARITY.
FT	DISULFID	1291	1305	BY SIMILARITY.
FT	DISULFID	1307	1320	BY SIMILARITY.
FT	DISULFID	1326	1339	BY SIMILARITY.
FT	DISULFID	1333	1348	BY SIMILARITY.
FT	DISULFID	1350	1361	BY SIMILARITY.
FT	DISULFID	1367	1380	BY SIMILARITY.
FT	DISULFID	1374	1389	BY SIMILARITY.
FT	DISULFID	1391	1402	BY SIMILARITY.
FT	DISULFID	1408	1420	BY SIMILARITY.
FT	DISULFID	1415	1429	BY SIMILARITY.
FT	DISULFID	1431	1444	BY SIMILARITY.
FT	DISULFID	1450	1461	BY SIMILARITY.
FT	DISULFID	1456	1470	BY SIMILARITY.
FT	DISULFID	1472	1485	BY SIMILARITY.
FT	DISULFID	1491	1502	BY SIMILARITY.
FT	DISULFID	1497	1511	BY SIMILARITY.
FT	DISULFID	1513	1526	BY SIMILARITY.
FT	DISULFID	1610	1622	BY SIMILARITY.
FT	DISULFID	1617	1631	BY SIMILARITY.
FT	DISULFID	1633	1646	BY SIMILARITY.
FT	DISULFID	1652	1663	BY SIMILARITY.
FT	DISULFID	1658	1672	BY SIMILARITY.
FT	DISULFID	1674	1687	BY SIMILARITY.

Query Match 3.3% Score 97.5; DB 1; Length 2871;
Best Local Similarity 22.6%; Pred. No. 60; Indels 129; Gaps 29;
Matches 93; Conservative 51; Mismatches 139;

Qy	124	GNPLPGGFNIN----	FVTPSGQRISPPMELLEKNINIKASTDLCRCAPFAKTVMADKN	179
Db	2173	GNPCGNGTKCKVIGFECTCEGEPGMWTC-----	DINECAQ-----N	2213
Qy	180	NKARKRYPPFYDCKKLLCHLLYVSMQMECKKCSYKGPDPDLTWYCFKR--	KSATV	236
Db	2214	PLLCAFRCVNTYGSYECKCPGVV--LRDRRMCKDEBCAEKHKDCTEKQMECKNLI	G	2270

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OY 237 NHHLYGSAYVGENDPATISKCPNQLRGYRGVWKGRCLD-----YT-ELTD-----T 285
DB 2271 TYMCGIGPGY-ORRPGD---EGCIDNECOTKPGICENGLTLGSLYCECNDGTAPT 2327
OY 286 VIERVESK-AQCWVTFPEN---DGVASDPHTYPLTSGAS--WMDWPLHOSDOPHSGGV 339
DB 2338 QDECDNNEGVCFSEVFEMWCOIGSSNNRPVT---KSECCCVGGRGWLHCEICFEFETV 2384
OY 340 -----GRNYGF-----YYVDTGEGKALSDQVDP-----CLVDSAAV 373
DB 2385 AYKCLCPHGR--GFMTNGADVDECKVIHDVCRNGEC-----VNDRGSYHCLCKTGYTPDI 2437
OY 374 SYTAGSLSE-ETP---NFIIPSNDPVTPRPETALCTADKFPSPF-----GAC-DV 421
DB 2438 TETSCVDLNECQAPKPCNFCIKMT-----EGSYQSC--PNGYILQEDGRSCKDL 2486
OY 422 QACKROKTSK-----VGS-----QIQTSTVD---CTADEONEGGS 453
DB 2487 DECATKQNNCPFLCVNTIGFTCKCPKPGFTQHTHTACIDNNECTSD-INLCGS 2537

RESULT 30
NX1B RAT STANDARD; PRT; 468 AA.
AC 063373;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Neurexin 1-beta precursor (Neurexin I-beta).
GN NRXN1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_Taxid=10116;
[1]
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Brain;
RX MEDLINE=92320296; PubMed=1621094;
RA Uehkaryov Y.A., Petrenko A.G., Geppert M., Suedhof T.C.;
RT "Neurexins: synaptic cell surface proteins related to the alpha-
RL latrotoxin receptor and laminin.";
Science 257:50-56(1992).
[2]
RP SEQUENCE OF N-TERMINUS, AND O-GLYCOSYLATION.
RC TISSUE=Brain;
RX MEDLINE=94216308; PubMed=8163501;
RA Uehkaryov Y.A., Hata Y., Ichchenko K., Moomaw C., Afendis S.,
RT "Slaughter C.A., Suedhof T.C.;"
RT "Conserved domain structure of beta-neurexins. Unusual cleaved signal
sequences in receptor-like neuronal cell-surface proteins.";
J. Biol. Chem. 269:11987-11992(1994).
[3]
RP FUNCTION, AND INTERACTION WITH NEUROLIGIN 1.
RX MEDLINE=97467410; PubMed=9325340;
RA Nguyen T., Suedhof T.C.;
RT "Binding properties of neuroligin 1 and neurexin 1beta reveal function
RT as heterophilic cell adhesion molecules.";
J. Biol. Chem. 272:26032-26039(1997).
[4]
RP INTERACTION WITH NLGN1, NLGN2 AND NLGN3.
RX MEDLINE=96162010; PubMed=8576240;
RA Ichchenko K., Nguyen T., Suedhof T.C.;
RT "Structures, alternative splicing, and neurexin binding of multiple
RT neuroligins.";
J. Biol. Chem. 271:2676-2682(1996).
[5]
RP INTERACTION WITH CASK.
RX MEDLINE=96256685; PubMed=8786425;
RA Hata Y., Butz S., Suedhof T.C.;
RT "CASK: a novel dlg/PSD95 homolog with an N-terminal
RT calmodulin-dependent protein kinase domain identified by interaction
RT with neurexins.";
J. Neurosci. 16:2488-2494(1996).

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RN [6]
RP INTERACTION WITH ALPHA-LATROTOXIN.
RX MEDLINE=99211386; PubMed=10197529;
RA Sugita S., Khvochtchey M., Suedhof T.C.;
RT "Neurexins are functional alpha-latrotoxin receptors.";
RL Neuron 22:489-496(1999).
[7]
RP INTERACTION WITH ALPHA-DYSTROGLYCAN.
RX MEDLINE=21363578; PubMed=11470830;
RA Sugita S., Saito F., Tang J., Satz J., Campbell K., Suedhof T.C.;
RT "A stoichiometric complex of neurexins and dystroglycan in brain.";
RL J. Cell Biol. 154:435-445(2001).
[8]
RN X-RAY CRYSTALLOGRAPHY (2.6 ANGSTROMS) OF 47-302.
RX MEDLINE=99449307; PubMed=10520997;
RA Rudenko G., Nguyen T., Chellish Y., Suedhof T.C., Deisenhofer J.;
RT "The structure of the ligand-binding domain of neurexin Ibeta:
RT regulation of LNS domain function by alternative splicing.";
RL Cell 99:93-101(1999).
CC -1- FUNCTION: Neuronal cell surface protein that may be involved in
CC cell recognition and cell adhesion by forming intracellular
CC junctions through binding to neuroligins. May play a role in
CC formation or maintenance of synaptic junctions. May mediate
CC intracellular signaling.
CC -1- SUBUNIT: The cytoplasmic C-terminal region binds to CASK. Isoforms
CC Beta 4b bind neuroligins NLGN1, NLGN2 and NLGN3, alpha-
CC dystroglycan and alpha-latrotoxin.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative promoter;
CC Comment=A number of isoforms, alpha-type and beta-type (shown
CC here), are produced by use of alternative promoters. Beta-type
CC isoforms differ from alpha-type isoforms in their N-terminus;
CC Event=Alternative splicing; Named isoforms=4;
CC Comment=There is a combination of two alternatively spliced
CC domains at sites 4 and 5 which are shared with alpha isoforms
CC (AC Q63372) and seem to be used independently. Experimental
CC confirmation may be lacking for some isoforms;
CC Name=1; Synonyms=Beta 4A5A;
CC IsoId=Q63373-1; Sequence=Displayed;
CC Name=2; Synonyms=Beta 4A5B;
CC IsoId=Q63373-2; Sequence=VSP_003497;
CC Name=3; Synonyms=Beta 4B5A;
CC IsoId=Q63373-3; Sequence=VSP_003496;
CC Name=4; Synonyms=Beta 4B5B;
CC IsoId=Q63373-4; Sequence=VSP_003496, VSP_003497;
CC -1- TISSUE SPECIFICITY: BRAIN.
CC -1- PTM: Highly O-glycosylated and minor N-glycosylated.
CC -1- SIMILARITY: Contains 1 laminin G-like domain.
CC -1- SIMILARITY: BELONGS TO THE NEUREXIN FAMILY.
CC -----
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CC -----
CC EMBL; M96375; AAA41705.1; -.
CC PIR; B40228; B40228.
CC PDB; 1CAR; 28-SEP-99.
CC InterPro; IPR001791; Laminin G.
CC InterPro; IPR003585; Neurexin-like.
CC Pfam; PF00054; Laminin_G_1.
CC SMART; SM00294; 4.1m; 1.
CC DR PROSITE; PSS0025; LAM G DOMAIN; 1.
CC Signal; Transmembrane; Cell adhesion; Glycoprotein;
CC Alternative splicing; Alternative promoter usage; 3D-structure.
CC FT SIGNAL 1 46
CC CHAIN 47 468 NEUREXIN 1-BETA.
CC DOMAIN 47 391 EXTRACELLULAR (POTENTIAL).

```


DB 425 ---GLANPTRVGGEPPYPSAEVIRESSSTGTVVAAAALCILLYAMY--KTRN 479
 QY 484 RNKGVOAAHEHEFQSDRGARKRPDLMQEAEPFWDPAENIE-ODGETHV 535
 DB 480 RDEG---SYHVESRNYSISNAGSNQAVYKEQPSASANKKCKKEYTV 529

RESULT 33
 AD22_HUMAN STANDARD; PRT; 906 AA.
 AC Q9P0K1: Q75075; Q9P0K2; Q9U1A1; Q9UKK2;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE ADAM 22 precursor (A disintegrin and metalloproteinase domain 22)
 DE (Metalloproteinase-like, disintegrin-like, and cysteine-rich protein
 2) (Metalloproteinase-disintegrin ADAM22-3).
 GN ADAM22 OR MDC2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RX MEDLINE=20504287; PubMed=11050470;
 RA Harada T., Nishie A., Torigoe K., Ikezaki K., Shono T., Maehara Y.,
 RA Kuwano M., Wada M.;
 RT "The specific expression of three novel splice variant forms of human
 RT metalloproteinase-like disintegrin-like cysteine-rich protein 2 gene
 RT in brain tissues and gliomas."
 RL Jpn. J. Cancer Res. 91:1001-1006(2000).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORMS 3 AND 4).
 RC TISSUE=Brain;
 RX MEDLINE=98359734; PubMed=9693107;
 RA Sagane K., Ohya Y., Hasegawa Y., Tanaka I.;
 RT "Metalloproteinase-like, disintegrin-like, cysteine-rich proteins MDC2
 RT and MDC3: novel human cellular disintegrins highly expressed in the
 RT brain";
 RL Biochem. J. 334:93-98(1998).
 RN [3]
 RP SEQUENCE FROM N.A. (ISOFORM 5).
 RC TISSUE=Brain;
 RA Wada M., Torigoe K., Harada T., Kuwano M.;
 RT "Isolation and tissue specific expression of novel ADAM family from
 RT Tg21.1 region.";
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE OF 40-906 FROM N.A. (ISOFORM 1).
 RC TISSUE=Cerebellum;
 RX MEDLINE=99453762; PubMed=10524237;
 RA Polinder K., Nelson N., Dubose R.F., Black R.A., Cerretti D.P.;
 RT "The identification of seven metalloproteinase-disintegrin (ADAM)
 RT genes from genomic libraries.";
 RL Gene 237:61-70(1999).
 CC -1- FUNCTION: PROBABLE LIGAND FOR INTEGRIN IN THE BRAIN. THIS IS A NON
 CC CATALYTIC METALLOPROTEINASE-LIKE PROTEIN.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=5;
 CC Name=1; Synonyms=Epsilon;
 CC IsoId=Q9P0K1-1; Sequence=Displayed;
 CC Name=2; Synonyms=Delta;
 CC IsoId=Q9P0K1-2; Sequence=VSP_005482, VSP_005484;
 CC Name=3; Synonyms=Alpha;
 CC IsoId=Q9P0K1-3; Sequence=VSP_005483;
 CC Name=4; Synonyms=Beta;
 CC IsoId=Q9P0K1-4; Sequence=VSP_005482, VSP_005483;
 CC Name=5;
 CC IsoId=Q9P0K1-5; Sequence=VSP_005482;
 CC -1- TISSUE SPECIFICITY: HIGHLY EXPRESSED IN THE BRAIN. DETECTED SLIGHTLY
 CC OR NOT AT ALL IN OTHER TISSUES.

CC -1- PTM: THE PRECURSOR IS CLEAVED BY A FURIN ENDOPEPTIDASE (BY
 CC SIMILARITY).
 CC -1- SIMILARITY: Belongs to peptidase family M12B.
 CC -1- SIMILARITY: Contains 1 EGF-like domain.
 CC -1- SIMILARITY: Contains 1 disintegrin domain.
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 CC -----
 CC EMBL: AF153382; AAF73289.1; -
 CC EMBL: AF153381; AAF73288.1; -
 CC EMBL: AB009671; BAA32349.1; -
 CC EMBL: AB009671; BAA32350.1; -
 CC EMBL: AF073291; AAF22476.2; -
 CC EMBL: AF158637; AAD55251.1; -
 CC HSSP: P18619; 1FVL.
 CC MEROPS: M12.978; -
 CC Genew: H9NC:201; ADAM22.
 CC MIM: 603709; -
 CC GO: GO:0016021; C:integral to membrane; NAS.
 CC GO: GO:0005178; F:integrin binding activity; NAS.
 CC GO: GO:0007162; F:negative regulation of cell adhesion; NAS.
 CC InterPro: IPR006585; ADAM_cysteine.
 CC InterPro: IPR001762; Disintegrin.
 CC InterPro: IPR006209; EGF-like.
 CC InterPro: IPR002870; Pep_M12B_propep.
 CC InterPro: IPR001590; Reptolysin.
 CC InterPro: IPR006025; Zn_MTPepdse.
 CC Pfam: PF01562; Pep_M12B_propep; 1.
 CC Pfam: PF01421; Reptolysin; 1.
 CC PRINTS: PR00289; DISINTEGRIN.
 CC ProDom: PD000664; Disintegrin; 1.
 CC SMART: SMO0608; ACR; 1.
 CC SMART: SMO0050; DISIN; 1.
 CC PROSITE: PS50215; ADAM_MEROP; 1.
 CC PROSITE: PS00427; DISINTEGRIN_1; FALSE_NEG.
 CC PROSITE: PS50214; DISINTEGRIN_2; 1.
 CC PROSITE: PS00022; EGF 1; 1.
 CC PROSITE: PS01186; EGF 2; FALSE_NEG.
 CC PROSITE: PS00142; ZINC_PROTEASE; FALSE_NEG.
 CC Signal: Glycoprotein; Transmembrane; EGF-like domain;
 CC Alternative splicing.
 CC FT SIGNAL 1 25
 CC FT PROPEP 26 222
 CC FT CHAIN 223 906
 CC FT DOMAIN 223 736
 CC FT TRANSMEM 737 757
 CC FT DOMAIN 758 906
 CC FT DOMAIN 223 438
 CC FT DOMAIN 444 531
 CC FT DOMAIN 532 678
 CC FT DOMAIN 532 712
 CC FT DISULFID 349 433
 CC FT DISULFID 503 516
 CC FT DISULFID 679 694
 CC FT DISULFID 688 700
 CC FT DISULFID 702 711
 CC FT CARBOHYD 175 175
 CC FT CARBOHYD 519 519
 CC FT CARBOHYD 634 634
 CC FT CARBOHYD 675 675
 CC FT VARSPLIC 768 803
 CC FT
 CC FT VARSPLIC 860 906
 CC FT
 CC FT VARSPLIC 859 859
 CC
 CC /FTid=VSP_005482.
 CC Missing (in isoform 3 and isoform 4).
 CC /FTid=VSP_005483.
 CC E -> EYLNPFKRDYVAVKVEDVKNKTEPPYR (1n

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FT      isoform 2).
FT      /FTID=VSP_005484.
FT      P -> R (IN REF. 3 AND 4).
FT      CONFLICT      81
SQ      SEQUENCE      906 AA; 100432 MM; 265ECDD0FA6C088B CRC64;
Query Match      3.3%; Score 97; DB 1; Length 906;
Beet Local Similarity 19.9%; Pred No. 14;
Matches 111; Conservative 61; Mismatches 233; Indels 154; Gaps 25;

QY      18 IFASGLSSTRSRESQTLASTSGNPFQANVEMKTF-MEREN-----LTHHQSGITY 68
DB      56 IYRSGGDESRHDLATRVRGDLGGQLTHVQOAFQVDAFGTSFLDVLVNHDDLSSEY 115
QY      69 VDL-----GQDREV-----DGLTYRPP-----AGLCPIV--GKHILEQOPDL 104
DB      116 IERHIEHGKTYEVKGEHCYQGHIRGNPDSFVALSTGHLMGYDGNHTYLLIEPEE- 174
QY      105 PYRNNPLEDVPTEKEYKQ-----SGNPLPGGFNLNFPVPSGORISPPFELLEKNINIK 159
DB      175 --NDTTOEDFPHSHVYSKRLPEFSLDDLSEFOQVNTTSKFLIKRP----- 220
QY      160 STDIGRCFAEFKTYAMDKNNKATKYRPFVYDSKRLCHILVSMQMEGKKYCSVGK- 218
DB      221 -----KRSKRQLRRYPRNVEETKYIELMIVNDHLMFKKRLSVVHT 262
QY      219 -----EPPDL-----TW-----YCKPKRSYVENHILYGSAYVE 249
DB      263 NTYAKSVVAMADLYKQDKTRIVLVAMETWATDNKFAISENPLTLTREPMKRRDIFE 322
QY      250 NPDA-----FISKCPQALRGVFGVWKKGRCDYELTDVIERVESKAQCVKTF 301
DB      323 KSDAVHLESGQSPESRSGAAYIGGICSLKGGVNEPFTDLMTLAOSLA----- 375
QY      302 ENDGVASDOPHTYPLTSQASWMDWPELHOSDOPHSGSGVNGYFYVDVTTEGCKALSDQ 361
DB      376 HNIIGIISDKRL--ASGECKCEDTW-----SGCIMDGYVLPKFTQ--CNI-BE 421
QY      362 VPDCLVSDAAYSYTAAGLSLSE--ETPNFIIPSNVTPPTP-----ETALQCTAK 411
DB      422 YHDFLMSGGACLFNPKSKLLDPPECGNGFETGEECDGCTPEVCVLEBAECCCKKTLTQ 481
QY      412 FPD-SFGACDVQACKRQKTSVCVGQIGSTSVDTADE-----ONEGCSNTALAGLAVG 465
DB      482 DSGCSGLC-----CKCKCFQPKMTVREAVNDCDIFETGSGNSQCAPNHNKMDGISC 537
QY      466 VLLALLLGGCYFPAKRLDR 484.
DB      538 VQGIC-FGGRG---KTRDR 552

RESULT 34
NX1A RAT STANDARD; PRT; 1514 AA.
ID NX1A RAT 063372;
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE Neurexin 1-alpha precursor (Neurexin 1-alpha).
GN NRXN1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN 1
RP SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.
RC TISSUE=Brain;
RX MEDLINE=92330296; PubMed=1621094;
RA Ushkaryov Y.A., Petrenko A.G., Geppert M., Suedhof T.C.;
RT "Neurexins: synaptic cell surface proteins related to the alpha-
RL latrotoxin receptor and laminin.";
RN Science 257:50-56(1992).
RP PARTIAL SEQUENCE FROM N.A., AND ALTERNATIVE SPLICING.

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RX MEDLINE=95209856; PubMed=7695896;
RA Ullrich B., Ushkaryov Y.A., Suedhof T.C.;
RT "Cartography of neurexins: more than 1000 isoforms generated by
RT alternative splicing and expressed in distinct subsets of neurons.";
RN Neuron 14:497-507(1995).
RN [3]
RX SEQUENCE OF N-TERMINUS, AND INTERACTION WITH NEUREXOPHILINS 1 AND 3.
RP MEDLINE=99074239; PubMed=9856994;
RA Miesler M., Hammer R.E., Suedhof T.C.;
RT "Neurexophilin binding to alpha-neurexins. A single LNS domain
RT functions as an independently folding ligand-binding unit.";
RN J. Biol. Chem. 273:34716-34723(1998).
RN [4]
RX INTERACTION WITH CASK.
RP MEDLINE=96256685; PubMed=8786425;
RA Hata Y., Butz S., Suedhof T.C.;
RT "CASK: a novel dig/PSD95 homolog with an N-terminal
RT calmodulin-dependent protein kinase domain identified by interaction
RT with neurexins.";
RN J. Neurosci. 16:2488-2494(1996).
RN [5]
RX INTERACTION WITH ALPHA-LATROTOXIN.
RP MEDLINE=99211386; PubMed=10197529;
RA Sugita S., Khvocholev M., Suedhof T.C.;
RT "Neurexins are functional alpha-latrotoxin receptors.";
RN Neuron 22:489-496(1999).
RN [6]
RX INTERACTION WITH ALPHA-DYSTROGLYCAN.
RP MEDLINE=21363578; PubMed=11470830;
RA Sugita S., Saito F., Tang J., Satz J., Campbell K., Suedhof T.C.;
RT "A stoichiometric complex of neurexins and dystroglycan in brain.";
RL J. Cell Biol. 154:435-445(2001).
CC -1- FUNCTION: Neuronal cell surface protein that may be involved in
CC cell recognition and cell adhesion. May mediate intracellular
CC signaling.
CC -1- SUBUNIT: The cytoplasmic C-terminal region binds to CASK. Laminin
CC alpha-like domain 2 binds to neurexophilin 1 and 3. Isoforms alpha 2C
CC and alpha 4C bind to alpha-dystroglycan. Isoforms alpha 4C bind to
CC alpha-latrotoxin.
CC -1- SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -1- ALTERNATIVE PRODUCTS:
CC Event=Alternative promoter;
CC Comment=A number of isoforms, alpha-type (shown here) and
CC beta-type, are produced by use of alternative promoters.
CC Beta-type isoforms differ from alpha-type isoforms in their
CC N-terminus;
CC Event=Alternative splicing; Named isoforms=1;
CC Comment=At least 96 isoforms may be produced by alternative
CC splicing. There is a combination of five alternatively spliced
CC domains at sites 1 to 5, each consisting of modular sequences
CC (A-G) that seem to be used independently. For splice site 1
CC additional splice modules might be possible thus increasing the
CC number of possible isoforms. Beta-type isoforms (AC Q63373)
CC share the combination of two alternatively spliced domains at
CC sites 4 and 5;
CC Name=Alpha 1A2A3A4A5A;
CC IsoId=Q63372-1; Sequence=Displayed;
CC -1- TISSUE SPECIFICITY: Brain (neuronal synapse).
CC -1- PTM: N- and O-glycosylated (By similarity).
CC -1- MISCELLANEOUS: Alpha-latrotoxin competes with alpha-dystroglycan for
CC binding.
CC -1- SIMILARITY: Contains 6 laminin G-like domains.
CC -1- SIMILARITY: Contains 3 EGF-like domains.
CC -1- SIMILARITY: BELONGS TO THE NEUREXIN FAMILY.
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DR EMBL, M96374; AAA41704.1; -.
DR PIR, A40228; A40228.
DR HSSP, Q63373; 1C4R.
DR InterPro: IPR000152; Asx_hydroxyl.
DR InterPro: IPR006209; EGF_like.
DR InterPro: IPR006210; IEGF.
DR InterPro: IPR003585; Neurexin-like.
DR Pfam; PF00008; EGF_3.
DR Pfam; PF00054; laminin_G_6.
DR SMART; SM00284; 4.1m.I.
DR SMART; SM00181; EGF_3.
DR SMART; SM00282; LamG_5.
DR PROSITE; PS00010; ASX_HYDROXYL_1.
DR PROSITE; PS00022; EGF_1; FALSE_NEG.
DR PROSITE; PS01186; EGF_2; FALSE_NEG.
DR PROSITE; PS50025; LAM_G_DOMAIN; 6.
KW Signal; Transmembrane; Repeat; Cell adhesion; Glycoprotein;
KW Alternative splicing; Alternative promoter usage.
FT SIGNAL 1
FT CHAIN 1 1514 NEUREXIN 1-ALPHA.
FT DOMAIN 31 1438 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 1439 1459 POTENTIAL.
FT DOMAIN 1460 1514 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 31 217 LAMININ G-LIKE 1.
FT DOMAIN 283 255 EGF-LIKE 1.
FT DOMAIN 487 679 LAMININ G-LIKE 2.
FT DOMAIN 683 720 LAMININ G-LIKE 3.
FT DOMAIN 725 898 EGF-LIKE 2.
FT DOMAIN 912 1087 LAMININ G-LIKE 4.
FT DOMAIN 1090 1127 LAMININ G-LIKE 5.
FT DOMAIN 1133 1331 LAMININ G-LIKE 6.
FT DOMAIN 1361 1364 POLY-THR.
FT DOMAIN 1446 1449 POLY-ALA.
FT CARBOHYD 125 125 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 190 190 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 797 797 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 1230 1230 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARSPLIC 258 258 Missing (in some isoforms Alpha 1C).
FT VARSPLIC 258 258 /FTid=VSP_003486.
FT VARSPLIC 258 277 Missing (in some isoforms Alpha 1G).
FT VARSPLIC 274 277 /FTid=VSP_003487.
FT VARSPLIC 379 393 Missing (in some isoforms Alpha 1D).
FT VARSPLIC 387 393 /FTid=VSP_003488.
FT VARSPLIC 387 393 Missing (in some isoforms Alpha 2C).
FT VARSPLIC 387 393 /FTid=VSP_003489.
FT VARSPLIC 387 393 Missing (in some isoforms Alpha 2B).
FT VARSPLIC 790 799 /FTid=VSP_003490.
FT VARSPLIC 790 799 DCIRINCNS -> G (in some isoforms Alpha
3B).
FT VARSPLIC 1247 1276 /FTid=VSP_003491.
FT VARSPLIC 1410 1411 Missing (in some isoforms Alpha 4B).
FT VARSPLIC 1410 1411 /FTid=VSP_003492.
FT VARSPLIC 1410 1411 Missing (in some isoforms Alpha 5B).
FT SEQUENCE 1514 AA; 166167 MW; D99492302860B0E14 CRC64;
Query Match 3.3%; Score 97; DB 1; Length 1514;
Best Local Similarity 22.3%; Pred. No. 28;
Matches 52; Conservative 38; Mismatches 103; Indels 40; Gaps 11;

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QY 484 RNKGVAHHHEHFEQSDRGARKRPPSDLMQAEPSFWDAAEENIE-ODGETHV 535
DB 1465 RDEG---SYHVEDERNATNSAGSNGAVKEKOPSSAKSNKKNKNDKEYIV 1514

RESULT 35
CYF_ATRBE STANDARD; PRT; 320 AA.
AC Q868M4;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Apocytochrome f precursor.
GN P6FA
OS Atropa belladonna (Belladonna) (Deadly nightshade).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Asterales; Lamiales; Solanales; Solanaceae; Atropa.
OX NCBI_Taxid=33113;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=AD5P(kan); PubMed=12200487;
RX MEDLINE=22189020;
RA Schmitz-Linneweber C., Regel R., Du T.G., Hupfer H., Herrmann R.G.,
RA Maier R.M.;
RT "The plastid chromosome of Atropa belladonna and its comparison with
RT that of Nicotiana tabacum: the role of RNA editing in generating
RT divergence in the process of plant speciation."
RL Mol. Biol. Evol. 19:1602-1612(2002).
CC -1- FUNCTION: Translocates protons across the thylakoid membrane and
CC transfers electrons from photosystem II to photosystem I. It
CC receives electrons from the Rieske iron-sulfur protein and passes
CC them to plastocyanin.
CC -1- SUBUNIT: Interacts with plastocyanin and Rieske iron-sulfur
CC protein (by similarity).
CC -1- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane. Membrane-
CC anchored (by similarity).
CC -1- SIMILARITY: Belongs to the cytochrome c family.
CC
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CC
DR EMBL; AJ116582; CAC88057.1; -.
DR HAMAP; MF_00610; -.
DR InterPro; IPR002325; Apocyt_F.
DR InterPro; IPR000345; Cytc_heme_bind.
DR Pfam; PF01333; Apocytochr_F_C1.
DR PROSITE; PS00190; CYTOCHROME_C_1.
KW Electron transport; Heme; Chloroplast; Thylakoid; Photosynthesis;
KW Photosystem I; Photosystem II; Transmembrane; Signal.
FT SIGNAL 1
FT CHAIN 1 320
FT TRANSMEM 286 305
FT METAL 36
FT BINDING 56 56 HEME (COVALENT) (BY SIMILARITY).
FT BINDING 59 59 HEME (COVALENT) (BY SIMILARITY).
FT METAL 60 60 IRON (HEME AXIAL LIGAND) (BY SIMILARITY).
FT SEQUENCE 320 AA; 35222 MW; BD6F5BD432A3A4 CRC64;
Query Match 3.3%; Score 95.5; DB 1; Length 320;
Best Local Similarity 21.2%; Pred. No. 4.5;
Matches 67; Conservative 40; Mismatches 90; Indels 119; Gaps 19;

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Db 48 REATGRIVCANCLANKRVEIEVPOAV-----LPDYFEAVLRIPYDMOLKQVLANCK 101
QY 129 GGFNLN--FVTPSG-----GRISPFMELLEKNKSNIKASTDLGCAEFAKTYVAMDKN 180
Db 102 GGLNVAVALILPEGEHAPSDRISP---EMKEKIGNL-----SFOSYAPNKKN 146
QY 181 KATKRRYFVYDSKKRLCHILYVSMQMEGKKYCVKKEPPDLTWYCKPRKSVTENHL 240
Db 147 -----LIVIGP--VPGKKY-----SEITPPIISPDPATKDVHF 178
QY 241 IYGSAYVGEN-----PDAFISKCPNOALRGYRFGWK-----GRCLDYELTD-- 284
Db 179 LKPYIVYGNNGRGQIYPDG--SKSNNTVYNATAGIYSKIRKKGVEITITDASGR 236
QY 285 TVIERVESKACQWKTFFENDGVAADPHTYPLTSGASWMDWPLHQSOPHSGVGRNYG 344
Db 237 QVVDIIPGPELVLS--EGESIKFDQ-----PLTS-----NPNVGGFGQ--- 273
QY 345 FYVYDTTGEKCALSD 360
Db 274 -----GDAEIVLD 282

RESULT 36
ID_CYP_ORYSA STANDARD; PRT; 320 AA.
AC P07888;
DT 01-AUG-1988 (Rel. 08, Created)
DT 01-OCT-1989 (Rel. 12, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Apocytochrome f precursor.
GN
OS Oryza sativa (Rice).
OC Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
OC Eriacoidae; Oryzae; Oryza.
OX NCBI_TaxID=4530;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Labelle;
RX MEDLINE=87219885; PubMed=2884170;
RA Mu N.-H., Cote J.C., Wu R.;
RT "Nucleotide sequence of the rice cytochrome f gene and the presence
RL of sequence variation near this gene.";
RN Gene 50:271-278(1986).
RP SEQUENCE FROM N.A.
RC STRAIN=cv. Nipponbare;
RX MEDLINE=89364698; PubMed=2770692;
RA Hiratsuka J., Shimada H., Whittier R., Ishibashi T., Sakamoto M.,
RA Mori M., Kondo C., Honji Y., Sun C.-R., Meng B.-Y., Li Y.-Q.,
RA Kanno A., Nishizawa Y., Hirai A., Shinozaki K., Sugiyama M.;
RT "The complete sequence of the rice (Oryza sativa) chloroplast genome:
RT intermolecular recombination between distinct rRNA genes accounts for
RT a major plastid DNA inversion during the evolution of the cereals.";
RN Mol. Gen. Gene. 217:185-194(1989).
RC -1- FUNCTION: Translocates protons across the thylakoid membrane and
CC transfers electrons from photosystem II to photosystem I. It
CC receives electrons from the Rieske iron-sulfur protein and passes
CC them to plastocyanin.
CC -1- SUBUNIT: Interacts with plastocyanin and Rieske iron-sulfur
CC protein (By similarity).
CC -1- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane. Membrane-
CC anchored (By similarity).
CC -1- SIMILARITY: Belongs to the cytochrome c family.
CC
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CC -----
CC EMBL; M15955; AAA84590.1; -.
DR EMBL; X15901; CAA33961.1; -.
DR PIR; J00239; CFEZ.
DR HSSP; P36438; IHCZ.
DR Gramene; P07888; -.
DR HAMAP; MF 00610; -.
DR InterPro; IPR002325; Apocyt_F.
DR InterPro; IPR000345; Cyt_c_heme_bind.
DR Pfam; PF01333; Apocytocch_F_C1.
DR PRINTS; PR00610; CYTOCHROME_F.
DR PROSITE; PS00190; CYTOCHROME_C_1.
KW Electron transport; Heme; Chloroplast; Thylakoid; Photosynthesis;
KW Photosystem I; Photosystem II; Transmembrane; Signal.
FT SIGNAL 1 35
FT CHAIN 36 305
FT TRANSMEM 286 305
FT METAL 36
FT BINDING 56 56
FT METAL 60 60
FT CONFLICT 14 14
FT CONFLICT 20 20
SQ SEQUENCE 320 AA; 35467 MW; 94628351A18018BF CRC64;
Query Match 3.3%; Score 95.5; DB 1; Length 320;
Best Local Similarity 21.5%; Pred. No. 4.5;
Matches 68; Conservative 39; Mismatches 90; Indels 119; Gaps 19;
QY 83 REPAGL-----CPIMGKHIEEQOPRLPYRNPFLE-----VPEKEVKQ--SGNPLP 128
Db 48 REATGRIVCANCLANKRVDIEVPOAV-----LPDYFEAVLRIPYDMOLKQVLANCK 101
QY 129 GGFNLN--FVTPSG-----GRISPFMELLEKNKSNIKASTDLGCAEFAKTYVAMDKN 180
Db 102 GGLNVAVALILPEGEHAPSDRISP---ELKEKIGNL-----SFOSYAPNKKN 146
QY 181 KATKRRYFVYDSKKRLCHILYVSMQMEGKKYCVKKEPPDLTWYCKPRKSVTENHL 240
Db 147 -----LIVIGP--VPGKKY-----SEITPPIISPDPATKDVHF 178
QY 241 IYGSAYVGEN-----PDAFISKCPNOALRGYRFGWK-----GRCLDYELTD-- 284
Db 179 LKPYIVYGNNGRGQIYPDG--SKSNNTVYNATAGIYSKIRKKGVEISYDASGR 236
QY 285 TVIERVESKACQWKTFFENDGVAADPHTYPLTSGASWMDWPLHQSOPHSGVGRNYG 344
Db 237 QVVDIIPGPELVLS--EGESIKLDQ-----PLTS-----NPNVGGFGQ--- 273
QY 345 FYVYDTTGEKCALSD 360
Db 274 -----GDAEIVLD 282

RESULT 37
ID_C166_MOUSE STANDARD; PRT; 583 AA.
AC C166_MOUSE 061490; O70136;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1999 (Rel. 38, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE CD166 antigen precursor (Activated leukocyte-cell adhesion molecule)
DE (ALCAM) (DM-GRASP protein).
GN ALCAM.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN
RP SEQUENCE FROM N.A.
RC STRAIN=NFS;

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RA MEDLINE=97353242; PubMed=9209500;
 RA Bowen M.A., Bajorath J., D'Egidio M., Whitney G.S., Palmer D.,
 RA Kobayashi J., Stirling G.C., Siadak A.W., Aruffo A.;
 RT "Characterization of mouse AlCAM (CD166): the CD6 binding domain is
 RT conserved in different homologs and mediates cross-species binding.";
 RL Eur. J. Immunol. 27:1465-1478(1997).
 RN [2]
 RP SEQUENCE OF 227-583 FROM N.A.
 RC STRAIN=BA1B/C; TISSUE=Brain;
 RX MEDLINE=94376084; PubMed=8089660;
 RA Kanki J.P., Chang S., Kawada J.Y.;
 RT "The molecular cloning and characterization of potential chick
 RT DM-GRASP homologs in zebrafish and mouse.";
 RL J. Neurobiol. 25:831-845(1994).
 CC -1- FUNCTION: CELL ADHESION MOLECULE THAT BINDS TO CD6. INVOLVED IN
 CC NEURITE EXTENSION BY NEURONS VIA HETEROPHILIC AND HOMOPHILIC
 CC INTERACTIONS. MAY PLAY A ROLE IN THE BINDING OF T AND B CELLS TO
 CC ACTIVATED LEUKOCYTES, AS WELL AS IN INTERACTIONS BETWEEN CELLS OF
 CC THE NERVOUS SYSTEM.
 CC -1- SUBCELLULAR LOCATION: Type I membrane protein.
 CC -1- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
 CC -1- SIMILARITY: Contains 2 immunoglobulin-like V-type domains.
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 CC -----
 DR EMBL; U95030; AAC06342.1; -;
 DR EMBL; L25274; AAA37528.1; -;
 DR HSSP; Q13740; IKXC
 DR MGD; MG1313266; Alcam.
 DR GO; GO:0019897; C:extrinsic to plasma membrane; IDA.
 DR GO; GO:0007165; P:signal transduction; IPI.
 DR InterPro; IPR007110; IG-1like.
 DR InterPro; IPR003599; IG.
 DR InterPro; IPR003066; IG_MHC.
 DR Pfam; PF00047; Ig_5.
 DR SMART; SM00409; Ig_3.
 DR PROSITE; PS00835; IG_LIKE; 4.
 DR PROSITE; PS00290; IG_MHC; FALSE NEG.
 KM Cell adhesion; Immunoglobulin domain; Glycoprotein; Transmembrane;
 KM Repeat; Signal.
 FT SIGNAL 1 27
 FT CHAIN 28 583
 FT DOMAIN 28 527
 FT TRANSMEM 528 549
 FT DOMAIN 550 583
 FT DOMAIN 28 120
 FT DOMAIN 125 234
 FT DOMAIN 245 328
 FT DOMAIN 333 409
 FT DOMAIN 416 501
 FT DISULFID 43 113
 FT DISULFID 157 220
 FT DISULFID 270 313
 FT DISULFID 354 392
 FT CARBOHYD 95 95
 FT CARBOHYD 167 167
 FT CARBOHYD 265 265
 FT CARBOHYD 306 306
 FT CARBOHYD 361 361
 FT CARBOHYD 457 457
 FT CARBOHYD 480 480
 FT CARBOHYD 499 499
 FT CONFLICT 227 232
 FT CONFLICT 454 454
 SQ SEQUENCE 583 AA; 65161 MM; E7BAFA8FCA8F9489 CRC64;

Query Match 3.3%; Score 95.5; DB 1; Length 583;
 Best Local Similarity 19.9%; Pred. No. 10;
 Matches 118; Conservative 66; Mismatches 179; Indels 229; Gaps 28;
 QY 31 ESQTSAS-----TSGNPQANVEKTM-----ERFYLTHHSGIYVD 70
 DB 94 ENYTLSTIANAKISDEKRFVCMLYVEDNVEAPTLVVKVQPSKPEIVKAPLELDQKK 153
 QY 71 LG----ODKEVDG--TLVREBAGCPIMGKIELOQPRRLRYNNFLDVPFEKYE--Q 122
 DB 154 LQDCISRSYDQNTWYRNGKVLQPVGEVALIFKKEIDP--GTYLYTSSLEFKYTR 211
 QY 123 SGNPLPGFNLFVTPSGQRI-----
 DB 212 SDIQWPFCSYTYGPGSQKITYSBEIFDIYPTQVTLQVLPKNAIKEGDNITLQCL 271
 QY 144 ---SPFMELL-----EKSNYKASTLGLRCAEAFPTVAMDKNKATKYRFRVY 191
 DB 272 GNGNPPPEEFMFYLPQDEGRSSNTYTLTVRRNATGDYCSLIDKENMA----- 323
 QY 192 DSKRLCHILVSMQMEGKKYCSVKGPDPULWYCFKPRKSYTENHLLIGSAVGENP 251
 DB 324 -STITVYLDLSL-----NPKGEVTKQ-----IG-- 347
 QY 252 DAFISKCPQALRGYRFGVWKKGR-----CLDYTE---LTDVIERVESKAQCW 297
 DB 348 DTLPSCTISASRNATV--VMKNKDIRLSSPSFSLHQDAGNYCETALQEVG----- 401
 QY 298 VKTFBNDSVADQHTYPLTISQASNDWMLHQSQDPHSGVGVRNGYVYDTGEGCA 357
 DB 402 LKKRESLTLVIEGKPOIKMTKK-----TDPGLSKXTI 433
 QY 358 LSDQVPCDLS--DSAAVSYTAAGSLs-----EETP-----NFILSPSPVPTPE 402
 DB 434 I-----CHVGCPKPAHMTITSGSVINOTESSPYNGRYKTLISPEBNV----- 482
 QY 403 TALQCTAD-KPPDSFGACDVQACKROKTSVCGQIOSTSVDTADEQNECSNTR-LIAG 460
 DB 483 -LCTAENQLERYTNSLNVSAISIP-----EHDEADDISDENKKNQDQKLLVG 531
 QY 461 LAVGVLLALLGGGCT--FAKR-----LDRKGVQAAHNEH 496
 DB 532 IVV-GLLIALVAGVYVWLVMKSKSTASKYHVKDGLGNMEKNKJLENNHKE 582
 RESULT 38
 MYCM_HUMAN
 ID MYCM_HUMAN STANDARD; PRT; 357 AA.
 AC P12525;
 DT 01-OCT-1989 (Rel. 12, Created)
 DT 01-OCT-1989 (Rel. 12, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DE L-myc-2 protein.
 GN MYC2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OK NCBI_TaxId=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89233129; PubMed=2541066;
 RA Morton C.C., Nussenzweig M.C., Sousa R., Sorenson G.D.,
 RA Pettengill O.S., Shows T.B.;
 RT "Mapping and characterization of an X-linked processed gene related
 RT to MYC1.";
 RL Genomics 4:367-375(1989).
 CC -1- SUBUNIT: EFFICIENT DNA BINDING REQUIRES DIMERIZATION WITH ANOTHER
 CC BHLH PROTEIN. BINDS DNA AS AN HETERODIMER WITH MAX.
 CC -1- SIMILARITY: BELONGS TO THE BASIC HELIX-LOOP-HELIX (BHLH) FAMILY OF
 CC TRANSCRIPTION FACTORS. BHLH-ZIP SUBFAMILY.
 CC -----
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EMBL, J03069; AAS59883.1; -
 DR PIR, A20146; TVHUL2.
 DR HSSP, P25912; IHLO.
 DR TRANSFAC, T03539; -
 DR Genew; HGNC:7556; MYCL2.
 DR MIM, 310310; -
 DR GO, GO:0003700; F:transcription factor activity; TMS.
 DR InterPro, IPR001092; HLM basic.
 DR InterPro, IPR002418; TF_Myc.
 DR Pfam; PF00010; HLM; 1.
 DR Pfam; PF01056; MYC_N term; 1.
 DR SMART; SMO0353; HLM_1.
 DR PROSITE; PS00018; HLM_1; 1.
 DR PROSITE; PS50888; HLM_2; 1.
 DR Nuclear protein; DNA-binding.
 DR DNA BIND 275
 FT DOMAIN 288 327
 SQ SEQUENCE 357 AA; 4113 MW; 4654F534716E0EC3 CRC64;

Query Match 3.3%; Score 95; DB 1; Length 357;
 Best Local Similarity 22.9%; Pred. No. 5.7; Indels 76; Gaps 17;
 Matches 69; Conservative 34; Mismatches 122;

238 HHLVGSAYGVENPDAFISCKPNOALRGYFGVWKKRGCLDYTELTD--TVIERVESKA 294
 Db 7 HHVFD--YDG-GEDEFYRSTTSE-----DIWKK-----FELVPPPTWTVRSREPEP 50

295 QCVKTFENDGVASDQPHYTP-----TSQASNDWMPHLOSQPHSGGGRNYGFPY 347
 Db 51 QLM-----SPGTWPVGCAGDETESQDYWKAM-----DANYASLIR----- 86

348 VTTTGEKCALSDQVP-DCLVSDSAVSTYAGSLSE-ETPFIIPSNSTVPPPETAL 405
 Db 87 -DCWMSG--FSTQELERAVSDLLAVGAPSGVSPREPAFPDY-----IPELEA 131

406 OCTADKFPDPSFACDVQACKROKTCVCGQIOISTVDCADBEQSGSTALIAVLAVG 465
 Db 132 GMLAPTFPLCEPKTQACSRSESP---SDSEEEEDIVYKKRQSLTKPIY--IAVNA 186

466 VLLALLGGGCVFAKRLDNRKGVQAANHEHEFQSDRGARKR-PSDLWGEABESFDEAE 524
 Db 187 DLLDPRMN---LFHISHQOHNVYAPPPESCFCGAGPKRMPKEALREBRAPGKDKXE 243

525 E 525
 Db 244 D 244

RESULT 39
 APC_MOUSE STANDARD; PRT; 2845 AA.
 AC Q61315; Q62044;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE Adenomatous polyposis coli protein (APC protein) (mAPC).
 GN APC.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2), AND VARIANTS.
 RC MEDLINE=C57BL/6J, and CAST/EiJ; TISSUE=Brain;
 RA Su L.-K., Kinzler K.W., Vogelstein B., Preisinger A.C., Moser A.R.,
 RA Luongo C., Gould K.A., Dove W.F.;

"Multiple intestinal neoplasia caused by a mutation in the murine homolog of the APC gene."
 RT Science 256:668-670(1992).
 RN [2]
 RP ERRATUM.
 RA Su L.-K., Kinzler K.W., Vogelstein B., Preisinger A.C., Moser A.R.,
 RA Luongo C., Gould K.A., Dove W.F.;
 RL Science 256:1114-1114(1992).
 RN [3]
 RP SEQUENCE OF 1-45 FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Liver;
 RA Dicker F., Lambert S., Reltmair A., Ballhausen W.G.;
 RT "The murine APC gene: alternative splicing of 5' untranslated region segments."
 RT Submitted (Oct-1993) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP ALTERNATIVE SPLICING.
 RX MEDLINE=94061824; PubMed=8242607;
 RA Oshima M., Sugiyama H., Kitagawa K., Takeo M.;
 RT "APC gene messenger RNA: novel isoforms that lack exon 7."
 RL Cancer Res. 53:5589-5591(1993).
 CC -1- FUNCTION: Tumor suppressor. Promotes rapid degradation of CTNNB1 and participates in Wnt signaling. APC activity is correlated with its phosphorylation state (By similarity).
 CC -1- SUBUNIT: Forms homooligomers. Associates with catenins. Binds axin (By similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event-Alternative splicing; Named isoforms=4;
 CC Name=1;
 CC IsoId=Q61315-1; Sequence=Displayed;
 CC Name=2;
 CC IsoId=Q61315-2; Sequence=VSP_004116;
 CC Name=3;
 CC IsoId=Q61315-3; Sequence=VSP_004117;
 CC Name=4;
 CC IsoId=Q61315-4; Sequence=VSP_004116, VSP_004117;
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN LIVER, SPLEEN, KIDNEY, HEART, LUNG, BRAIN, STOMACH, INTESTINE, TESTIS AND OVARY.
 CC -1- PTM: PHOSPHORYLATED BY GSK-3B (BY SIMILARITY).
 CC -1- SIMILARITY: Contains 7 ARM repeats.
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EMBL, M88127; AAB59632.1; -
 DR EMBL, U02937; AAB03443.1; -
 DR PIR, I49505; I49505.
 DR HSSP, 002248; 3BCT..
 DR MGD, MGI:88039; APC.
 DR GO, GO:0005737; Cytoplasm; IDA.
 DR GO, GO:0005634; Cnucleus; IDA.
 DR GO, GO:0008013; F:beta-catenin binding activity; IDA.
 DR GO, GO:0016055; P:Wnt receptor signaling pathway; IDA.
 DR InterPro, IPR000225; Armadillo.
 DR Pfam; PF00514; Armadillo_seg; 4.
 DR SMART; SMO0185; ARM; 5.
 DR PROSITE; PS50176; ARM_REPEAT; 1.
 KW Wnt signaling pathway; Anti-oncogene; Phosphorylation;
 KW Alternative splicing; Repeat; Coiled coil.
 FT DOMAIN 1 61
 FT DOMAIN 125 245
 FT DOMAIN 245 284
 FT REPEAT 451 493 ARM 1.
 FT REPEAT 503 545 ARM 2.
 FT REPEAT 546 589 ARM 3.
 FT REPEAT 590 636 ARM 4.
 FT REPEAT 637 681 ARM 5.
 FT REPEAT 682 723 ARM 6.

```

FT REPEAT 724 765 ARM 7.
FT DOMAIN 739 2834 SER-RICH.
FT DOMAIN 1130 1156 ASP/GLU-RICH (ACIDIC).
FT DOMAIN 1556 1575 ASP/GLU-RICH (ACIDIC).
FT DOMAIN 1864 1891 HIGHLY CHARGED.
FT VARSPIC 243 276 Missing (in isoform 2 and isoform 4).
FT VARSPIC 310 410 Missing (in isoform 3 and isoform 4).
FT VARSPIC 310 410 Missing (in isoform 3 and isoform 4).
FT VARIANT 120 120 T -> A (IN STRAIN CAST/ET).
FT VARIANT 493 493 V -> I (IN STRAIN CAST/ET).
FT VARIANT 797 797 Y -> F (IN STRAIN CAST/ET).
FT VARIANT 1330 1330 A -> T (IN STRAIN CAST/ET).
FT VARIANT 1618 1618 A -> S (IN STRAIN CAST/ET).
FT VARIANT 2294 2294 G -> A (IN STRAIN CAST/ET).
FT VARIANT 2496 2496 H -> Q (IN STRAIN CAST/ET).
FT VARIANT 2523 2523 T -> A (IN STRAIN CAST/ET).
FT VARIANT 2813 2813 T -> S (IN STRAIN CAST/ET).
SQ SEQUENCE 2845 AA; 311086 MW; 145CA73CF570A499 CRC64;

Query Match 3.3%; Score 95; DB 1; Length 2845;
Best Local Similarity 18.5%; Pred. No. 91;
Matches 103; Conservative 65; Mismatches 185; Indels 204; Gaps 23;

QY 19 PASGLSSSTRRESQTLASSTGNPFOANVEMKTFMERFNL-----THHQSG-----I 67
DB FSTATSLSDLTIESPPNELAT-GDVRAIGSQSGEKEKRDITPTGSRSTDQAQKGISIV 1707
QY 68 YVDDGGQKENVDTLYREBAGCPIWKGKIEIQDRLPYRNNFLQEDVTEKEYQSGNPL 127
DB TPDLDDNKAERGDDTLAECINSAMPRGK-----SHKFR-----VKIMDOVQOASST 1754
QY 128 PGCFNLNFTVPSGOR-----ISPPMEL-----LEKSNIKASTDLGRCAEPAF-----K 172
DB 1755 SSGANKQVDTKKKKKPSVPMQNTREYRVRKNTDSKNNV-----TEETFSNDKSK 1810
QY 173 TVAMDKNNAKATYRP-----FYVDSKKRLCHLLVYSMQLMEKKYCSVKGEPPDL 223
DB 1811 KPSIQTNAAKAFNEKLPNNEDVRGTFALDSPHH-----YPIEGTP--- 1851
QY 224 TWVGFRRKRSYTEHNLHLYGSAVYGENPDATISCPNOLALGVRFGVKKRCCLDYELT 283
DB 1852 --YCFSRNDSL-----SLDFDDDDVLSREKAL-----RKGEKSKDSBAK 1891
QY 284 DTV-----IERVESKACQWV-----TFENDVVASDOPHTYPLTQASWMDWMLHQSDQ 333
DB 1892 VTCPREPNSSQQAASKQASIKHPANRAQSKPVLOKQD-TPPOSSK-----DG 1938
QY 334 PHSGVGVRNYGFYVDTTGECKALSDQVPCLVSDSAVSYTAAGLS----- 382
DB 1939 PDRG-----AATBEKLNLAIENTPVCFSSNSSLSSLDIDQENNN 1979
QY 383 ---EETNFNFIIPSPSVTPPTETALCTADKPFDSGACVQACROKTSVCGQIOST 439
DB 1980 NKSEPIKEAFAPASQGEPSKQ-----ASGYAPKSFHVEITPTVCFSSNNS-----LSL 2029
QY 440 SVDCTADEQNECGSNTALLIAGLAVGVLLALLGGGCVFAFKLRNKGCVQAHHNEHROS 499
DB 2030 SIBEDDLQECISAM----- 2046
QY 500 DRGARKRPDLMQEA 516
DB 2047 ---PKKKRPRLKSESE 2060

RESULT 40
CYF_SPTOL STANDARD; PRT; 320 AA.
AC P16013; Q9M3L3;
DT 01-APR-1990 (Rel. 14, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE Apocytochrome f precursor.

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GN PETA.
OS Spinacia oleracea (Spinach).
OS Chloroplast.
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
OC Caryophyllidae; Caryophyllales; Chenopodiaceae; Spinacia.
OX NCBI_TaxID=3562;
RN [1]
RP SEQUENCE FROM N.A.
RA Alt J., Herrmann R.G.;
RT "Nucleotide sequence of the gene for pre-apocytochrome f in the
RT spinach plastid chromosome.";
RL Curr. Genet. 8:551-557(1984).
RN [2]
RP SEQUENCE FROM N.A.
RA MEDLINE=2187424; PubMed=11292076;
RX Schmitz-Linneweber C., Mäler R.M., Alcaraz J.-P., Cottet A.,
RA Herrmann R.G., Maché R.;
RT "The plastid chromosome of spinach (Spinacia oleracea): complete
RT nucleotide sequence and gene organization.";
RL Plant Mol. Biol. 45:307-315(2001).
CC -1- FUNCTION: Translocates protons across the thylakoid membrane and
CC transfers electrons from photosystem II to photosystem I. It
CC receives electrons from the Rieske iron-sulfur protein and passes
CC them to plastocyanin.
CC -1- SUBUNIT: Interacts with plastocyanin and Rieske iron-sulfur
CC protein (by similarity).
CC -1- SUBCELLULAR LOCATION: Chloroplast thylakoid membrane. Membrane-
CC anchored (by similarity).
CC -1- SIMILARITY: Belongs to the cytochrome c family.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
DR EMBL; M36602; AAA84632.1; -.
DR EMBL; AJ400848; CAB88742.1; -.
DR PIR; S00430; S00430.
DR HSSP; P36438; 1HCZ.
DR HAMAP; MF_00610; -; 1.
DR InterPro; IPR002325; Apocyt_f.
DR InterPro; IPR000345; Cytc_heme_bind.
DR Pfam; PF01333; Apocytochr_F_C; 1.
DR PRINTS; PR00610; CYTOCHROME_F.
DR PROSITE; PS00190; CYTOCHROME_C; 1.
KW Electron transport; Heme; Chloroplast; Thylakoid; Photosynthesis;
KW Photosystem I; Photosystem II; Transmembrane; Signal.
FT SIGNAL 1 35
FT CHAIN 36 320
FT TRANSMEM 286 305
FT METAL 36
FT BINDING 56 56
FT BINDING 59 59
FT METAL 60 60
FT CONFLICT 235 235
SQ SEQUENCE 320 AA; 35319 MW; 33B9FE0D02F19C36 CRC64;

Query Match 3.2%; Score 94.5; DB 1; Length 320;
Best Local Similarity 20.9%; Pred. No. 5.4;
Matches 66; Conservative 42; Mismatches 89; Indels 119; Gaps 19;

QY 83 REPAGL-----CPWKGKIELOQDRLPYRNNFLQD-----VPTKEYKQ-SGNPLP 128
DB 48 REATGRIVCANCHIANPVIDEIVQAV-----LPDVFPAVRIPIYDMQLKVLANGKK 101
QY 129 GGFNIN--FVTPSG-----QRISSPPMELLEKNKSNKASTDLGRCAEPAFKTVAMDKN 180

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Db      102 GGLNVGAVLILPEGFELAPDDRISP--EMKEKMGNL-----SFOSTYRPNKON 146
OY      181 KATKYRYPFVYDSKKRLCHILYVSMQIMEGKKYCSVKGEPPDLTWYCFKPRKSVTENHHL 240
Db      147 -----ILVIGP--VPGOKY-----SEITFPILAPDPATKQDVHF 178
OY      241 IYGSAYGEN-----PDAFISKCPNQLRGYRFGVWK-----GRCLDYTELTD-- 284
Db      179 LKYPYVGNRGQIYPPDG--SKSNNTVYNSTATGIVKIVRKEKGGYEINIADASDGR 236
OY      285 TVIERVESKACQWKTENDGVASDQPHTYPLTSQASWMDWPLHQSDQPHSGGVGRNYG 344
Db      237 EVVDIIPRGPELVS--EGESIKLDQ---PLTS-----NPNVGGFRGQ--- 273
OY      345 FYVVDTTGEGKCALSD 360
Db      274 -----GDAEVVLQD 282

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Search completed: October 2, 2003, 15:49:45
 Job time : 31 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 2, 2003, 15:52:30 ; Search time 83 Seconds
(without alignments)
1034.591 Million cell updates/sec

Title: US-10-039-770A-1
Perfect score: 541
Sequence: 1 MGLVGVQVLVLVADCTIFA.....EAEENIEDQETHWVWEGDY 541

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 1107863 seqs, 158726573 residues

Word size: 0

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 1000 summaries

Database:

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24: /SIDSI/gcgdata/geneSeq/geneSeq-emb1/AA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	86	15.9	86	ABP56991	Toxoplasma gondii
2	8	1.5	39	AA607963	Arabidopsis thaliana
3	8	1.5	39	AA649409	Arabidopsis thaliana
4	8	1.5	60	AA64731	Human 5' EST relat
5	8	1.5	75	ABP56974	E. tenella microne
6	8	1.5	106	AAO21315	Soybean KCP-like p
7	8	1.5	133	ABP63392	Drosophila melanog
8	8	1.5	200	ABU05787	M. tuberculosis an
9	8	1.5	238	ABP58791	Breast and ovarian

10	8	1.5	255	AA674269	Human colon cancer
11	8	1.5	256	AA670923	Alternatively spliced
12	8	1.5	266	AA68706	Human transcriptio
13	8	1.5	276	AA609922	Human CLAR1 protei
14	8	1.5	287	AA60577	Eimeria tenella 54
15	8	1.5	287	AA605216	Antigen GX5401 an
16	8	1.5	437	AA667722	Human tumour anti
17	8	1.5	437	AA667733	PRO1663, a novel t
18	8	1.5	437	AA667750	Human PRV-1 protei
19	8	1.5	437	AA67261	Human signal pepti
20	8	1.5	437	AA66737	Membrane-bound pro
21	8	1.5	437	AA612404	Human PRO181 poly
22	8	1.5	437	AA670851	Human PRV-1 protei
23	8	1.5	437	AA65260	Human PRO181 (UNQ
24	8	1.5	437	ABG31399	Human PRO1863 poly
25	8	1.5	437	ABG91359	Novel human secret
26	8	1.5	437	ABG92707	Human secreted pro
27	8	1.5	437	AA683672	Human PRO protein,
28	8	1.5	437	AA680767	Human granulocyte
29	8	1.5	437	ABU66802	Human PRO polypept
30	8	1.5	437	ABU67078	Human secreted/tra
31	8	1.5	437	ABU59883	Novel secreted and
32	8	1.5	437	ABU60811	Human secreted/tra
33	8	1.5	437	ABG73312	Human secreted/tra
34	8	1.5	437	ABU59153	Human PRO1863 poly
35	8	1.5	437	ABU59300	Novel human secret
36	8	1.5	437	ABU59449	Human secreted/tra
37	8	1.5	437	ABU60584	Human secreted/tra
38	8	1.5	437	ABU58075	Human PRO polypept
39	8	1.5	437	ABU59006	Human secreted/tra
40	8	1.5	437	ABU13966	Human PRO181 poly
41	8	1.5	437	ABU10921	Human PRO polypept
42	8	1.5	535	AA651249	Rat liver anion tr
43	8	1.5	585	AA63788	Human polypeptide,
44	8	1.5	616	AA19347	Human PRO113 (UNQ
45	8	1.5	616	AA629102	Human PRO polypept
46	8	1.5	616	AA66096	Protein of the inv
47	8	1.5	616	ABU71190	Human PRO113 prote
48	8	1.5	616	ABU56647	Human secreted/tra
49	8	1.5	616	ABU55980	Novel human secret
50	8	1.5	616	ABU67484	Human secreted/tra
51	8	1.5	616	ABU65342	Human PRO polypept
52	8	1.5	616	ABU58478	Human PRO polypept
53	8	1.5	616	ABU6014	Human secreted/tra
54	8	1.5	616	ABU57009	Human PRO polypept
55	8	1.5	616	ABU10588	Human secreted/tra
56	8	1.5	692	ABP57859	Plasmodium falciparum
57	8	1.5	1129	ABG20477	Novel human diapo
58	8	1.5	2189	AA605222	Antigen GX5401FL e
59	8	1.5	2189	ABP56960	E. maxima 250 kDa
60	8	1.5	3433	ABP70647	Amino acid sequenc
61	8	1.5	3433	ABP88821	West Nile virus BC
62	8	1.3	10	AA632582	West Nile virus (W
63	8	1.3	13	AA674276	Immunoglobulin E F
64	8	1.3	32	AA65179	Human cytochrome c
65	8	1.3	35	AA620409	Human microtubule
66	8	1.3	41	AA670553	Heterologous signa
67	8	1.3	50	ABP03189	Human ORF protein
68	8	1.3	52	AAU44403	Protoninbacterium
69	8	1.3	53	ABP26162	Streptococcus poly
70	8	1.3	56	AAU60385	Protoninbacterium
71	8	1.3	59	ABG57756	Human liver peptid
72	8	1.3	59	ABP42311	Peptide #9837 enco
73	8	1.3	59	ABP35822	Protein #7821 enco
74	8	1.3	59	AA663217	Human brain expres
75	8	1.3	59	AA676030	Human bone marrow
76	8	1.3	59	AA620777	Peptide #7211 enco
77	8	1.3	59	AA636137	Peptide #10174 enco
78	8	1.3	59	ABG5438	Human peptide enco
79	8	1.3	70	ABG58999	Human liver peptid
80	8	1.3	70	ABP43622	Peptide #1118 enco
81	8	1.3	70	AA64563	Human brain expres
82	8	1.3	70	AA677366	Human bone marrow

83	7	1.3	70	22	AAW21289	Peptide #7723 enco	156	7	1.3	182	21	AAW6234	Recombinant human
84	7	1.3	70	22	AAW37516	Peptide #1553 enco	157	7	1.3	183	21	AAW6232	Recombinant human
85	7	1.3	70	23	ABG46380	Human peptide enco	158	7	1.3	193	17	AAW9281	IgE high affinity
86	7	1.3	70	24	ABP56985	Sarcocystis muris	159	7	1.3	193	22	AAU3487	Enterococcus faeca
87	7	1.3	77	22	AAU48074	Propionibacterium	160	7	1.3	197	15	AAW5778	Human dihydrofolat
88	7	1.3	80	22	ABG51385	Human liver peptid	161	7	1.3	197	22	AAW1586	A Fc epsilon recep
89	7	1.3	80	22	ABW31332	Peptide #3983 enco	162	7	1.3	198	22	ABW66920	Drosophila melanog
90	7	1.3	80	22	ABW36538	Peptide #4044 enco	163	7	1.3	198	22	ABW66930	Streptococcus agal
91	7	1.3	80	22	ABW21879	Protein #3878 enco	164	7	1.3	202	21	AAW6806	N. gonorrhoeae ami
92	7	1.3	80	22	AAW57300	Human brain expres	165	7	1.3	202	24	ABP76743	N. gonorrhoeae ami
93	7	1.3	80	22	AAW69705	Human bone marrow	166	7	1.3	202	24	ABP79559	Pept. Bacillus amy
94	7	1.3	80	22	AAW17517	Peptide #3951 enco	167	7	1.3	215	14	AAW38690	Bacillus subtilis
95	7	1.3	80	22	AAW30039	Peptide #4076 enco	168	7	1.3	215	14	AAW41759	Bacillus subtilis
96	7	1.3	80	22	AAW05189	Peptide #3871 enco	169	7	1.3	215	14	AAW3315	Polypeptide subclis
97	7	1.3	80	23	ABG39320	Human peptide enco	170	7	1.3	216	20	AAW69013	Human secreted pro
98	7	1.3	86	22	AAW09816	Human polypeptide	171	7	1.3	216	22	ABW51091	Human secreted pro
99	7	1.3	88	22	AAW57891	Propionibacterium	172	7	1.3	217	22	AAW64401	Novel human diagno
100	7	1.3	89	22	AAU45812	Propionibacterium	173	7	1.3	221	23	AAW17599	E. gossypii protein
101	7	1.3	92	22	AAU55470	Human ORFX ORF290	174	7	1.3	221	23	AAW56236	Human secreted pro
102	7	1.3	95	21	AAW40526	Human ORFX ORF290	175	7	1.3	222	21	AAW56236	Novel human diagno
103	7	1.3	95	22	AAW07633	Human polypeptide	176	7	1.3	232	22	AAW31585	Novel human diagno
104	7	1.3	100	20	AAW89015	Polypeptide triagme	177	7	1.3	234	22	ABG10662	Olfactory receptor
105	7	1.3	100	22	ABW51093	Human secreted pro	178	7	1.3	234	22	AAW73028	Soybean 3-hydroxy
106	7	1.3	107	22	ABW17371	Human nervous syst	179	7	1.3	234	23	AAW19930	Human FcBRI alpha
107	7	1.3	112	21	AAW21372	Zea mays protein f	180	7	1.3	235	13	AAW26064	Propionibacterium
108	7	1.3	112	23	AAW64006	Novel secreted pro	181	7	1.3	238	22	AAU39177	Arabidopsis thalia
109	7	1.3	112	23	AAW83335	Novel secreted pro	182	7	1.3	246	21	AAW59547	Listeria monocytog
110	7	1.3	113	22	AAW63171	Propionibacterium	183	7	1.3	247	23	ABW49250	Aspergillus fumiga
111	7	1.3	113	22	AAW804068	Rat zeytor 10 cyto	184	7	1.3	247	24	ABW25658	Arabidopsis thalia
112	7	1.3	115	22	ABG25336	Novel human diagno	185	7	1.3	250	21	AAW17920	Arabidopsis thalia
113	7	1.3	123	21	AAW64607	Propionibacterium	186	7	1.3	250	21	AAW59272	Arabidopsis thalia
114	7	1.3	127	21	AAW64657	Human 5' EST relat	187	7	1.3	250	21	AAW59546	Human protein SEQ
115	7	1.3	129	23	ABP32868	Human complement p	188	7	1.3	252	22	AAW79289	Human polypeptide
116	7	1.3	130	22	AAW47977	Propionibacterium	189	7	1.3	253	23	ABW6108	Listeria monocytog
117	7	1.3	131	22	AAW65178	Human cytochrome c	190	7	1.3	253	23	ABW49402	C. glutamicum prote
118	7	1.3	133	22	AAW57948	Propionibacterium	191	7	1.3	256	22	AAW92545	Alpha subunit of h
119	7	1.3	136	13	AAW22387	Antigen cc-33c. E	192	7	1.3	257	10	AAW90385	Alpha subunit of h
120	7	1.3	137	20	AAW91442	Murine GLIR protei	193	7	1.3	257	11	AAW05025	Human Fc(epsilon)R
121	7	1.3	137	21	AAW91442	Human secreted pro	194	7	1.3	257	12	AAW14772	Human FcBRI alpha
122	7	1.3	137	22	AAW64531	Gene 35 human secr	195	7	1.3	257	14	AAW42316	Alpha subunit of h
123	7	1.3	139	22	ABG28850	Novel human diagno	196	7	1.3	257	18	AAW24066	The alpha chain of
124	7	1.3	148	22	ABG52204	Human liver peptid	197	7	1.3	257	19	AAW61190	Human IgG receptor
125	7	1.3	148	22	ABG58832	Human liver peptid	198	7	1.3	257	19	AAW48094	Human immunoglobul
126	7	1.3	148	22	ABW32148	Peptide #4799 enco	199	7	1.3	257	22	AAW74667	Amino acid sequenc
127	7	1.3	148	22	ABW37398	Peptide #4904 enco	200	7	1.3	257	22	AAW31584	Human IgE receptor
128	7	1.3	148	22	ABW43456	Peptide #10962 enc	201	7	1.3	257	23	ABW32801	Human B2S binding
129	7	1.3	148	22	ABW14896	Human nervous syst	202	7	1.3	257	23	ABW45241	Aspergillus fumiga
130	7	1.3	148	22	ABW26425	Protein #8424 enco	203	7	1.3	258	24	ABW26258	Human Fc receptor,
131	7	1.3	148	22	AAW64387	Human brain expres	204	7	1.3	260	21	AAW96230	Bacillus megaterium
132	7	1.3	148	22	AAW70527	Human bone marrow	205	7	1.3	271	21	AAW95751	Bifidobacterium lo
133	7	1.3	148	22	AAW77209	Human bone marrow	206	7	1.3	277	23	ABW5842	Streptococcus poly
134	7	1.3	148	22	AAW18365	Peptide #4799 enco	207	7	1.3	277	23	ABP28865	Hybrid Fc(epsilon)
135	7	1.3	148	22	AAW21140	Peptide #7574 enco	208	7	1.3	281	12	AAW13867	Hybrid Fc(epsilon)
136	7	1.3	148	22	AAW37345	Peptide #11382 enc	209	7	1.3	281	12	AAW13868	Hybrid Fc(epsilon)
137	7	1.3	148	22	AAW05965	Peptide #4647 enco	210	7	1.3	281	12	AAW13869	Hybrid Fc(epsilon)
138	7	1.3	148	23	ABG46220	Human peptide enco	211	7	1.3	281	12	AAW13870	Listeria monocytog
139	7	1.3	149	22	ABG10601	Novel human diagno	212	7	1.3	291	23	ABW47465	Novel human diagno
140	7	1.3	156	23	ABP30498	Streptococcus poly	213	7	1.3	301	22	ABW05867	Arabidopsis thalia
141	7	1.3	156	23	ABP30498	Novel human secret	214	7	1.3	312	21	AAW17919	Arabidopsis thalia
142	7	1.3	160	21	AAW21371	Zea mays protein f	215	7	1.3	312	21	AAW59271	Arabidopsis thalia
143	7	1.3	162	23	ABP26616	Streptococcus poly	216	7	1.3	312	21	AAW59545	Lactococcus lactis
144	7	1.3	166	23	ABP28342	Streptococcus poly	217	7	1.3	314	23	ABW54787	Human ileal sodi
145	7	1.3	172	20	AAW33185	Human sFC-epsilon	218	7	1.3	325	23	ABW76899	Rat phospholipase
146	7	1.3	172	21	AAW94211	Human sFC-epsilon	219	7	1.3	344	13	AAW10899	Phospholipase A2 i
147	7	1.3	172	21	AAW31587	A Fc epsilon recep	220	7	1.3	344	13	AAW21775	Phospholipase A2 i
148	7	1.3	176	21	AAW94210	Human sFC-epsilon	221	7	1.3	344	15	AAW51948	N. gonorrhoeae ami
149	7	1.3	176	22	AAW65597	Amino acid sequenc	222	7	1.3	345	24	ABP80534	Human protein sequ
150	7	1.3	176	22	AAW65597	Hepatitis GB virus	223	7	1.3	349	12	AAW10900	Human phospholip
151	7	1.3	177	16	AAW81432	Hepatitis GB virus	224	7	1.3	349	13	AAW21776	Phospholipase A2 i
152	7	1.3	177	21	ABW09009	Hepatitis GB virus	225	7	1.3	349	13	AAW51949	Phospholipase A2 i
153	7	1.3	178	22	ABW17489	Human nervous syst	226	7	1.3	361	15	AAW59270	Arabidopsis thalia
154	7	1.3	178	22	AAU27668	Human protein AFP6	227	7	1.3	361	21	AAW17918	Arabidopsis thalia
155	7	1.3	178	22	AAW03375	Human gene 2 encod	228	7	1.3	367	21	AAW17918	Arabidopsis thalia

229	7	1.3	377	23	AAE28936	Human sodium/bile-
230	7	1.3	377	24	AAE29906	Human transporter
231	7	1.3	390	22	ABBS9303	Drosophila melanog
232	7	1.3	399	23	ABBS5336	Lactococcus lactis
233	7	1.3	399	24	AAE31967	Bacillus subtilis
234	7	1.3	406	21	AAE33205	Human ORFX ORF2969
235	7	1.3	424	24	AAE18745	Pseudomonas aerugi
236	7	1.3	456	24	AAO16594	Human GLYT1 protei
237	7	1.3	458	24	ABP57706	Saccharopolyspora
238	7	1.3	459	21	AAE57687	Streptococcus pneu
239	7	1.3	459	23	AAU83249	S. pneumoniae ABC
240	7	1.3	459	24	ABU00977	S. pneumoniae type
241	7	1.3	460	21	AAE81545	Streptococcus pneu
242	7	1.3	469	23	AAU72939	Neisseria meningit
243	7	1.3	470	19	AAU47172	Glucosyl transfera
244	7	1.3	470	20	AAU06274	Tomato dehydrodico
245	7	1.3	471	20	AAU98009	Medium-chain UDP-g
246	7	1.3	474	22	ABG19636	Novel human diagno
247	7	1.3	492	22	AAE92209	C glutamincum prote
248	7	1.3	495	23	ABBS1922	Human fibroblast g
249	7	1.3	517	23	ABBS7872	Human ankyrin homo
250	7	1.3	518	22	ABBS6436	Drosophila melanog
251	7	1.3	526	14	AAE33375	Brevibacterium fla
252	7	1.3	526	22	AAE91406	Corynebacterium gl
253	7	1.3	526	22	AAE79695	Novel human thromb
254	7	1.3	548	23	ABG70356	Drosophila melanog
255	7	1.3	550	22	ABBS0211	Drosophila melanog
256	7	1.3	554	22	ABBS1243	Drosophila melanog
257	7	1.3	554	22	ABBS1246	Drosophila melanog
258	7	1.3	557	22	ABBS6631	Drosophila melanog
259	7	1.3	563	23	ABBS1144	Herbicidally activ
260	7	1.3	570	21	AAE91944	Human chaperrone pr
261	7	1.3	570	21	AAE94912	Human secreted pro
262	7	1.3	572	23	ABPA1775	Human ovarian anti
263	7	1.3	578	20	AAE90965	Human complement E
264	7	1.3	582	21	AAE19338	Amino acid sequenc
265	7	1.3	600	23	ABBS1520	Herbicidally activ
266	7	1.3	635	22	AAE31594	Fc epsilon recepto
267	7	1.3	638	23	AAU93126	Arabidopsis transc
268	7	1.3	657	22	ABG14461	Novel human diagno
269	7	1.3	660	22	AAE31593	Fc epsilon recepto
270	7	1.3	669	23	ABBS09771	Amino acid sequenc
271	7	1.3	669	23	ABBS09781	Amino acid sequenc
272	7	1.3	679	22	ABBS2564	Novel human diagno
273	7	1.3	690	22	ABBS1234	Drosophila melanog
274	7	1.3	712	23	ABG18031	Novel human diagno
275	7	1.3	727	23	AAU74448	Human protein sequ
276	7	1.3	731	22	AAE31591	Amino acid sequenc
277	7	1.3	746	17	AAE33270	GST-INL fusion int
278	7	1.3	756	22	AAE31590	Amino acid sequenc
279	7	1.3	775	22	AAU67605	Propionibacterium
280	7	1.3	782	23	ABBS9330	Herbicidally activ
281	7	1.3	795	22	ABBS1567	Drosophila melanog
282	7	1.3	802	23	AAE16588	Human fibroblast g
283	7	1.3	804	23	ABP64757	Human protein SEQ
284	7	1.3	831	22	AAE78806	Human protein SEQ
285	7	1.3	839	23	AAU86145	Human PEO7168 poly
286	7	1.3	839	23	ABG34056	Human pro peptide
287	7	1.3	840	22	ABG03702	Novel human diagno
288	7	1.3	840	22	ABG33955	Novel human diagno
289	7	1.3	867	22	AAE79790	Human protein SEQ
290	7	1.3	885	17	AAE85754	Human axl receptor
291	7	1.3	885	23	AAU84262	Human endometrial
292	7	1.3	891	22	AAE78870	Human protein SEQ
293	7	1.3	894	17	AAE85753	Human axl receptor
294	7	1.3	894	22	AAE90763	Human shear stress
295	7	1.3	947	22	ABG2182	Novel human diagno
296	7	1.3	971	22	ABG05866	Novel human diagno
297	7	1.3	976	22	ABG07373	Novel human diagno
298	7	1.3	978	19	AAE48096	Human serum albumi
299	7	1.3	978	23	ABG3803	Human iGF receptor
300	7	1.3	995	22	ABG2184	Novel human diagno
301	7	1.3	1009	23	AAE25387	Human NZMS-11 prot

302	7	1.3	1009	23	AAU84380	Novel human secret
303	7	1.3	1013	21	AAE4687	Amino acid sequenc
304	7	1.3	1013	22	AAE11053	Ashbya gossypii GT
305	7	1.3	1078	22	ABBS3389	Drosophila melanog
306	7	1.3	1085	22	ABG27847	Novel human diagno
307	7	1.3	1091	23	ABBS48258	Listeria monocytog
308	7	1.3	1097	22	ABG25216	Novel human diagno
309	7	1.3	1151	22	AAE83939	Amino acid sequenc
310	7	1.3	1192	22	ABG02038	Novel human diagno
311	7	1.3	1202	22	AAE78807	Human protein SEQ
312	7	1.3	1225	22	ABG03949	Novel human diagno
313	7	1.3	1234	24	ABG72921	Human prostate can
314	7	1.3	1239	21	AAE84279	Human ORFX ORF2493
315	7	1.3	1240	22	AAU30861	Novel human secret
316	7	1.3	1251	16	AAE79475	Mouse lTRP-3. Mus
317	7	1.3	1251	22	AAE61481	Murine lTRP-3 prot
318	7	1.3	1251	22	AAE61483	Human TANGO 300 ex
319	7	1.3	1253	21	AAE12271	Mouse Latent TGF-b
320	7	1.3	1253	22	AAE61420	Murine TANGO 275 p
321	7	1.3	1270	24	ABU11749	Human MDR1 polypep
322	7	1.3	1398	22	ABBS4629	Drosophila melanog
323	7	1.3	1540	22	ABG25976	Novel human diagno
324	7	1.3	1592	18	AAW34623	Human C3 protein m
325	7	1.3	1611	18	AAW22604	Tylosine synthase
326	7	1.3	1635	18	AAW34624	Human C3 protein m
327	7	1.3	1657	18	AAW34629	Human C3 protein m
328	7	1.3	1659	24	ABBS1332	Streptococcus pneu
329	7	1.3	1659	24	ABU00861	S. pneumoniae type
330	7	1.3	1661	18	AAW34625	Human C3 protein m
331	7	1.3	1663	17	AAE94028	Human C3 precursor
332	7	1.3	1663	17	AAE94029	Human modified C3
333	7	1.3	1663	17	AAE94030	Human modified C3
334	7	1.3	1663	18	AAW34620	Human C3 protein m
335	7	1.3	1663	18	AAW34620	Human C3 protein m
336	7	1.3	1663	18	AAW34621	Human C3 protein m
337	7	1.3	1663	18	AAW34627	Human C3 protein m
338	7	1.3	1663	18	AAW34628	Human C3 protein m
339	7	1.3	1663	18	AAW34630	Human C3 protein m
340	7	1.3	1663	18	AAW40988	Human C3 protein m
341	7	1.3	1663	18	AAW40989	Human C3 protein m
342	7	1.3	1663	18	AAW40990	Human C3 protein m
343	7	1.3	1663	18	AAW34611	Human C3 protein m
344	7	1.3	1663	18	AAW34612	Human C3 protein m
345	7	1.3	1663	18	AAW34608	Human C3 protein m
346	7	1.3	1663	18	AAW34609	Human C3 protein m
347	7	1.3	1663	18	AAW34610	Human C3 protein m
348	7	1.3	1663	18	AAW34611	Human C3 protein m
349	7	1.3	1663	18	AAW34612	Human C3 protein m
350	7	1.3	1663	18	AAW34613	Human C3 protein m
351	7	1.3	1663	18	AAW34614	Human C3 protein m
352	7	1.3	1663	18	AAW34615	Human C3 protein m
353	7	1.3	1663	18	AAW34616	Human C3 protein m
354	7	1.3	1663	18	AAW34617	Human C3 protein m
355	7	1.3	1663	18	AAW34618	Human C3 protein m
356	7	1.3	1667	18	AAW34626	Human C3 protein m
357	7	1.3	1667	18	AAW34631	Human C3 protein m
358	7	1.3	1782	22	ABBS5685	Drosophila melanog
359	7	1.3	1795	22	ABBS59806	Drosophila melanog
360	7	1.3	1836	24	ABE25404	Aspergillus fumiga
361	7	1.3	1857	24	ABE26004	Aspergillus fumiga
362	7	1.3	1916	22	ABBS2423	Drosophila melanog
363	7	1.3	1916	22	ABBS6089	Drosophila melanog
364	7	1.3	1964	20	AAE95557	Mus musculus notch
365	7	1.3	1980	22	ABBS7589	Drosophila melanog
366	7	1.3	2047	22	ABBS9541	Human CLASP-7 prot
367	7	1.3	2047	23	ABG61707	Human cadherin-11k
368	7	1.3	2062	23	AAU99400	Human tumour suppr
369	7	1.3	2067	24	ABU11831	Human MDR1 polypep
370	7	1.3	3080	10	AAE93285	Sequence of clone
371	7	1.3	3210	9	AAE81771	Deduced sequence e
372	7	1.3	3257	22	ABBS7502	Drosophila melanog
373	7	1.3	3931	24	ABU07377	Human protein NOV9
374	7	1.3	7	20	AAE30095	Cyclin binding dom

375	6	1.1	7	23	ABG7648	Targeting peptide	448	6	1.1	22	22	ABG79009	Consensus signal s
376	6	1.1	8	16	AAR7413	Human TSH receptor	449	6	1.1	22	22	AAR53402	Consensus signal p
377	6	1.1	9	20	AAV5442	HuA binding p1u-1	450	6	1.1	22	22	AAV52570	Consensus signal p
378	6	1.1	9	20	AAV46021	Immunogenic peptid	451	6	1.1	22	22	AAE13132	Consensus signal p
379	6	1.1	9	20	AAV46424	Immunogenic peptid	452	6	1.1	22	22	AAE12406	Consensus signal p
380	6	1.1	9	20	AAV46487	Immunogenic peptid	453	6	1.1	22	23	ABG71500	Consensus signal p
381	6	1.1	9	20	AAV00811	HuA-A24 antigenic	454	6	1.1	22	23	ABG96476	Human myeloid prog
382	6	1.1	9	20	AAW97259	Cytotoxic T-cell e	455	6	1.1	22	23	AAU99514	Consensus signal s
383	6	1.1	9	22	AAH88457	HER2/NEU DR superm	456	6	1.1	22	23	ABG63324	Synthetic signal p
384	6	1.1	9	22	AAH88591	HER2/NEU DR superm	457	6	1.1	22	23	AAE20851	Consensus signal p
385	6	1.1	9	22	AAH88959	HER2/neu epitope H	458	6	1.1	22	23	AAU79154	Synthetic consensu
386	6	1.1	9	22	AAU02236	HuA binding TADG-1	459	6	1.1	22	23	AAU75223	Consensus signal p
387	6	1.1	9	22	AAU02263	HuA binding TADG-1	460	6	1.1	22	23	AAU75412	Tumour necrosis fa
388	6	1.1	9	22	AAU02274	HuA binding TADG-1	461	6	1.1	23	21	AAV54009	Calcineurin bindin
389	6	1.1	9	22	AAU02293	HuA binding TADG-1	462	6	1.1	24	14	AAH42318	EBV VCA-p18 fragme
390	6	1.1	9	22	AAU02297	HuA binding TADG-1	463	6	1.1	24	16	AAH74987	Epstein-Barr virus
391	6	1.1	9	22	AAU02315	HuA binding TADG-1	464	6	1.1	24	24	AAO26957	EBV virus peptide
392	6	1.1	9	22	AAU02334	HuA binding TADG-1	465	6	1.1	25	22	AAH66870	Human EtB2 CD4+ T
393	6	1.1	10	22	AAH97586	Human complementar	466	6	1.1	25	22	AAH66885	Human EtB2 CD4+ T
394	6	1.1	10	22	AAH97593	Saccharomyces cere	467	6	1.1	25	23	AAH62679	Bacterial DnaB1
395	6	1.1	10	22	AAH97842	Saccharomyces cere	468	6	1.1	25	23	AAH29090	Cloned bovine inte
396	6	1.1	10	22	AAH97843	Saccharomyces cere	469	6	1.1	26	23	AAO17005	Pro-opiomelanocort
397	6	1.1	10	22	AAH98179	Saccharomyces cere	470	6	1.1	26	24	AAH96841	Human PRGF N-term
398	6	1.1	11	7	AAH60959	Gamma-odn which i	471	6	1.1	26	24	AAH75012	Human secreted pro
399	6	1.1	11	23	AAH66008	Modified I-TAC che	472	6	1.1	27	19	AAH74895	Human novel secret
400	6	1.1	12	21	AAH56322	Triglycylylvaopres	473	6	1.1	27	19	AAH75012	Human novel secret
401	6	1.1	13	13	AAH26040	Oligopeptide P96-1	474	6	1.1	27	23	AAH95147	Human novel secret
402	6	1.1	13	13	AAH26332	Murine GM-CSF P96-	475	6	1.1	27	23	AAH95147	Human novel secret
403	6	1.1	13	21	AAH54010	Calcineurin bindin	476	6	1.1	28	15	AAH51784	Der p II derived p
404	6	1.1	13	24	AAH99850	Human GM-CSF MHC c	477	6	1.1	28	19	AAH71959	Der matopagoides s
405	6	1.1	13	24	AAH99851	Human GM-CSF MHC c	478	6	1.1	28	20	AAH50416	Der matopagoides s
406	6	1.1	14	19	AAH47507	Human beta-HCG scr	479	6	1.1	28	22	AAH50046	Wild-type IL-4 pep
407	6	1.1	14	19	AAH50067	Human chorionic go	480	6	1.1	28	22	AAH50047	Mutant IL-4 pepid
408	6	1.1	14	19	AAH50102	Human chorionic go	481	6	1.1	28	22	AAH19016	T-cell epitope con
409	6	1.1	15	14	AAH42321	EBV VCA peptide.	482	6	1.1	28	24	AAH30288	Human Lp317 protei
410	6	1.1	15	21	AAH98838	HuA class II bindi	483	6	1.1	30	24	AAH02679	S. pneumoniae type
411	6	1.1	15	21	AAH98839	HuA class II bindi	484	6	1.1	31	21	AAH20889	Human Lhx3b immuno
412	6	1.1	15	21	AAH70813	Secretory signal s	485	6	1.1	31	21	AAH20891	Porcine Lhx3b prot
413	6	1.1	15	22	AAH88386	HER2/NEU DR superm	486	6	1.1	32	17	AAH03347	HCV core1+2+3 epit
414	6	1.1	15	22	AAH88450	HER2/NEU DR superm	487	6	1.1	32	22	AAH28266	Novel human secret
415	6	1.1	15	22	AAH88458	HER2/NEU DR superm	488	6	1.1	32	22	AAH75127	Human secreted pro
416	6	1.1	15	22	AAH88458	HER2/NEU DR superm	489	6	1.1	35	19	AAH75127	Human secreted pro
417	6	1.1	15	22	AAH88592	HER2/NEU DR superm	490	6	1.1	36	22	AAH71209	Peptide #11246 enc
418	6	1.1	15	22	AAH88658	HER2/NEU DR superm	491	6	1.1	38	17	AAH97677	Chick yee proto-on
419	6	1.1	15	22	AAH89007	HER2/neu DR super	492	6	1.1	39	20	AAH74050	Human hept1 bindi
420	6	1.1	15	22	AAH89008	HER2/neu DR super	493	6	1.1	42	22	ABG18775	Novel human diago
421	6	1.1	15	22	AAH89009	HER2/neu DR super	494	6	1.1	44	22	ABG47722	Human liver peptid
422	6	1.1	15	22	AAH89048	HER2/neu DR super	495	6	1.1	44	22	ABH27699	Human peptide #350
423	6	1.1	15	22	AAH89049	HER2/neu DR super	496	6	1.1	44	22	ABH32870	Peptide #376 encod
424	6	1.1	15	23	ABG62477	Eubacterial Duf72	497	6	1.1	44	22	AAH18352	Protein #351 encod
425	6	1.1	15	23	AAH8430	Insulin/insulin-1i	498	6	1.1	44	22	AAH53672	Human brain expres
426	6	1.1	15	23	AAH48206	Human baesophil gra	499	6	1.1	44	22	AAH6056	Human bone marrow
427	6	1.1	16	23	AAH14608	Interleukin-4 heil	500	6	1.1	44	22	AAH6056	Human bone marrow
428	6	1.1	17	22	AAH73392	Rat SSeCKS cyclin	501	6	1.1	44	22	AAH26331	Peptide #359 encod
429	6	1.1	17	23	AAU08978	Human CDC25A inhib	502	6	1.1	44	23	AAH01668	Peptide #350 encod
430	6	1.1	18	17	AAU75740	Anti-(MCP)-1 antih	503	6	1.1	44	23	ABU51287	Helicobacter pylor
431	6	1.1	18	22	AAU75740	Amphiphilic antim	504	6	1.1	45	20	AAH35704	Human peptide enco
432	6	1.1	18	22	ABG48839	Human liver peptid	505	6	1.1	45	22	AAH45284	Human secreted pro
433	6	1.1	18	22	ABH28833	Peptide #1484 enco	506	6	1.1	46	22	AAH16675	Signal peptide for
434	6	1.1	18	22	ABH34018	Peptide #1524 enco	507	6	1.1	46	23	AAH66029	Human 5' EST secre
435	6	1.1	18	22	ABH19459	Protein #1458 enco	508	6	1.1	47	20	AAH12862	Nucleic acid selec
436	6	1.1	18	22	AAH54786	Human brain expres	509	6	1.1	47	23	AAH91263	Human liver peptid
437	6	1.1	18	22	AAH67173	Human bone marrow	510	6	1.1	48	22	ABH66599	Drosophila melanog
438	6	1.1	18	22	AAH15032	Peptide #1466 enco	511	6	1.1	48	22	ABH66599	Peptide #8662 enco
439	6	1.1	18	22	AAH15032	Peptide #1508 enco	512	6	1.1	48	22	AAH41156	Protein #7191 enco
440	6	1.1	18	22	AAH15032	Peptide #1444 enco	513	6	1.1	48	22	AAH62016	Human brain expres
441	6	1.1	18	23	ABG71572	Mycobacteriophage	514	6	1.1	48	22	AAH74818	Human poly peptide
442	6	1.1	18	23	ABG36835	Human peptide enco	515	6	1.1	48	22	AAO05521	Human polypeptide
443	6	1.1	19	10	AAH90312	Alpha-helix-formin	516	6	1.1	48	22	AAH4934	Human peptide enco
444	6	1.1	19	10	AAH90312	Lysine oxidase pro	517	6	1.1	48	22	AAH44605	Peptide #8971 enco
445	6	1.1	20	12	AAH11966	Human interleukin-	518	6	1.1	50	22	AAH52970	Human peptide enco
446	6	1.1	22	16	AAH85180	GM-CSF receptor bl	519	6	1.1	50	22	AAH03940	Human musculoskele
447	6	1.1	22	17	AAH04410	Circumsporozoite p	520	6	1.1	50	23	ABP06712	Human ORF protein

521	6	1.1	50	24	ABU13234	Novel human muscul	594	6	1.1	66	21	AA02678	Human secreted pro
522	6	1.1	51	22	AAU40783	Proionbacterium	595	6	1.1	66	21	AA93417	Amino acid sequenc
523	6	1.1	51	22	AAU59883	Proionbacterium	596	6	1.1	66	22	AA97349	Human immune/haema
524	6	1.1	51	23	ABP32097	Human ORP1070 prot	597	6	1.1	66	23	AB877029	Human protein sequ
525	6	1.1	52	22	AAU39818	Proionbacterium	598	6	1.1	66	23	ABG64907	Human albumin fusi
526	6	1.1	52	23	AAO17043	Human pro-opiomela	599	6	1.1	66	23	ABP33374	Human nuclease-1lx
527	6	1.1	53	22	AAU48443	Proionbacterium	600	6	1.1	67	16	AA979507	Branched-chain alp
528	6	1.1	54	21	AA852020	Human secreted pro	601	6	1.1	67	20	AA941696	Human PRO617 prote
529	6	1.1	54	22	AAU5867	Proionbacterium	602	6	1.1	67	21	AA844252	Human PRO617 (UNQ3
530	6	1.1	54	22	AAU56762	Proionbacterium	603	6	1.1	67	21	AA819581	Human PRO617 used
531	6	1.1	54	22	AAU65571	Proionbacterium	604	6	1.1	67	21	AA800473	Human secreted pro
532	6	1.1	54	22	ABG28926	Novel human diagno	605	6	1.1	67	22	AAU47924	Proionbacterium
533	6	1.1	55	19	AAW50261	Mouse BID truncate	606	6	1.1	67	22	AAU28155	Novel human secret
534	6	1.1	55	20	AA929334	Human secreted pro	607	6	1.1	67	23	AAU79607	Human clone DNA483
535	6	1.1	55	23	ABBS5769	Mycobacterium spec	608	6	1.1	67	24	ABU610982	Human PRO617 polyp
536	6	1.1	55	20	AA907809	Human secreted pro	609	6	1.1	68	22	AAU52189	Proionbacterium
537	6	1.1	55	20	AA911793	Human 5' EST seque	610	6	1.1	68	22	AAU54459	Proionbacterium
538	6	1.1	55	22	AAU39060	Human secreted pro	611	6	1.1	68	22	AAU61499	Human novel foetal
539	6	1.1	55	22	AAW92035	Human digestive sy	612	6	1.1	68	24	ABP77907	N. gonorrhoeae ami
540	6	1.1	55	23	ABBS5769	Human polypeptide	613	6	1.1	69	21	AA839425	Human secreted pro
541	6	1.1	56	16	AAW74989	Epoetin-Barr virus	614	6	1.1	69	22	AAU48474	Proionbacterium
542	6	1.1	56	22	AAW91222	Human immune/haema	615	6	1.1	69	23	ABP1893	Human ORP866 prote
543	6	1.1	56	23	ABBS4793	Lactococcus lactis	616	6	1.1	70	22	ABG09739	Novel human diagno
544	6	1.1	57	22	ABG54874	Human liver peptid	617	6	1.1	70	22	ABB17856	Human nervous syst
545	6	1.1	57	22	AAU56904	Proionbacterium	618	6	1.1	70	22	AAW79621	Human protein SBO
546	6	1.1	57	22	AAU64825	Proionbacterium	619	6	1.1	70	22	AAW8784	Peptide #2821 enco
547	6	1.1	57	22	ABBS39784	Peptide #7290 enco	620	6	1.1	70	22	AAW86365	Human gastric canc
548	6	1.1	57	22	ABBS2405	Protein #6404 enco	621	6	1.1	70	23	ABG38068	Human peptide enco
549	6	1.1	57	22	AAW60505	Human brain expres	622	6	1.1	70	23	ABP03136	Human ORFX protein
550	6	1.1	57	22	AAW73158	Human bone marrow	623	6	1.1	70	23	AAO16979	Human secreted pro
551	6	1.1	57	22	AAW19863	Peptide #6297 enco	624	6	1.1	71	19	AAW58982	Pro-opiomelanocort
552	6	1.1	57	22	AAW33371	Peptide #7408 enco	625	6	1.1	71	23	AAO16980	Homo sapiens adult
553	6	1.1	57	22	AAW06402	Human foetal prote	626	6	1.1	72	20	AAV07892	Adrenocorticotroph
554	6	1.1	57	22	ABG43004	Human peptide enco	627	6	1.1	72	21	AAW08954	Human secreted pro
555	6	1.1	58	20	AAW99320	Epoetin-Barr virus	628	6	1.1	73	21	AAW01106	Human secreted pro
556	6	1.1	58	22	AAU48641	Proionbacterium	629	6	1.1	73	21	AAW01228	Human secreted pro
557	6	1.1	58	22	AAW91931	Human digestive sy	630	6	1.1	73	22	AAW82180	Human immune/haema
558	6	1.1	58	23	ABP40976	Human liver associ	631	6	1.1	73	23	ABP05456	Human ORFX protein
559	6	1.1	58	23	ABP40837	Human liver antiqf	632	6	1.1	73	23	AAO16981	Adrenocorticotroph
560	6	1.1	59	20	AAW89036	Sequence ID #736 f	633	6	1.1	74	22	AAU47759	Proionbacterium
561	6	1.1	59	22	ABG54184	Human liver peptid	634	6	1.1	74	22	AAU66372	Proionbacterium
562	6	1.1	59	22	AAU57143	Proionbacterium	635	6	1.1	74	23	AAO16982	Adrenocorticotroph
563	6	1.1	59	22	ABBS39240	Peptide #6746 enco	636	6	1.1	74	23	AAO16983	Alpha-MSH-f consti
564	6	1.1	59	22	ABBS1161	Human secreted pro	637	6	1.1	75	21	AAW32763	Eucalyptus grandis
565	6	1.1	59	22	AAW72493	Human bone marrow	638	6	1.1	75	24	ABP56973	E. maxima immuno
566	6	1.1	59	23	ABG42313	Human peptide enco	639	6	1.1	76	21	AAW55660	Arabidopsis thalia
567	6	1.1	60	22	AAU54186	Proionbacterium	640	6	1.1	76	21	AAW55755	Arabidopsis thalia
568	6	1.1	60	23	ABP34807	Human ORF3780 prot	641	6	1.1	76	22	AAW47587	Mouse heat shock a
569	6	1.1	61	21	AAW08913	Human secreted pro	642	6	1.1	76	22	AAW47589	Rat CD24 peptide.
570	6	1.1	61	22	AAW80465	Human haematologic	643	6	1.1	77	22	AAU42054	Proionbacterium
571	6	1.1	61	22	AAW82055	Human secreted pro	644	6	1.1	77	22	AAW83526	Human immune/haema
572	6	1.1	61	20	AAW5279	Fragment of human	645	6	1.1	77	22	AAU02981	Angiotensin conver
573	6	1.1	62	20	AAW67929	Zea mays protein f	646	6	1.1	77	23	ABP43357	Human secreted pro
574	6	1.1	62	21	AAW33049	Human secreted pro	647	6	1.1	77	23	ABP08119	Human ORFX protein
575	6	1.1	62	21	AAW03233	Proionbacterium	648	6	1.1	77	24	ABP56106	Human IGFBP6 amino
576	6	1.1	62	22	AAU56522	Novel human diagno	649	6	1.1	78	21	AAW54008	Calcineurin bindin
577	6	1.1	63	22	ABG22753	Proionbacterium	650	6	1.1	79	21	AAW43962	Human cancer assoc
578	6	1.1	63	23	AAW52943	Proionbacterium	651	6	1.1	79	23	ABP07114	Human ORFX protein
579	6	1.1	63	23	ABP35402	Human ORF4375 prot	652	6	1.1	80	22	AAU44362	Proionbacterium
580	6	1.1	64	13	AAW24332	Tracheal antimicro	653	6	1.1	80	22	AAU46205	Proionbacterium
581	6	1.1	64	16	AAW66205	Bovine tracheal an	654	6	1.1	80	22	AAU61639	Proionbacterium
582	6	1.1	64	16	AAW66204	Bovine tracheal an	655	6	1.1	80	22	AAW47588	Human CD24 peptide
583	6	1.1	64	17	AAW66894	Prepro-LAP. Bos t	656	6	1.1	80	22	AAW65481	Human immune/haema
584	6	1.1	64	19	AAW69696	Human tracheal ant	657	6	1.1	80	22	AAW87092	Human immune/haema
585	6	1.1	64	21	AAW05993	Human secreted pro	658	6	1.1	80	23	ABP68613	Human pancreatic c
586	6	1.1	64	22	AAW59393	Proionbacterium	659	6	1.1	80	23	ABP64138	Human ORF508. Hom
587	6	1.1	64	22	ABW03561	Human musculoskele	660	6	1.1	80	24	ABW47940	Breast cancer asso
588	6	1.1	64	23	AAU90965	Transplant media a	661	6	1.1	80	24	ABP75965	Human GENSER prote
589	6	1.1	64	24	AAU12855	Novel human muscul	662	6	1.1	80	24	ABP76132	Human GENSER prote
590	6	1.1	65	17	AAW68896	Prepro-LAP #2. Sy	663	6	1.1	81	13	AAW26875	Rat intestinal tre
591	6	1.1	65	22	AAW58392	Proionbacterium	664	6	1.1	81	18	AAW27630	Rat trefolil factor
592	6	1.1	65	22	AAW81287	Human AFP protein	665	6	1.1	81	21	AAW99887	Rat intestinal tre
593	6	1.1	66	21	AAW00326	Human secreted pro	666	6	1.1	81	21	AAW59318	Arabidopsis thalia

667	6	1.1	81	21	AAV54567	Amino acid sequenc	740	6	1.1	93	23	ABP40341	Staphylococcus epi
668	6	1.1	81	22	ABG18234	Novel human diagno	741	6	1.1	94	21	AAV53925	Arabiidopsis thalia
669	6	1.1	81	22	ABG20201	Novel human diagno	742	6	1.1	94	21	AAV53038	Human secreted pro
670	6	1.1	81	23	AAE16433	Rat intestinal tre	743	6	1.1	94	22	AAU22535	Novel human colon
671	6	1.1	82	19	AAW56582	Petlecan splice va	744	6	1.1	94	22	AAW82544	Human immune/haema
672	6	1.1	82	21	AAW53397	Human secreted pro	745	6	1.1	94	22	AAW92490	Human immune/haema
673	6	1.1	82	21	AAW56557	Arabiidopsis thalia	746	6	1.1	95	20	AAW19661	Human digestive sy
674	6	1.1	82	22	AAV66045	Proponibacterium	747	6	1.1	95	21	AAW11541	SSQ ID NO 379 from
675	6	1.1	82	22	AAW24316	Human EST encoded	748	6	1.1	95	22	AAW84249	Arabiidopsis thalia
676	6	1.1	82	23	ABJ10914	Human secreted pro	749	6	1.1	95	23	AAW81283	Human immune/haema
677	6	1.1	82	23	ABP07904	Human ORFX protein	750	6	1.1	96	17	AAW91279	Corn KCP -like prot
678	6	1.1	82	23	ABE29929	Human Lp321 protei	751	6	1.1	96	19	AAW23999	Fat-specific gene
679	6	1.1	83	20	AAV21863	Mouse agouti-relat	752	6	1.1	96	20	AAW30616	Mouse fat-specific
680	6	1.1	83	22	ABW96420	Human testicular a	753	6	1.1	96	21	AAW27016	Protein associated
681	6	1.1	83	22	AAU50182	Proponibacterium	754	6	1.1	96	21	AAV97996	Mouse fat-specific
682	6	1.1	83	22	AAU51473	Proponibacterium	755	6	1.1	96	22	AAW87642	Bovine mammary tis
683	6	1.1	83	22	ABG26049	Novel human diagno	756	6	1.1	96	23	AAO21287	Corn KCP -like prot
684	6	1.1	83	22	AAW95889	Human reproductive	757	6	1.1	96	23	ABP08650	Human ORFX protein
685	6	1.1	83	23	ABP10957	Human ORFX protein	758	6	1.1	97	18	AAW44126	Streptococcus pneu
686	6	1.1	84	21	AAV32887	Zea mays protein f	759	6	1.1	97	19	AAV86076	S. pneumoniiae deri
687	6	1.1	84	21	AAV59026	Arabiidopsis thalia	760	6	1.1	97	21	AAW043325	Arabiidopsis thalia
688	6	1.1	84	21	AAV59317	Arabiidopsis thalia	761	6	1.1	97	21	AAW234454	Arabiidopsis thalia
689	6	1.1	84	22	ABG50231	Human liver peptid	762	6	1.1	97	21	AAV54007	Calcineurin bindin
690	6	1.1	84	22	ABG11106	Novel human diagno	763	6	1.1	97	22	ABG01911	Novel human diagno
691	6	1.1	84	22	ABW30201	Peptide #2852 enco	764	6	1.1	97	22	ABP40455	Staphylococcus epi
692	6	1.1	84	22	ABW35364	Peptide #2870 enco	765	6	1.1	97	24	ABP97706	Amino acid sequenc
693	6	1.1	84	22	ABW15019	Human nervous syst	766	6	1.1	97	24	ABJ37124	NOVX protein seque
694	6	1.1	84	22	ABW20806	Protein #2805 enco	767	6	1.1	98	22	AAO13900	Human polypeptide
695	6	1.1	84	22	AAW56195	Human brain expres	768	6	1.1	98	22	AAO13900	Plant SDF encoded
696	6	1.1	84	22	AAW68568	Human bone marrow	769	6	1.1	99	21	ABW03550	Human musculoskele
697	6	1.1	84	22	AAW16376	Peptide #2810 enco	770	6	1.1	99	22	ABW03550	Human ORF1471 prot
698	6	1.1	84	22	AAW28873	Peptide #2910 enco	771	6	1.1	99	23	ABP32498	Novel human muscul
699	6	1.1	84	22	AAW04112	Peptide #2794 enco	772	6	1.1	99	24	ABU012844	S. pneumoniiae type
700	6	1.1	84	23	ABP43617	PR02160 protein.	773	6	1.1	99	24	ABU01412	Human 5'

813	6	1.1	109	21	AAB40429	Human ORFX ORF193
814	6	1.1	109	23	ABP01336	Human ORFX protein
815	6	1.1	110	21	AAB40867	Human ORFX-ORF631
816	6	1.1	110	21	AA632886	zee maye protein f
817	6	1.1	110	22	AAU52797	Proiontobacterium
818	6	1.1	110	23	ABP07862	Human ORFX protein
819	6	1.1	111	13	AAAR26955	Human T lymphocyte
820	6	1.1	111	22	ABBB71018	Drosophila melanog
821	6	1.1	111	22	AAAG64616	Human brain expres
822	6	1.1	111	22	AAAG5087	Human brain expres
823	6	1.1	111	23	ABBB2268	Herbicidally activ
824	6	1.1	112	14	AAAR3433	LT-8-2. Ganoderma
825	6	1.1	112	21	AAAB33149	Pinus radiata tran
826	6	1.1	112	22	AAU47112	Proiontobacterium
827	6	1.1	112	22	AAU49273	Proiontobacterium
828	6	1.1	112	22	AAU57895	Proiontobacterium
829	6	1.1	112	22	ABBI5275	Proiontobacterium
830	6	1.1	112	22	AAAB23810	Human nervous syst
831	6	1.1	112	23	ABP38038	Human EST encoded
832	6	1.1	112	23	AAAB49275	Staphylococcus epi
833	6	1.1	112	23	AAAB49275	Human cell signal/
834	6	1.1	113	20	AAV21866	Amino acid sequenc
835	6	1.1	113	21	AAAB44227	Human cancer asoc
836	6	1.1	113	22	ABBB70281	Drosophila melanog
837	6	1.1	113	22	AAU48609	Proiontobacterium
838	6	1.1	113	22	ABG19319	Novel human diagn
839	6	1.1	113	22	AAAG90165	C glutamicum prote
840	6	1.1	113	23	ABP08125	Human ORFX protein
841	6	1.1	114	22	AAU42767	Proiontobacterium
842	6	1.1	114	22	AAU48548	Proiontobacterium
843	6	1.1	114	22	AAAB78304	Human bone marrow
844	6	1.1	114	22	AAAG92226	Human immune/haema
845	6	1.1	114	22	AAAG92226	C glutamicum prote
846	6	1.1	114	23	ABP34022	Human transport pr
847	6	1.1	115	18	AAAB9769	NOVX protein sequ
848	6	1.1	116	22	ABG18098	Staphylococcus aur
849	6	1.1	116	22	AAAB79486	Novel human diagn
850	6	1.1	117	20	AAV21867	Human protein SBO
851	6	1.1	117	21	AAAG15659	Amino acid sequenc
852	6	1.1	117	22	ABUS2900	Arabidopsis thalia
853	6	1.1	117	22	ABG12950	Human uterus-deriv
854	6	1.1	117	22	ABAB72462	Novel human diagn
855	6	1.1	118	6	AAAP50294	Partial WSIP. Ory
856	6	1.1	118	11	AAAR07611	Sequence of mamma
857	6	1.1	118	22	AAAB39722	Murine granulocyte
858	6	1.1	118	22	AAAB68611	Human VAPB-1. Ho
859	6	1.1	118	23	ABG32647	Human vacuolar pro
860	6	1.1	118	24	ABU18744	Peptidomonas aerugi
861	6	1.1	119	22	AAU64551	Proiontobacterium
862	6	1.1	119	22	ABG101820	Novel human diagn
863	6	1.1	119	22	ABBI17376	Human nervous syst
864	6	1.1	120	21	AAAG00195	Human secreted pro
865	6	1.1	120	22	AAU51164	Proiontobacterium
866	6	1.1	120	22	AAU51164	Proiontobacterium
867	6	1.1	120	23	AAU51164	Hepatitis C virus
868	6	1.1	120	23	AAU51164	Human polypeptide
869	6	1.1	121	17	AAAM07541	Clone 99, human pr
870	6	1.1	121	22	AAAB58441	Human liver peptid
871	6	1.1	121	22	AAAB58441	Human brain expres
872	6	1.1	122	19	AAAB58441	Human protein sequ
873	6	1.1	122	19	AAAB58441	Mouse BID truncate
874	6	1.1	122	20	AAAB58441	Protein which is s
875	6	1.1	122	22	AAAB58441	Enterococcus faeca
876	6	1.1	122	22	AAAB58441	Novel human diagn
877	6	1.1	122	23	ABBB97768	Human secretory po
878	6	1.1	122	23	ABBB97768	E faecalis EF046 p
879	6	1.1	122	23	ABBB97768	Human cytochrome x
880	6	1.1	122	23	AAU575737	AAV293 anti- (MCP) -
881	6	1.1	122	23	AAU575737	AAV293 anti- (MCP) -
882	6	1.1	122	24	ABU13592	Enterococcus faeca
883	6	1.1	123	24	ABP79046	N. gonorrhoeae ami
884	6	1.1	123	23	ABP31574	Human ORF547 prote
885	6	1.1	124	17	AAAB42908	DDD4 polypeptide #
	6	1.1	124	21	AAAB42908	Human ORFX ORF2672
886	6	1.1	124	21	AAAB08733	Amino acid sequenc
887	6	1.1	124	21	AAAB3165	MAGE5 polypeptide.
888	6	1.1	124	22	AAU48123	Proiontobacterium
889	6	1.1	124	22	AAU55784	Proiontobacterium
890	6	1.1	124	22	AAU55784	Proiontobacterium
891	6	1.1	124	22	AAAB01820	Human gene 12 enco
892	6	1.1	124	23	ABG64131	Human albumin fusi
893	6	1.1	125	21	ABP31689	Human ORF62 prote
894	6	1.1	125	22	AAAG33726	Arabidopsis thalia
895	6	1.1	125	22	AAU62578	Proiontobacterium
896	6	1.1	125	22	ABG00193	Novel human diagn
897	6	1.1	126	13	AAAR22188	Sequence of rat C-
898	6	1.1	126	21	AAAG3056	Human secreted pro
899	6	1.1	126	22	AAAG3056	Human polypeptide
900	6	1.1	126	22	AAAB48092	Protein encoded by
901	6	1.1	126	24	AAAB33512	Streptococcus pneu
902	6	1.1	126	24	AAAB33512	Streptococcus pneu
903	6	1.1	126	24	AAAB00447	S. pneumoniae type
904	6	1.1	127	10	AAAP1061	Human granulocyte-
905	6	1.1	127	11	AAAP1890	Amino acid sequenc
906	6	1.1	127	12	AAAR08268	Crystalline recombi
907	6	1.1	127	12	AAAR13215	Oxidised GM-CSF.
908	6	1.1	127	14	AAAR1540	r-h-GM-CSF. Homo
909	6	1.1	127	14	AAAR33774	Recombinant human
910	6	1.1	127	14	AAAR33775	Human Leu23-GM-CSF
911	6	1.1	127	16	AAAR72357	Human granulocyte
912	6	1.1	127	16	AAAM13057	HIV-2 provirus--enc
913	6	1.1	127	20	AAV49918	Human GM-CSF prote
914	6	1.1	127	20	AAV35046	Chlamydia pneumonia
915	6	1.1	127	21	AAAG59024	Arabidopsis thalia
916	6	1.1	127	21	AAV69025	Amino acid sequenc
917	6	1.1	127	22	ABG29256	Human liver peptid
918	6	1.1	127	22	ABBB4421	Peptide #1907 enco
919	6	1.1	127	22	AAAB33117	Peptide #1927 enco
920	6	1.1	127	22	AAAB33118	Mature human GM-CS
921	6	1.1	127	22	ABBB19833	Mature rat GM-CSF
922	6	1.1	127	22	AAAB55211	Protein #1832 enco
923	6	1.1	127	22	AAAB55211	Human brain expres
924	6	1.1	127	22	AAAB67606	Human bone marrow
925	6	1.1	127	22	AAAB54513	Peptide #1847 enco
926	6	1.1	127	22	AAAB79902	Peptide #1939 enco
927	6	1.1	127	23	AAAB03175	Peptide #1857 enco
928	6	1.1	127	23	ABBB78399	Amino acid sequenc
929	6	1.1	127	23	ABG37196	Human peptide enco
930	6	1.1	127	24	ABBB99813	Human granulocyte
931	6	1.1	128	9	AAAB1001	Sequence (I) of hu
932	6	1.1	128	10	AAAP00115	Synthetic human gr
933	6	1.1	128	10	AAAP00118	Synthetic human gr
934	6	1.1	128	11	AAAR03199	New human granular
935	6	1.1	128	16	AAAR79338	PMON13012 peptide.
936	6	1.1	128	16	AAAB00328	Modified human col
937	6	1.1	128	16	AAAB00329	Modified human col
938	6	1.1	128	17	AAAB00102	Granulocyte macroph
939	6	1.1	128	17	AAAB00103	Granulocyte macroph
940	6	1.1	128	19	AAAB09041	D3D4 polypeptide #
941	6	1.1	128	19	AAAB54144	GM-KSF activity ex
942	6	1.1	128	21	AAV53217	Human G-CSF mutant
943	6	1.1	128	22	AAAB14011	Chemically modifie
944	6	1.1	128	23	ABG97784	Human gene 6 encod
945	6	1.1	128	23	ABG64481	Human interleukin-
946	6	1.1	128	24	ABG64185	Human albumin fusi
947	6	1.1	129	8	AAAP70616	Human interleukin
948	6	1.1	129	8	AAAP70616	Mammal interleukin-
949	6	1.1	129	12	AAAR12788	Human IL-4 and pep
950	6	1.1	129	14	AAAR47182	Human IL-4 mutein. Homo
951	6	1.1	129	14	AAAR47183	IL-4 mutein Y124X.
952	6	1.1	129	14	AAAR47184	IL-4 mutein Y124G.
953	6	1.1	129	15	AAAB58630	Human interleukin-
954	6	1.1	129	20	AAV37560	Protein involved i
955	6	1.1	129	21	AAAB1881	Human ORFX ORF1645
956	6	1.1	129	21	AAAG12569	zee maye protein f
957	6	1.1	129	21	AAV57324	Human interleukin-
958	6	1.1	129	21	AAV69035	Amino acid sequenc

959	6	1.1	129	21	AAV53593	Rat agouti-related
960	6	1.1	129	22	ABG60262	Human ovarian anti-
961	6	1.1	129	22	AAW94546	Human reproductive
962	6	1.1	129	22	AAW41508	Human polypeptide
963	6	1.1	129	23	ABG92913	Human interleukin-
964	6	1.1	129	23	ABG61733	Novel ovarian rela
965	6	1.1	129	23	ABG60658	Human interleukin-
966	6	1.1	129	23	ABP31472	Human ORF445 prote
967	6	1.1	129	23	AAO14758	Mature human Inter
968	6	1.1	129	23	AAU83552	Arbuckle wild type h
969	6	1.1	130	21	AAO07664	Arabidopsis thaliana
970	6	1.1	130	21	AAAG53925	Arabidopsis thaliana
971	6	1.1	130	21	AAAG53960	Arabidopsis thaliana
972	6	1.1	130	22	AAW90325	Human immune/haema
973	6	1.1	130	22	AAO01995	Human polypeptide
974	6	1.1	130	23	ABP43871	Clone RPS-855D21.
975	6	1.1	130	23	ABP26330	Streptococcus poly
976	6	1.1	131	7	AAW60350	Human granulocyte
977	6	1.1	131	8	AAW70364	Sequence of human
978	6	1.1	131	8	AAW70351	Sequence of granul
979	6	1.1	131	19	AAW26779	Mouse agouti-regul
980	6	1.1	131	20	AAV49104	Mouse agouti-relat
981	6	1.1	131	22	AAO09636	Human polypeptide
982	6	1.1	131	22	AAW38858	Human polypeptide
983	6	1.1	131	22	AAO19090	Human granulocyte-
984	6	1.1	131	23	ABG31632	Human granulocyte-
985	6	1.1	131	23	ABW08135	Human GM-CSF polype
986	6	1.1	132	8	AAW70363	Sequence of human
987	6	1.1	132	21	AAW44085	Human cancer assoc
988	6	1.1	132	22	ABW96173	Human testicular a
989	6	1.1	132	22	AAW95489	Human reproductive
990	6	1.1	132	22	AAW59518	Human secreted pro
991	6	1.1	132	23	ABW51422	Helicobacter pylori
992	6	1.1	133	12	AAW13164	Human interleukin-
993	6	1.1	133	15	AAW66997	Human interleukin-
994	6	1.1	133	16	AAW72358	Human granulocyte
995	6	1.1	133	19	AAW61232	Streptococcus pneu
996	6	1.1	133	22	ABW62907	Drosophila melanog
997	6	1.1	133	23	ABW54650	S. pneumoniae SP10
998	6	1.1	133	23	ABG59943	Human DITP polype
999	6	1.1	133	24	ABW98963	Phosphatase 2A cat
1000	6	1.1	134	16	AAW91236	Interleukin-4 circ

ALIGNMENTS

RESULT 1

ABP56991 standard; Peptide; 86 AA.

XX	ABP56991;	
AC	ABP56991;	
XX	10-APR-2003 (first entry)	
DT		
XX	Toxoplasma gondii AMA1 amino acid sequence fragment.	
DE		
XX	Elmeria maxima; 250 kDa antigen; sporozoite; merozoite; infection;	
KW	vacine; antiparasitic; gene therapy.	
XX	Toxoplasma gondii.	
OS	Synthetic.	
XX	WO2003004684-A2.	
PN		
XX	16-JAN-2003.	
PD		
XX	03-JUL-2002; 2002WO-US21237.	
PF		
XX	06-JUL-2001; 2001US-303670P.	
PR		
XX	(WITC/) WITCOMBE D.	
PA	(SMIT/) SMITH N C.	

PA	(WALL/) WALLACH M.	
XX		
PI	Witcombe D, Smith NC, Wallach M;	
XX		
DR	WPI; 2003-201556/19.	
XX		
PT	New nucleic acid comprising a sequence encoding a 250 kDa polypeptide	
PR	from sporozoites/merozoites of Elmeria maxima, useful for preparing a	
PT	vaccine against Elmeria infection	
XX		
PS	Example 5; Fig 33; 198pp; English.	
XX		
CC	The present invention describes a nucleic acid (1) comprising a	
CC	sequence encoding a 250 kDa polypeptide from Sporozoites/Merozoites of	
CC	Elmeria maxima or its homologue or complement. Also described: (1) a	
CC	vector comprising the nucleic acid; (2) a host cell comprising the	
CC	vector; (3) a plasmid comprising the nucleic acid; (4) a transformed	
CC	cell comprising the nucleic acid; (5) producing a recombinant 250 kDa	
CC	polypeptide; (6) a recombinant polypeptide; (7) a vaccine against	
CC	E. tenella, E. acervulina, E. necatrix, E. praecox, E. maxima, E. mitis	
CC	or E. brunetti or a microorganism expressing an immunologically	
CC	cross-reactive antigen; (8) immunising a subject against infection by	
CC	Elmeria, or a microorganism expressing an immunologically cross-reactive	
CC	antigen; (9) conferring upon a newborn subject of an avian species	
CC	maternal immunity against infection by Elmeria; (10) a fertilised egg	
CC	from an avian species having an air sac, where the air sac is inoculated	
CC	with the vaccine; and (11) reducing the output of Elmeria oocytes in	
CC	faeces from a newborn subject of an avian species. (1) has antiparasitic	
CC	activity and can be used in a vaccine and in gene therapy. The nucleic	
CC	acid is useful for preparing a vaccine against E. tenella, E. acervulina,	
CC	E. necatrix, E. praecox, E. maxima, E. mitis or E. brunetti infection.	
CC	The present sequence represents an amino acid sequence used in an example	
CC	from the present invention.	
XX		
SQ	Sequence 86 AA;	
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	Best Local Similarity 100.0%; Pred. No. 3.7e-76;	
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DB	1 ALIAGLVGCVLLALLGGCGCFARLRDNRNGVQAHHHEHFGOSRGARKRPSDLMGEA 60	
QY	516 EPSFWDEAENIEODGETHWVEGDY 541	
DB	61 EPSFWDEAENIEODGETHWVEGDY 86	
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XX	AAW07963;	
AC	AAW07963;	
XX	17-OCT-2000 (first entry)	
DT		
XX	Arabidopsis thaliana protein fragment SEQ ID NO: 5315.	
DE		
XX	Arabidopsis thaliana protein identification; signal transduction pathway; metabolic pathway;	
KW	hybridisation assay; genetic mapping; gene expression control; promoter;	
XX	termination sequence.	
OS	Arabidopsis thaliana.	
XX		
PN	EP1033405-A2.	
XX		
PD	06-SEP-2000.	
XX		
PF	25-FEB-2000; 2000EP-0301439.	
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PR	25-FEB-1999; 99US-0121825.	
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PR	05-MAR-1999; 99US-0123180.	

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Best Local Similarity 100.0%; Pred. No. 8;
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Db 17 GVLLIALL 24

RESULT 3

AA049409
ID AA049409 standard; Protein; 39 AA.

XX AC AA049409;

XX DT 18-OCT-2000 (first entry)

XX DE Arabidopsis thaliana protein fragment SEQ ID NO: 62504.

XX KW protein identification; signal transduction pathway; metabolic pathway;

KW hybridisation assay; genetic mapping; gene expression control; promoter;

KW termination sequence.

OS Arabidopsis thaliana.

PN EP1033405-A2.

XX PD 06-SEP-2000.

XX PF 25-FEB-2000; 2000EP-0301439.

XX PR 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

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PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161922.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 1.5%; Score 8; DB 21; Length 39;
Best Local Similarity 100.0%; Pred. No. 8;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 465 GVLLALL 472
DB 17 GVLLALL 24

RESULT 4
ID AAY64731 standard; Protein; 60 AA.
XX AAY64731;
XX AC AAY64731;
XX DT 01-FEB-2000 (first entry)
XX DE Human 5' EST related polypeptide SEQ ID NO:892.
XX KW Human; 5' EST; expressed sequence tag; secreted protein; diagnosis;
KW gene therapy; chromosome mapping; upstream regulatory sequence;
KW forensic; location; development; protein synthesis; stability;
XX regulation; identification.
XX OS Homo sapiens.
XX PN WO9953051-A2.
XX PD 21-OCT-1999.
XX PF 09-APR-1999; 99WO-IB00712.
XX PR 09-APR-1998; 98US-0057719.
XX PR 28-APR-1998; 98US-0069047.
XX PA (GSET) GENSET.
XX PI Dumas Milne Edwards J, Duclert A, Giordano J;
XX WP1; 2000-038446/03.
XX DR N-PSDB; AAZ42345.
XX PT Novel secreted protein 5' expressed sequence tag sequences used in
XX diagnostic, forensic, gene therapy, and chromosome mapping procedures
XX Claim 3; Page 625; 837pp; English.
XX

```

CC AA242265 to AA243075 represent novel 5' expressed sequence tag (EST) sequences, corresponding to human secreted proteins. AAY64651 to CC AAY65438 represent the EST-related proteins corresponding to AA242265 to CC AAY63052. The 5' ESTs can be used for producing secreted human gene products. They can be used to identify and isolate 5' untranslated CC regions (UTRs) and upstream regulatory regions which control the CC location, development stage, rate, and quantity of protein synthesis, as CC well as stability of mRNA. The ESTs are also useful as probes for CC chromosome mapping, and to obtain full length cDNA clones. The ESTs can CC also be used in forensic procedures to identify individuals, or in CC diagnostic procedures to identify individuals having genetic diseases CC resulting from abnormal gene expression. The products may also be used in CC gene therapy protocols. The nucleic acids encoding signal peptides can be CC used for directing extracellular secretion of a polypeptide or the CC insertion of a polypeptide into a membrane, or importing a polypeptide CC into a cell. The proteins encoded by the EST sequences may be useful in CC treating a variety of human conditions. Secreted proteins have CC therapeutic value, and the identification of new secreted proteins is CC valuable. AA242249 to AA242264 and AAY64644 to AAY64650 represent CC sequences used in the exemplification of the present invention.

XX SQ Sequence 60 AA;

Query Match 1.5%; Score 8; DB 21; Length 60;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 466 VLLALLLG 473
Db 4 VLLALLLG 11

RESULT 5
ID ABP56974 standard; Peptide; 75 AA.
XX AC ABP56974;
XX DT 10-APR-2003 (first entry)
XX DE E. tenella microneme 4 protein amino acid sequence fragment.
XX KW Eimeria maxima; 250 kDa antigen; sporozoite; merozoite; infection;
XX KM vaccine; antiparasitic; gene therapy.
XX OS Eimeria tenella.
XX OS Synthetic.
XX PN WO2003004684-A2.
XX PD 16-JUN-2003.
XX PF 03-JUL-2002; 2002WO-US21237.
XX PR 06-JUL-2001; 2001US-303670P.
XX PA (WITC/) WITCOMBE D.
XX PA (SMIT/) SMITH N C.
XX PA (WALL/) WALLACH M.
XX PI WITCOMBE D, Smith NC, Wallach M;
XX DR WPI; 2003-201556/19.
XX PT New nucleic acid comprising a sequence encoding a 250 kDa polypeptide
XX PT from sporozoites/merozoites of Eimeria maxima, useful for preparing a
XX PT vaccine against Eimeria infection -
XX PS Example 5; Fig 33; 198pp; English.
XX CC The present invention describes a nucleic acid (1) comprising a
XX CC sequence encoding a 250 kDa polypeptide from Sporozoites/Merozoites of
XX CC Eimeria maxima or its homologue or complement. Also described: (1) a

CC vector comprising the nucleic acid; (2) a host cell comprising the
CC vector; (3) a plasmid comprising the nucleic acid; (4) a transformed
CC cell comprising the nucleic acid; (5) producing a recombinant 250 kDa
CC polypeptide; (6) a recombinant polypeptide; (7) a vaccine against
CC E. tenella, E. acerulina, E. necatrix, E. praecox, E. maxima, E. mittle
CC or E. brunetti or a microorganism expressing an immunologically
CC cross-reactive antigen; (8) immunising a subject against infection by
CC Eimeria, or a microorganism expressing an immunologically cross-reactive
CC antigen; (9) conferring upon a newborn subject of an avian species
CC maternal immunity against infection by Eimeria; (10) a fertilised egg
CC from an avian species having an air sac, where the air sac is inoculated
CC with the vaccine; and (11) reducing the output of Eimeria oocytes in
CC faeces from a newborn subject of an avian species. (1) has antiparasitic
CC activity and can be used in a vaccine and in gene therapy. The nucleic
CC acid is useful for preparing a vaccine against E. tenella, E. acerulina,
CC E. necatrix, E. praecox, E. maxima, E. mittle or E. brunetti infection.
CC The present sequence represents an amino acid sequence used in an example
CC from the present invention.

XX SQ Sequence 75 AA;

Query Match 1.5%; Score 8; DB 24; Length 75;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 463 VGVVLLLA 470
Db 7 VGVVLLLA 14

RESULT 6
ID AAO21315 standard; Protein; 106 AA.
XX AC AAO21315;
XX DT 05-AUG-2002 (first entry)
XX DE Soybean KCP-like protein, SEQ ID NO 70.
XX KW Antimicrobial, transgenic; plant; potato snakin antimicrobial protein;
XX KM GAS44; GAS45; GAS71 homologue; lysine- and cysteine- rich peptide;
XX KM KCP-like polypeptide; modulating; disease resistance.
XX OS Glycine max.
XX PN WO200222821-A2.
XX PD 21-MAR-2002.
XX PF 13-SEP-2001; 2001WO-US28429.
XX PR 13-SEP-2000; 2000US-232569P.
XX PR 11-SEP-2001; 2001US-0950933.
XX PA (PION-) PIONEER HI-BRED INT INC.
XX PI Simmons CR, Navarro Acevedo PA;
XX DR WPI; 2002-425842/45.
XX DR N-PSDB; AAL37842.
XX PT New polynucleotide encoding lysine- and cysteine-rich peptides-like
XX PT polypeptide useful for modulating the polypeptide level in a plant
XX PT cell, enhancing disease resistance -
XX PS Claim 1; Page 152; 163pp; English.
XX CC The invention relates to an isolated polynucleotide encoding a
XX CC polypeptide which is related to potato snakin antimicrobial protein and
XX CC GAS44 or GAS45 or GAS71 homologues, which is referred to as lysine- and
XX CC cysteine- rich peptides (KCP)-like polypeptide, having a nucleotide
XX CC sequence from 36 sequences of defined base pairs, given in the

CC specification. A recombinant expression cassette comprising the isolated
 CC polynucleotide of the invention is useful for modulating the level of
 CC (KCP)-like polypeptides in a plant cell, where the level of (KCP)-like
 CC polypeptides is increased, and disease resistance is enhanced. This
 CC sequence represents a KCP-like protein encoded by an isolated
 CC polynucleotide of the invention.

XX Sequence 106 AA;

Query Match 1.5%; Score 8; DB 23; Length 106;

Best Local Similarity 100.0%; Pred. No. 20;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 466 VLLALLG 473
 |||||
 9 VLLALLG 16

Db

RESULT 7

ABB69392 standard; Protein; 133 AA.

XX ABB69392;

DT 26-MAR-2002 (first entry)

DE Drosophila melanogaster polypeptide SEQ ID NO 34968.

XX Drosophila; developmental biology; cell signalling; insecticide;

KM pharmaceutical.

XX Drosophila melanogaster.

PN WO200171042-A2.

PD 27-SEP-2001.

PF 23-MAR-2001; 2001WO-US09231.

PR 23-MAR-2000; 2000US-191637P.

PR 11-JUL-2000; 2000US-0614150.

XX (PEKE) PE CORP NY.

PI Venter JC, Adams M, Li PWD, Myers EW;

DR WPI; 2001-655860/75.

XX N-PSDB; ABL13495.

PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions -

PS Disclosure; SEQ ID NO 34968; 21pp + Sequence Listing; English.

CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (AB16176-AB130511), expressed DNA
 CC sequences (AB101840-AB16175) and the encoded proteins
 CC (AB85737-AB872072).

CC The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pcc_sequences.

XX Sequence 133 AA;

Query Match 1.5%; Score 8; DB 22; Length 133;

Best Local Similarity 100.0%; Pred. No. 24;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 466 VLLALLG 473
 |||||
 6 VLLALLG 13

Db

RESULT 8

ABU05787 standard; Protein; 200 AA.

XX ABU05787;

DT 08-APR-2003 (first entry)

DE M. tuberculosis and M. leprae marker protein #438.

XX Mycobacteriosis; survival; virulence; protective antigen; vaccine;

KM mycobacterial disease; tuberculosis; leprosy.

XX Mycobacterium tuberculosis.

OS Mycobacterium leprae.

PN WO200274903-A2.

PD 26-SEP-2002.

PF 22-FEB-2002; 2002WO-IB01973.

PR 22-FEB-2001; 2001US-270123P.

XX (INSP) INST PASTEUR.

PI Cole S;

DR WPI; 2002-759885/82.

PT Identifying and selecting genes for survival or virulence of
 PT mycobacteria by a comparative genomic analysis of the sequences of
 PT Mycobacterium tuberculosis and M. leprae -

XX Claim 17; Page 640-642; 874pp; English.

CC This invention relates to a novel method for identifying essential genes
 CC for survival or virulence of mycobacteria species. The method comprises
 CC aligning the genomic sequence of a first mycobacterium species on a
 CC genomic sequence of a second mycobacterium species and selecting a
 CC polynucleotide sequence that is highly conserved in both genomes with no
 CC counterparts in other bacterial genomic sequences and that corresponds
 CC to an essential gene for the survival or virulence of mycobacterium
 CC species. The method of the invention is useful for detecting M.
 CC tuberculosis or M. leprae infection. The method reduces the number of
 CC potential new targets and protective antigens for new drugs and vaccine
 CC compositions to treat and prevent mycobacterial diseases, particularly
 CC tuberculosis and leprosy. The present sequence represents a marker
 CC protein from Mycobacterium tuberculosis and Mycobacterium leprae
 CC identified using the method of the invention.

XX Sequence 200 AA;

Query Match 1.5%; Score 8; DB 23; Length 200;

Best Local Similarity 100.0%; Pred. No. 35;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 467 VLLALLG 474
 |||||
 8 VLLALLG 95

Db

RESULT 9

AAB58791 standard; Protein; 238 AA.

XX AAB58791;

DT 27-MAR-2001 (first entry)
 XX Breast and ovarian cancer associated antigen protein sequence SEQ ID 499.
 DE
 XX Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;
 KW nocotropic; neuroprotective; antiviral; antiallergic; hepatotropic;
 KW antidiabetic; antiinflammatory; antitumor; vulnery; anticonvulsant;
 KW antibacterial; antifungal; antiparasitic; cardiac; immune disorder;
 KW Addison's disease; allergy; autoimmune haemolytic anaemia;
 KW autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
 KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
 KW cardiovascular disorder; wound healing; neurological disease.
 KW
 OS Homo sapiens.
 PN WO200055173-A1.
 XX
 XX 21-SEP-2000.
 PD
 XX 08-MAR-2000; 2000WO-US05881.
 PF
 XX 12-MAR-1999; 99US-0124270.
 PR
 XX (HUMA-) HUMAN GENOME SCI INC.
 PA
 XX Rosen CA, Ruben SM;
 PI
 XX WPI; 2000-611515/58.
 DR
 XX N-PSDB; AAF21694.
 XX
 PT New human breast and ovarian cancer associated gene sequences and the
 PT polypeptides encoded by these genes, useful in the prevention,
 PT treatment and diagnosis of cancer, immune disorders, cardiovascular
 PT disorders and neurological diseases -
 XX
 PS Claim 11; Page 931; 1299pp; English.
 XX
 CC Sequences AAF21614 - AAF22031 represent DNA sequences encoding human
 CC proteins AAB5711 - AAB59128. The DNA and protein sequences are
 CC associated with breast and ovarian cancer. Included in the invention are
 CC sequences AAF22032 - AAF22040 and AAB59129 which are used in the
 CC isolation and characterisation of the DNA and protein sequences of the
 CC invention. The breast and ovarian cancer associated DNA, protein, agonist
 CC or antagonist sequences exhibit cytostatic; immunosuppressive;
 CC nocotropic; neuroprotective; antiviral; antiallergic; hepatotropic;
 CC antidiabetic; antiinflammatory; antitumor; vulnery; anticonvulsant;
 CC antibacterial; antifungal; antiparasitic and cardiac activity. The
 CC polynucleotide and protein sequences are used in the diagnosis of cancer,
 CC particularly breast and ovarian cancer. The nucleic acid sequences,
 CC proteins, agonists and antagonists may also be used in the diagnosis,
 CC prevention and treatment of immune disorders e.g. Addison's disease,
 CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
 CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
 CC arthritis and ulcerative colitis; cardiovascular disorders such as
 CC myocardial ischaemia; wound healing; neurological diseases such as
 CC cerebral anoxia and epilepsy; and infectious diseases.
 CC
 XX
 SQ Sequence 238 AA;
 XX
 Query Match 1.5%; Score 8; DB 21; Length 238;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX
 DT 03-SEP-2001 (first entry)
 XX Human colon cancer antigen protein SEQ ID NO:5033.
 DE
 XX Human; colon cancer; colon cancer antigen; diagnosis; detection;
 KW colorectal carcinoma.
 KW
 OS Homo sapiens.
 PN WO200122920-A2.
 XX
 XX 05-APR-2001.
 PD
 XX 28-SEP-2000; 2000WO-US26524.
 PF
 XX 29-SEP-1999; 99US-0157137.
 PR
 XX 03-NOV-1999; 99US-0163280.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 PI
 XX Ruben SM, Barash SC, Birse CE, Rosen CA;
 PI
 XX WPI; 2001-235357/24.
 DR
 XX N-PSDB; AAH33700.
 XX
 PT Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
 PT useful for preventing, diagnosing and/or treating colorectal cancers -
 XX
 PS Claim 11; Page 6764-6765; 9803pp; English.
 XX
 CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
 CC cancer-associated nucleic acid molecules (N) and proteins (P), where
 CC the proteins are collectively known as colon cancer antigens. The colon
 CC cancer antigens have cytostatic activity and can be used in gene
 CC therapy and vaccine production. N and P may be used in the prevention,
 CC diagnosis and treatment of diseases associated with inappropriate P
 CC expression. For example, N and P may be used to treat disorders
 CC associated with decreased expression by rectifying mutations or deletions
 CC in a patient's genome that affect the activity of P by expressing
 CC inactive proteins or to supplement the patient's own production of P.
 CC Additionally, N may be used to produce the colon cancer-associated P,
 CC by inserting the nucleic acids into a host cell and culturing the cell
 CC to express the proteins. N and P can be used in the prevention, diagnosis
 CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
 CC and AAB77789 represent sequences used in the exemplification of the
 CC present invention.
 CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
 CC missing at time of publication, meaning no sequences are present for
 CC SEQ ID NO:1027 to 1052, 7921 and 7922.
 CC
 XX
 SQ Sequence 255 AA;
 XX
 Query Match 1.5%; Score 8; DB 22; Length 255;
 Best Local Similarity 100.0%; Pred. No. 44;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

XX
 DT 28-MAY-1999 (first entry)
 XX Alternatively spliced Human CLAR1 protein sequence.
 DE
 XX CLAR1, human; late stage-specific marker; prostate cancer progression;
 KW

XX	Cancer susceptibility; diagnosis; therapy.
XX	
OS	Homo sapiens.
XX	
PN	WO9909215-A1.
XX	
PD	25-FEB-1999.
XX	
PF	13-AUG-1998; 98WO-US16768.
XX	
PR	13-AUG-1997; 97US-0055285.
XX	
PA	(FOXC-) FOX CHASE CANCER CENT.
XX	
PI	Rondineelli R, Triccoli JV;
XX	
DR	WPI, 1999-181061/15.
XX	
DR	N-PSDB; AAX27245.
XX	
PT	Newly isolated CLAR1 nucleic acid molecule (including complements
XX	and allelic variants) encoding a polypeptide - useful as a late
PT	stage-specific marker for the prognosis and diagnosis of prostate
XX	cancer progression
XX	
PS	Claim 14; Page 44; 70pp; English.
XX	
CC	This sequence is the human CLAR1 of the invention. CLAR1 was
CC	isolated from a human adult heart cDNA library and is a late
CC	stage-specific marker for prostate cancer progression. The CLAR1 nucleic
CC	acid molecules (including oligonucleotides as probes/primers) and
CC	antibodies against CLAR1 form kits for detecting expression of the CLAR1
CC	gene associated with a susceptibility to cancer. The nucleic acids are
CC	also useful for identifying and characterizing related genes from other
CC	species. They are useful for identifying genes encoding proteins that
CC	interact with CLAR1, which facilitates further study of the role of these
CC	cellular signaling mechanisms in cancer progression. The nucleic acids
CC	are also useful for controlling CLAR1 protein production. The CLAR1
CC	polypeptides are useful in screening for molecules (especially
CC	antibodies) that affect or modulate its activity or function. Such
CC	molecules may be therapeutically useful. The isolated CLAR1 nucleic acid
CC	molecule enables the generation of a transgenic animal, which can be
CC	used as a model for prostate cancer to allow screening and identification
CC	of compounds for the treatment of prostate cancer. Such an animal
CC	expresses the CAR1 protein at a higher level than that of a normal
CC	animal.
SO	
Sequence	256 AA;
Query Match	1.5%; Score 8; DB 20; Length 256;
Best Local Similarity	100.0%; Pred. No. 44;
Matches 8; Conservative	0; Mismatches 0; Indels 0; Gaps 0
QY	379 GSLSEETP 386
DB	154 GSLSEETP 161
RESULT 12	
AA048706	
ID	AA048706 standard; Protein; 266 AA.
XX	
AC	AA048706;
XX	
DT	21-MAR-2002 (first entry)
XX	
DE	Human transcription factor 29.26.
XX	
KW	Human; transcription factor 29.26; gene therapy; cytostatic; virucidal;
KW	immunomodulatory; antiinflammatory; haemostatic; malignant tumour;
KW	human immunodeficiency virus; HIV; infection; immunological disease.
XX	
OS	Homo sapiens.
XX	

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PN WO200192515-A1.
PD 06-DEC-2001.
XX 21-MAY-2001; 2001WO-CN00821.
PF 24-MAY-2000; 2000CN-0115813.
XX PR
XX (SHAN-) SHANGHAI BIOWINDOW GENE DEV INC.
XX PA
XX MAO Y, XIE Y;
XX PI
XX WPI; 2002-090044/12.
XX DR
XX N-PSDB; ABA96344.
XX
XX Human transcription factor 29.26 and encoding polynucleotide, used in
PT diagnosis and treatment of malignant tumours, haemopathy, human
PT immunodeficiency virus infection, immunological diseases and
PT inflammation -
XX
XX Claim 1; Page 30-31, 35pp; Chinese.
XX PS
XX
XX The invention relates to human transcription factor 29.26 with
CC cytosolic, virucidal, immunomodulatory, anti-inflammatory and
CC haemostatic activity. The protein and encoding polynucleotide are used
CC in diagnosis and treatment of malignant tumour, haemopathy, human
CC immunodeficiency virus (HIV) infection, immunological diseases and
CC various inflammations. The polynucleotide is useful in gene therapy.
XX
XX Sequence 266 AA;
SQ
QY 384 ETPNFIIP 391
  |||||
Db 116 ETPNFIIP 123

```

PT cancer progression
 XX
 PS Claim 13, Page 44; 70pp; English.
 CC This sequence is the human CLAR1 of the invention. CLAR1 was
 CC isolated from a human adult heart cDNA library and is a late
 CC stage-specific marker for prostate cancer progression. The CLAR1 nucleic
 CC acid molecules (including oligonucleotides as probes/primers) and
 CC antibodies against CLAR1 form kits for detecting expression of the CLAR1
 CC gene associated with a susceptibility to cancer. The nucleic acid are
 CC also useful for identifying and characterizing related genes from other
 CC species. They are useful for identifying genes encoding proteins that
 CC interact with CLAR1, which facilitates further study of the role of these
 CC cellular signalling mechanisms in cancer progression. The nucleic acids
 CC are also useful for controlling CLAR1 protein production. The CLAR1
 CC polypeptides are useful in screening for molecules (especially
 CC antibodies) that affect or modulate its activity or function. Such
 CC molecules may be therapeutically useful. The isolated CLAR1 nucleic acid
 CC molecule enables the generation of a transgenic animal, which can be
 CC used as a model for prostate cancer to allow screening and identification
 CC of compounds for the treatment of prostate cancer. Such an animal
 CC expresses the CAR1 protein at a higher level than that of a normal
 CC animal.
 XX
 SQ Sequence 276 AA;
 Query Match 1.5%; Score 8; DB 20; Length 276;
 Best Local Similarity 100.0%; Pred. No. 47;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 379 GSLSEETP 386
 Db 174 GSLSEETP 181
 RESULT 14
 AAP60577
 ID AAP60577 standard; Protein; 287 AA.
 XX
 AC AAP60577;
 XX
 DT 25-MAR-2003 (updated)
 DT 31-JUL-1991 (first entry)
 XX
 DE Eimeria tenella S401 sporozoite antigen.
 XX
 KW Antigen; vaccine; poultry; fowl; avian coccidiosis; immunization.
 XX
 OS Eimeria tenella.
 XX
 PN WO8600528-A.
 XX
 PD 30-JAN-1986.
 XX
 PF 05-JUL-1985; 85WO-US01274.
 XX
 PR 19-JUN-1985; 85US-0746520.
 PR 05-JUL-1984; 84US-0627811.
 XX
 PA (GENEX) GENEX CORP.
 XX
 PI Anderson DM, McCandliss RJ;
 DR WPI; 1986-042037/06.
 DR N-PSDB; AAN60488.
 XX
 PT New cloned gene expressing Eimeria antigen - useful in vaccines
 PT for protecting poultry against coccidiosis
 XX
 PS Claim 42; Fig 1; 82pp; English.
 XX
 CC The antigenic protein binds with an antibody directed against an
 CC antigenic protein of avian coccidia, (esp. a protein of E. tenella

CC sporozoite). It may be used for immunising birds against avian
 CC coccidiosis.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 287 AA;
 Query Match 1.5%; Score 8; DB 7; Length 287;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 463 VGVILLLA 470
 Db 219 VGVILLLA 226
 RESULT 15
 AAR05216
 ID AAR05216 standard; protein; 287 AA.
 XX
 AC AAR05216;
 XX
 DT 25-MAR-2003 (updated)
 DT 02-AUG-1990 (first entry)
 XX
 DE Antigens GX5401 and GX3264 encoded by cDNA of Eimeria tenella oocyte.
 XX
 KW Eimeria tenella; antigen GX5401; antigen GX3264; avian coccidiosis.
 XX
 OS Eimeria tenella.
 XX
 PN WO9000403-A.
 XX
 PD 25-JAN-1990.
 XX
 PF 05-JUL-1989; 89WO-US02918.
 XX
 PR 05-JUL-1988; 88US-0215162.
 XX
 PA (GENEX) GENEX CORP.
 XX
 PI Anderson DM, McCandliss RJ, Strauberg SL, Strauberg RL;
 DR WPI; 1990-051586/07.
 DR N-PSDB; AAG03317.
 XX
 PT Cloned gene or fragment encoding antigenic protein -
 PT which binds with antibodies against avian coccidia, and
 PT transformed cells used in vaccine
 XX
 PS Claim 1; Page 93; Fig 1; 134pp; English.
 XX
 CC They are antigenic proteins (AP) which bind with a monoclonal antibody
 CC (Mab) or polyvalent Ab directed against an AP of avian coccidia. GX5401
 CC is claimed in claim 1, and GX3264 is claimed in claim 2. Also new
 CC are an expression vector contg. their cloned gene, and host cells
 CC transformed with the vector. The transformed cells are used in a
 CC vaccine to immunise birds against avian coccidiosis. By labelling the
 CC peptides, they can be used as a type-specific probe. The Abs are used to
 CC used in an assay to detect Ab against the coccidia. They may also be
 CC identify transformed cells contg. the DNA.
 CC (Updated on 25-MAR-2003 to correct PA field.)
 XX
 SQ Sequence 287 AA;
 Query Match 1.5%; Score 8; DB 11; Length 287;
 Best Local Similarity 100.0%; Pred. No. 48;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 463 VGVLLLLA 470
XX |||||
Db 219 VGVLLLLA 226

RESULT 16

AAW67722 standard; Protein; 437 AA.

AAW67722;

16-MAR-1999 (first entry)

Human tumour antigen zsig15 protein sequence.

Secretion; differentiation marker; tumour; epithelial cell; colon; blood; breast; prostate; growth; development; antagonist; receptor; bone marrow; cancer; metastasis.

Homo sapiens.

WO9850552-A1.

12-NOV-1998.

06-MAY-1998; 98WO-US09584.

06-MAY-1997; 97US-0045703.

(ZYMO) ZYMOGENETICS INC.

Grossmann A, Shepard PO;

WPI; 1999-034723/03.

N-PSDB; AAV81394.

New nucleic acid encoding secreted polypeptide zsig15 - used as a marker for tumour cells, useful for diagnosis and treatment of cancer, inflammation and hyperplasia

Claim 16; Page 81-84; 100pp; English.

This sequence is of a secreted polypeptide, designated zsig15, which is a marker for differentiation in normal and tumour cells (particularly epithelial cells and derived tumours of colon, breast and prostate). The zsig15 protein is useful for the promotion of growth and development of epithelial cells; to identify specific (ant)agonists, also where conjugated to a toxin, to deliver these to cells expressing the cognate receptor (e.g. to kill cells of blood, colon, breast and bone marrow cancer), and to identify/isolate receptors involved in cancer metastases. The sequence was isolated from a colon cancer library after screening an EST (expressed sequence tag) database for sequences containing putative secretion signal sequences.

Sequence 437 AA;

Query Match 1.5%; Score 8; DB 20; Length 437;

Best Local Similarity 100.0%; Pred. No. 71;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 466 VLLALLLG 473
XX |||||
Db 4 VLLALLLG 11

RESULT 17

AA96733 standard; Protein; 437 AA.

AA96733;

26-SEP-2000 (first entry)

PRO1863, a novel transmembrane protein.

PRO1863; secreted protein; transmembrane protein; recombinant production; gene therapy.

Homo sapiens.

Key Location/Qualifiers

Peptide 1..15

Modified-site /label= Signal_peptide

Modified-site /note= "N-glycosylation site"

Modified-site /note= "Glycosaminoglycan attachment site"

Modified-site /note= "N-myristoylation site"

Modified-site /note= "N-myristoylation site"

Modified-site /note= "N-myristoylation site"

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Modified-site /note= "N-myristoylation site"

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PR 10-FEB-1999; 99US-0119537.
PR 12-FEB-1999; 99US-0119965.
PR 02-JUN-1999; 99WO-US12252.
XX
XX (GETH ) GENENTECH INC.
XX
XX Borstein D, Desnoyers L, Ferrara N, Fong S, Gao W, Goddard A;
PI Gurrey AL, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK;
PI Wood WI;
XX
XX WPI; 2000-431586/37.
DR N-PSDB; AAA51263.
XX
XX Isolated nucleic acid molecule encodes a PRO polypeptide which is a
PT transmembrane polypeptide
XX
XX Claim 12; Fig 10; 154BP; English.
XX
XX This is PRO1863, a novel transmembrane protein. The invention
CC concerns novel secreted and transmembrane proteins, designated PRO
CC polypeptides. The cDNA and gene sequences are useful in the recombinant
CC production of PRO polypeptides, as a hybridization probe to screen
CC libraries to isolate cDNAs with sequence identity to PRO polypeptides or
CC to map the gene encoding the PRO polypeptides and analyzing genetic
CC disorders. The cDNA/gene can also be used to produce transgenic animals
CC useful for the development and screening of therapeutically useful
CC reagents. They can also be used in gene therapy, e.g. to replace a
CC defective gene.
XX
XX Sequence 437 AA:
SQ
Query Match 1.5%; Score 8; DB 21; Length 437;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 466 VLLALLLG 473
DB 4 VLLALLLG 11
RESULT 18
AAV87750
ID AAV87750 standard; Protein; 437 AA.
XX
XX AAV87750;
AC
XX
XX 17-AUG-2000 (first entry)
DT
XX
XX Human PRV-1 protein.
DE
XX
XX PRV-1; human; polycythaemia rubra vera; PRV; antiproliferative;
KW treatment; detection; diagnosis.
XX
XX Homo sapiens.
OS
XX
XX DE19849044-A1.
PN
XX
XX 27-APR-2000.
PD
XX
XX 23-OCT-1998; 98DE-1049044.
PF
XX
XX 23-OCT-1998; 98DE-1049044.
PR
XX
XX (UYFR-) UNIV FREIBURG KLINIKUM ALBERT-LUDWIGS.
PA
XX
XX Pahl H, Temerinac S;
PI
XX
XX WPI; 2000-319347/28.
DR
XX
XX N-PSDB; AAA12386.
XX
XX New polycythemia rubra vera-related polypeptide useful for diagnosis
PT and for developing therapeutic antibodies
XX

```

```

PS Claim 6; Fig 2; 6pp; German.
XX
XX This invention describes a novel PRV-1 protein (I) detected in humans
CC suffering from the condition polycythaemia rubra vera (PRV). The product
CC of the invention has antiproliferative activity. The encoding nucleic
CC acid sequence is used to express recombinant PRV-1 polypeptides and as a
CC source of antisense sequences that can be expressed in vivo for treatment
CC of PRV. (I) is used to raise specific mono or polyclonal antibodies and
CC these are used to diagnose PRV (by detecting (I), or its epitopes, in
CC immunoassays) or for treatment of PRV (optionally when coupled to a
CC cytotoxin). This sequence represents the human PRV-1 protein described in
CC the method of the invention.
XX
XX Sequence 437 AA:
SQ
Query Match 1.5%; Score 8; DB 21; Length 437;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 466 VLLALLLG 473
DB 4 VLLALLLG 11
RESULT 19
AAV87261
ID AAV87261 standard; Protein; 437 AA.
XX
XX AAV87261;
AC
XX
XX 11-MAY-2000 (first entry)
DT
XX
XX Human signal peptide containing protein HSP6-38 SEQ ID NO:38.
DE
XX
XX Human; signal peptide-containing protein; HSP6; diagnosis; cancer;
KW inflammation; cardiovascular disease; anticancer; anti-inflammatory;
KW antimicrobial; neuroprotective; cardiovascular; hepatotropic;
KW antiaslomatic; gene therapy; cell proliferation; neurological disorder;
KW reproductive disorder; developmental disorder; arteriosclerosis;
KW cirrhosis; psoriasis; acquired immune deficiency syndrome; anaemia;
KW asthma; Crohn's disease; infection; Alzheimer's disease; schizophrenia;
KW Parkinson's disease; Huntington's disease; ovulatory defect;
KW muscular dystrophy.
XX
XX Homo sapiens.
OS
XX
XX WO200000610-A2.
PN
XX
XX 06-JAN-2000.
PD
XX
XX 25-JUN-1999; 99WO-US14484.
PF
XX
XX 26-JUN-1998; 98US-0090762.
PR
XX
XX 31-JUL-1998; 98US-0094983.
PR
XX
XX 01-OCT-1998; 98US-0102686.
PR
XX
XX 11-DEC-1998; 98US-0112129.
XX
XX (INCY-) INCYTE PHARM INC.
PA
XX
XX Lal P, Tang YT, Gorgone GA, Corley NC, Guejler KJ, Baughn MR;
PI Akerblom IE, Au-Yang J, Yue H, Patterson C, Reddy R, Hillman JL;
PI Bandman O;
XX
XX WPI; 2000-160673/14.
DR
XX
XX N-PSDB; AA298146.
XX
XX New human signal peptide-containing proteins useful in treatment,
PT prevention and diagnosis of e.g. cancer, inflammation and
PT cardiovascular disease
XX
XX Claim 1; Page 185-186; 327pp; English.
PS
XX
XX AA298109 to AA298242 encode AAV87224 to AAV87357 which represent the
XX

```

CC human signal peptide-containing protein HSP-1 to HSP-134. HSPs have
CC anticancer, anti-inflammatory, antimicrobial, neurotrophic, hepatotropic,
CC neuroprotective, cardiovascular and antistatic activities, and can
CC be used in gene therapy. HSPs can be used to treat or prevent disorders
CC associated with decreased activity or function of HSP. Antagonists of
CC HSP are used to treat or prevent disorders associated with increased
CC activity or function of HSP. Such diseases include cell proliferation
CC (including cancer), inflammation, cardiovascular, neurological,
CC reproductive or developmental disorders, (e.g. arteriosclerosis,
CC cirrhosis, psoriasis, acquired immune deficiency syndrome, anaemia,
CC asthma, Crohn's disease, microbial or other infections, congestive or
CC ischaemic heart disease, Alzheimer's, Parkinson's or Huntington's
CC diseases, schizophrenia, ovulatory defects, muscular dystrophy). HSP
CC nucleic acids can be used for the recombinant production of HSP, for
CC detecting HSP in standard hybridisation and amplification assays (for
CC diagnosis and monitoring), in gene therapy, as antisense,
CC triplex-forming or ribosome therapeutics, for detecting related sequences
CC or genetic variations, and for chromosomal mapping. HSP are also used to
CC raise specific antibodies (Ab) and to screen for agonists and
CC antagonists (potential therapeutic agents). Ab are used to diagnose, or
CC monitor, HSP-related diseases (in usual immunoassays), as therapeutic
CC antagonists, in competitive drug screens, and for purification of HSP
CC from natural sources.

XX Sequence 437 AA;

Query Match 1.5%; Score 8; DB 21; Length 437;

Best Local Similarity 100.0%; Pred. No. 71; Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 466 VLLALLLG 473
|||
4 VLLALLLG 11

Db

RESULT 20

AA66737

ID AA66737 standard; protein; 437 AA.

XX AA66737;

XX 05-APR-2000 (first entry)

DE Membrane-bound protein PRO1181.

XX Membrane-bound polypeptide; PRO polypeptide; LDL receptor; TIE ligand;

KW pharmaceutical; receptor immunoadhesin; gene mapping.

OS Homo sapiens.

PN MO963088-A2.

PD 09-DEC-1999.

PF 02-JUN-1999; 99WO-US12252.

XX 02-JUN-1998; 98US-0087607.

PR 02-JUN-1998; 98US-0087609.

PR 03-JUN-1998; 98US-0087759.

PR 04-JUN-1998; 98US-0088021.

PR 04-JUN-1998; 98US-0088025.

PR 04-JUN-1998; 98US-0088028.

PR 04-JUN-1998; 98US-0088030.

PR 04-JUN-1998; 98US-0088033.

PR 05-JUN-1998; 98US-0088167.

PR 05-JUN-1998; 98US-0088202.

PR 05-JUN-1998; 98US-0088212.

PR 09-JUN-1998; 98US-0088655.

PR 10-JUN-1998; 98US-0088730.
PR 10-JUN-1998; 98US-0088734.
PR 10-JUN-1998; 98US-0088738.
PR 10-JUN-1998; 98US-0088740.
PR 10-JUN-1998; 98US-0088741.
PR 10-JUN-1998; 98US-0088742.
PR 10-JUN-1998; 98US-0088810.
PR 10-JUN-1998; 98US-0088811.
PR 10-JUN-1998; 98US-0088825.
PR 10-JUN-1998; 98US-0088826.
PR 10-JUN-1998; 98US-0088858.
PR 11-JUN-1998; 98US-0088861.
PR 11-JUN-1998; 98US-0088863.
PR 11-JUN-1998; 98US-0088876.
PR 12-JUN-1998; 98US-0089090.
PR 12-JUN-1998; 98US-0089105.
PR 16-JUN-1998; 98US-0089440.
PR 16-JUN-1998; 98US-0089512.
PR 16-JUN-1998; 98US-0089514.
PR 17-JUN-1998; 98US-0089532.
PR 17-JUN-1998; 98US-0089538.
PR 17-JUN-1998; 98US-0089598.
PR 17-JUN-1998; 98US-0089599.
PR 17-JUN-1998; 98US-0089600.
PR 17-JUN-1998; 98US-0089653.
PR 18-JUN-1998; 98US-0089801.
PR 18-JUN-1998; 98US-0089907.
PR 18-JUN-1998; 98US-0089908.
PR 19-JUN-1998; 98US-0089947.
PR 19-JUN-1998; 98US-0089948.
PR 19-JUN-1998; 98US-0089952.
PR 22-JUN-1998; 98US-0090246.
PR 22-JUN-1998; 98US-0090252.
PR 23-JUN-1998; 98US-0090254.
PR 23-JUN-1998; 98US-0090349.
PR 23-JUN-1998; 98US-0090355.
PR 24-JUN-1998; 98US-0090429.
PR 24-JUN-1998; 98US-0090431.
PR 24-JUN-1998; 98US-0090435.
PR 24-JUN-1998; 98US-0090444.
PR 24-JUN-1998; 98US-0090445.
PR 24-JUN-1998; 98US-0090461.
PR 24-JUN-1998; 98US-0090472.
PR 24-JUN-1998; 98US-0090535.
PR 24-JUN-1998; 98US-0090538.
PR 24-JUN-1998; 98US-0090540.
PR 24-JUN-1998; 98US-0090557.
PR 25-JUN-1998; 98US-0090676.
PR 25-JUN-1998; 98US-0090678.
PR 25-JUN-1998; 98US-0090688.
PR 25-JUN-1998; 98US-0090690.
PR 25-JUN-1998; 98US-0090691.
PR 25-JUN-1998; 98US-0090694.
PR 25-JUN-1998; 98US-0090695.
PR 25-JUN-1998; 98US-0090696.
PR 26-JUN-1998; 98US-0090862.
PR 26-JUN-1998; 98US-0090863.
PR 01-JUL-1998; 98US-0091358.
PR 01-JUL-1998; 98US-0091360.
PR 01-JUL-1998; 98US-0091544.
PR 02-JUL-1998; 98US-0091478.
PR 02-JUL-1998; 98US-0091486.
PR 02-JUL-1998; 98US-0091519.
PR 02-JUL-1998; 98US-0091626.
PR 02-JUL-1998; 98US-0091628.
PR 02-JUL-1998; 98US-0091633.
PR 02-JUL-1998; 98US-0091646.
PR 02-JUL-1998; 98US-0091673.
PR 07-JUL-1998; 98US-0091978.
PR 07-JUL-1998; 98US-0091982.
PR 09-JUL-1998; 98US-0092182.
PR 10-JUL-1998; 98US-0092472.

CC	20-JUL-1998;	98US-0093339.
PR	30-JUL-1998;	98US-00934651.
PR	04-AUG-1998;	98US-0095282.
PR	04-AUG-1998;	98US-0095285.
PR	04-AUG-1998;	98US-0095301.
PR	04-AUG-1998;	98US-0095302.
PR	04-AUG-1998;	98US-0095318.
PR	04-AUG-1998;	98US-0095321.
PR	04-AUG-1998;	98US-0095325.
PR	10-AUG-1998;	98US-0095916.
PR	10-AUG-1998;	98US-0095929.
PR	10-AUG-1998;	98US-0096012.
PR	11-AUG-1998;	98US-0096143.
PR	11-AUG-1998;	98US-0096146.
PR	12-AUG-1998;	98US-0096329.
PR	17-AUG-1998;	98US-0096757.
PR	17-AUG-1998;	98US-0096766.
PR	17-AUG-1998;	98US-0096768.
PR	17-AUG-1998;	98US-0096773.
PR	17-AUG-1998;	98US-0096791.
PR	17-AUG-1998;	98US-0096867.
PR	17-AUG-1998;	98US-0096891.
PR	17-AUG-1998;	98US-0096895.
PR	17-AUG-1998;	98US-0096897.
PR	18-AUG-1998;	98US-0096949.
PR	18-AUG-1998;	98US-0096950.
PR	18-AUG-1998;	98US-0096959.
PR	18-AUG-1998;	98US-0096960.
PR	18-AUG-1998;	98US-0097022.
PR	19-AUG-1998;	98US-0097141.
PR	20-AUG-1998;	98US-0097218.
PR	24-AUG-1998;	98US-0097661.
PR	26-AUG-1998;	98US-0097951.
PR	26-AUG-1998;	98US-0097952.
PR	26-AUG-1998;	98US-0097954.
PR	26-AUG-1998;	98US-0097955.
PR	26-AUG-1998;	98US-0097971.
PR	26-AUG-1998;	98US-0097974.
PR	26-AUG-1998;	98US-0097978.
PR	26-AUG-1998;	98US-0097979.
PR	26-AUG-1998;	98US-0097986.
PR	26-AUG-1998;	98US-0098014.
PR	31-AUG-1998;	98US-0098525.
PR	16-SEP-1998;	98US-0100634.
PR	12-JAN-1999;	99US-0115565.
XX	(GETH) GENENTECH INC.	
PA		
PI	Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;	
PI	Wood WI, Yuan J;	
XX		
DR	WPI: 2000-072883/06.	
DR	N-PSDB; AA265083.	
XX		
XX	Membrane-bound proteins and related nucleotide sequences -	
PT		
XX		
PS	claim 12; Fig 250; 822pp; English.	
XX		
XX	The invention provides membrane-bound PRO polypeptides and	
CC	polynucleotides encoding them. The PRO sequences of the invention were	
CC	identified based on extracellular domain homology screening. The PRO	
CC	sequences have homology with proteins including LDL receptors, TIE	
CC	ligands and various enzymes. The membrane-bound proteins and receptor	
CC	molecules are useful as pharmaceutical and diagnostic agents. Receptor	
CC	immunoadhesins, for instance, can be used as therapeutic agents to block	
CC	receptor-ligand interactions. The membrane-bound proteins can also be	
CC	employed for screening of potential peptide or small molecule inhibitors	
CC	of the relevant receptor/ligand interaction. The PRO encoding sequences	
CC	are useful as hybridization probes, in chromosome and gene mapping and in	
CC	the generation of antisense RNA and DNA. PRO nucleic acid sequences	
CC	will also be useful for the preparation of PRO polypeptides, especially	
CC	by recombinant techniques.	

XX	Sequence	437 AA;
XX	Query Match	1.5%; Score 8; DB 21; Length 437;
XX	Best Local Similarity	100.0%; Pred. No. 71;
XX	Matches	8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY	466 VLLALLAG 473	
Db	4 VLLALLAG 11	
RESULT 21		
AAUI2404		
ID	AAUI2404 standard; Protein; 437 AA.	
XX		
AC	AAUI2404;	
XX		
DT	24-OCT-2001 (first entry)	
XX		
DE	Human PRO1181 polypeptide sequence.	
XX		
KW	Human secretory and transmembrane; PRO; mammalian; cancer; lung;	
KW	breast; prostate; cervical; tumour necrosis factor-alpha; TNF-alpha;	
KW	cartilage; ear; proliferation; glucose; free fatty acid; skeletal muscle;	
KW	adipocyte; A-peptide; factor VIIa; gene therapy.	
XX		
OS	Homo sapiens.	
XX		
PN	WO200140466-A2.	
XX		
PD	07-JUN-2001.	
XX		
PF	01-DEC-2000; 2000MO-US32678.	
XX		
PR	01-DEC-1999; 99MO-US28301.	
PR	01-DEC-1999; 99MO-US28634.	
PR	02-DEC-1999; 99MO-US28551.	
PR	02-DEC-1999; 99MO-US28564.	
PR	02-DEC-1999; 99MO-US28565.	
PR	09-DEC-1999; 98US-0170262.	
PR	16-DEC-1999; 99MO-US30095.	
PR	20-DEC-1999; 99MO-US30911.	
PR	20-DEC-1999; 99MO-US30999.	
PR	30-DEC-1999; 99MO-US31243.	
PR	06-JAN-2000; 2000MO-US00277.	
PR	06-JAN-2000; 2000MO-US00376.	
PR	11-FEB-2000; 2000MO-US03565.	
PR	18-FEB-2000; 2000MO-US04341.	
PR	18-FEB-2000; 2000MO-US04342.	
PR	22-FEB-2000; 2000MO-US04414.	
PR	24-FEB-2000; 2000MO-US04914.	
PR	24-FEB-2000; 2000MO-US05004.	
PR	01-MAR-2000; 2000MO-US05601.	
PR	20-MAR-2000; 2000MO-US07377.	
PR	21-MAR-2000; 2000MO-US07532.	
PR	30-MAR-2000; 2000MO-US08439.	
PR	17-MAY-2000; 2000MO-US13705.	
PR	22-MAY-2000; 2000MO-US14042.	
PR	30-MAY-2000; 2000MO-US14941.	
PR	02-JUN-2000; 2000MO-US15264.	
PR	10-NOV-2000; 2000MO-US30873.	
XX		
PA	(GENTECH) GENENTECH INC.	
XX		
PI	Baker KP, Beresini M, DeGeorge L, Desnoyers L, Filvaroff E, Gao W;	
PI	Gerlitsen ME, Goddard A, Godowski PJ, Gunney AU, Sherwood S;	
PI	Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WT, Zhang Z;	
XX		
DR	WPI: 2001-408281/43.	
DR	N-PSDB; AAS21476.	
XX		
PT	Isolated, secretory and transmembrane PRO polypeptide used to detect	

other PRO polypeptides, link bioactive molecules to cells expressing
 PT lung, breast, prostate, cervical -
 XX
 XX
 XX
 XX

Claim 12; Fig 466; 813pp; English.

AAU12172-AAU12446 represent novel human secretory and transmembrane
 CC PRO polypeptides. The PRO polypeptides are useful to detect other
 CC PRO polypeptides, to link bioactive molecules to cells expressing
 CC PRO polypeptides, to modulate biological activities of cells expressing
 CC PRO polypeptides, and to detect the presence of mammalian lung, colon,
 CC breast, prostate, rectal, cervical or liver tumours by comparing PRO
 CC polypeptide expression in a cell sample to that in a control sample.
 CC Some of the 275 sequences are also useful to stimulate the release of
 CC tumour necrosis factor-alpha (TNF-alpha) from human blood, the
 CC proliferation or differentiation of chondrocytes, the proliferation or
 CC gene expression in pericyte cells, the release of proteoglycans from
 CC cartilage, the proliferation of inner ear utricular supporting cells or
 CC of T-lymphocytes, the release of a cytokine from peripheral blood
 CC monocytes (PBMCs), or the proliferation of endothelial cells. Some of
 CC the PRO polypeptides may modulate glucose or free fatty acid uptake by
 CC skeletal muscle cells or by adipocytes; or inhibit binding of A-peptide
 CC to factor VIIa. The PRO polypeptides can be used in assays to identify
 CC molecules involved in binding interactions. The polynucleotides encoding
 CC PRO polypeptides can be used to generate probes, antisense RNA/DNA,
 CC transgenic or knock out animals and can be used in gene therapy.

Sequence 437 AA;

Query Match 1.5%; Score 8; DB 22; Length 437;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 466 VLLALALG 473
 |||||
 Db 4 VLLALALG 11

RESULT 22
 AAB70851

ID AAB70851 standard; Protein; 437 AA.

XX AAB70851;

DT 29-JUN-2001 (first entry)

XX Human PRV-1 protein.

KW PRV-1; human; hemostatic; polycythemia rubra vera; antisense therapy;
 KW treatment; diagnosis; pancytopenia; bone-marrow; blood; growth factor;
 KW pancytopenia; hematopoietic system disorder.

XX Homo sapiens.

PN DE19947010-A1.

XX 05-APR-2001.

PD 30-SEP-1999; 99DE-1047010.

XX 30-SEP-1999; 99DE-1047010.

PA (UNIV-) UNIVERSITAETSKLINIKUM FREIBURG.

XX Pahl H;

XX WPI; 2001-246167/26.

DR N-PSDB; AAF61560.

PT New cloned PRV-1 gene associated with polycythemia rubra vera, e.g.
 PT useful for preparing antisense molecules or polypeptides for treatment
 PT or diagnosis of disorders of the hematopoietic system -
 XX

PS Claim 3; Fig 2; 10pp; German.

XX This invention describes a novel cloned PRV-1 gene (1) which has
 CC hemostatic activity and is associated with polycythemia rubra vera
 CC (PRV). (1) is useful for: (1) producing a recombinant PRV-1 polypeptide;
 CC (2) producing antisense molecules useful for diagnosis and treatment of
 CC PRV; (3) preparing medicaments for treating pancytopenia and
 CC pancytopenias of the bone-marrow and blood. The polypeptide is useful:
 CC (1) as a growth factor for inducing hematopoietic stem cells to form
 CC erythroid colonies; (2) for preparing medicaments for treating
 CC pancytopenias and pancytopenias of the bone-marrow and blood; (3) for
 CC treating and/or multiplying autologous cells and/or established cell
 CC lines ex vivo or in vitro; and (4) for producing antibodies useful for
 CC diagnosis of PRV or other disorders of the hematopoietic system. This
 CC sequence represents the human PRV-1 protein described in the invention.

Sequence 437 AA;

Query Match 1.5%; Score 8; DB 22; Length 437;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 466 VLLALALG 473
 |||||
 Db 4 VLLALALG 11

RESULT 23
 AAB65260

ID AAB65260 standard; Protein; 437 AA.

XX AAB65260;

DT 02-APR-2001 (first entry)

XX Human PRO1181 (UNQ595) protein sequence SEQ ID NO:355.

KW Human; secreted and transmembrane protein; PRO; cytostatic;
 KW cell death; cancer; chromosomal mapping; gene mapping; tissue typing;
 KW diagnostic assay.

XX Homo sapiens.

PN WO200073454-A1.

XX 07-DEC-2000.

PF 30-MAR-2000; 2000WO-US08439.

XX 02-JUN-1999; 99WO-US12252.

PR 23-JUN-1999; 99US-0141037.

PR 07-JUL-1999; 99US-0143048.

PR 20-JUL-1999; 99US-0144758.

PR 26-JUL-1999; 99US-0145698.

PR 28-JUL-1999; 99US-0146222.

PR 17-AUG-1999; 99US-0149396.

PR 15-SEP-1999; 99WO-US21090.

PR 15-SEP-1999; 99WO-US21547.

PR 08-OCT-1999; 99US-0158663.

PR 30-NOV-1999; 99WO-US28301.

PR 01-DEC-1999; 99WO-US28301.

PR 16-DEC-1999; 99WO-US30095.

PR 20-DEC-1999; 99WO-US30911.

PR 05-JAN-2000; 2000WO-US00219.

PR 06-JAN-2000; 2000WO-US00376.

PR 11-FEB-2000; 2000WO-US03565.

PR 18-FEB-2000; 2000WO-US04341.

PR 22-FEB-2000; 2000WO-US04414.

PR 24-FEB-2000; 2000WO-US04914.

PR 02-MAR-2000; 2000WO-US05004.

PR 15-MAR-2000; 2000WO-US05841.

PR 20-MAR-2000; 2000WO-US06884.

PR 20-MAR-2000; 2000WO-US07377.

XX (GETH) GENENTECH INC.
 PA Ashkenazi AJ, Baker KP, Botstein D, Desnayers L, Eaton DL;
 XX Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi CJ, Gunney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI,
 PI Zhang Z;
 XX WPI, 2001-032160/04.
 DR N-PSDB; AAF44229.
 XX
 PT PRO polynucleotides used to produce polypeptides used to target
 PT bioactive molecules such as toxins, radiolabels or antibodies, to
 PT specific cells, to cause targeted cell death -
 XX
 PS Claim 12; Fig 250; 935pp; English.
 XX
 CC The present invention describes human secreted and transmembrane PRO
 CC proteins. The PRO proteins have cytototoxic activity. The PRO proteins
 CC can be used for targeted delivery of bioactive molecules, such as
 CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
 CC sequences, and their fragments, can be used as hybridisation probes, in
 CC chromosomal and gene mapping, and in the generation of anti-sense RNA
 CC and DNA. They may also be used to produce transgenic animals which are
 CC used to develop and screen therapeutically useful reagents. The PRO
 CC nucleotide and protein sequence can be used for tissue typing and in
 CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
 CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used
 CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and
 CC AAB5515 to AAB55300 represent human PRO polynucleotide and protein
 CC sequences given in the exemplification of the present invention.
 XX
 SQ Sequence 437 AA:
 QY
 466 VLLALLLG 473
 |||||
 4 VLLALLLG 11
 Db
 RESULT 24
 ABG31399 1.5%; Score 8; DB 22; Length 437;
 ID ABG31399 standard; Protein; 437 AA.
 XX
 AC ABG31399;
 XX
 DT 29-NOV-2002 (first entry)
 XX
 XX Human PRO1863 polypeptide.
 XX
 KW Human; secreted and transmembrane polypeptide; PRO polypeptide;
 KW T-lymphocyte proliferation; inflammatory disease; rheumatoid arthritis;
 KW inflammatory bowel disease; Sjogren's syndrome; thyroiditis;
 KW autoimmune haemolytic anaemia; diabetes mellitus; multiple sclerosis;
 KW hepatitis; contact dermatitis; allergic disease; psoriasis; vitreous;
 KW immune related disease; kidney disease; antiinflammatory; antithyroid;
 KW antihemetic; antiarthritis; immunosuppressive; antianaemic;
 KW antidiabetic; neuroprotective; hepatocytic; antiinflammatory;
 KW dermatological; anti-allergic; antipsoriatic; PRO1863.
 KW
 XX Homo sapiens.
 XX
 OS
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..15
 FT /label= signal_peptide
 FT Protein 16..437
 FT /label= Mature_PRO1863
 FT Modified-site 46..49
 FT /note= "N-glycosylation site"

FT Region
 FT 51..54
 FT /note= "Glycosaminoglycan attachment site"
 FT 54..59
 FT /note= "N-myristoylation site"
 FT 75..80
 FT /note= "N-myristoylation site"
 FT 141..146
 FT /note= "N-myristoylation site"
 FT 154..159
 FT /note= "N-myristoylation site"
 FT 168..173
 FT /note= "N-myristoylation site"
 FT 169..174
 FT /note= "N-myristoylation site"
 FT 189..192
 FT /note= "N-glycosylation site"
 FT 198..203
 FT /note= "N-myristoylation site"
 FT 243..260
 FT /label= Transmembrane_domain
 FT 254..259
 FT /note= "N-myristoylation site"
 FT 261..266
 FT /note= "N-myristoylation site"
 FT 269..274
 FT /note= "N-myristoylation site"
 FT 284..289
 FT /note= "N-myristoylation site"
 FT 333..338
 FT /note= "N-myristoylation site"
 FT 347..352
 FT /note= "N-myristoylation site"
 FT 359..362
 FT /note= "Glycosaminoglycan attachment site"
 FT 360..365
 FT /note= "N-myristoylation site"
 FT 361..366
 FT /note= "N-myristoylation site"
 FT 382..385
 FT /note= "N-glycosylation site"
 FT 388..393
 FT /note= "N-myristoylation site"
 FT 408..413
 FT /note= "N-myristoylation site"
 FT 419..424
 FT /note= "N-myristoylation site"
 FT
 XX US2002098507-A1.
 PN
 XX
 PD 25-JUL-2002.
 XX
 PP 27-DEC-2001; 2001US-0033326.
 XX
 XX 02-JUN-1999; 99WO-US12252.
 PR 01-DEC-1999; 99WO-US28634.
 PR 02-DEC-1999; 99WO-US28551.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 16-DEC-1998; 98US-113145P.
 PR 22-DEC-1998; 98US-113111P.
 PR 12-JAN-1999; 99US-115558P.
 PR 12-JAN-1999; 99US-115565P.
 PR 12-JAN-1999; 99US-115733P.
 PR 09-FEB-1999; 99US-119341P.
 PR 10-FEB-1999; 99US-119537P.
 PR 12-FEB-1999; 99US-119965P.
 PR 29-OCT-1999; 99US-162506P.
 XX

PA (GETH) GENENTECH INC.
XX Botstein D, Desnoyers L, Ferrara N, Fong S, Gao W, Goddard A;
PI Gurney AL, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK;
XX Wood WI;
XX WPI; 2002-673823/72.
DR N-PSDB; ABS53475.
XX
XX Novel PRO polypeptides and nucleic acids encoding the polypeptides,
PT useful for preparing a medicament for the treatment of inflammatory and
PT immune related disorders -
XX
XX Claim 12; Fig 10; 125pp; English.
XX
XX The present invention relates to the isolation of novel human
CC secreted and transmembrane polypeptides, designated PRO polypeptides,
CC and the polynucleotide sequences encoding them. The PRO polypeptides
CC of the invention include PRO1800, PRO539, PRO982, PRO1434, PRO1863,
CC PRO1917, PRO1868, PRO3434 and PRO1927. The PRO polypeptides can
CC inhibit the stimulation of T-lymphocyte proliferation. The PRO
CC polypeptides are useful for the diagnosis and treatment of inflammatory
CC diseases (e.g. inflammatory bowel disease, rheumatoid arthritis, diabetes
CC Sjogren's syndrome, autoimmune haemolytic anaemia, thyroiditis, diabetes
CC mellitus, multiple sclerosis, hepatitis, contact dermatitis, allergic
CC diseases and psoriasis), immune related diseases, and kidney diseases
CC in humans. The present sequence represents human PRO1863 polypeptide.
XX
XX Sequence 437 AA;
SQ
Query Match 1.5%; Score 8; DB 23; Length 437;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 466 VLLALLLG 473
Db 4 VLLALLLG 11
RESULT 25
ABG91359
ID ABG91359 standard; Protein; 437 AA.
XX
XX ABG91359;
XX
XX 29-NOV-2002 (first entry)
XX
XX Novel human secreted protein #5.
XX
XX Human; secreted protein; transmembrane protein; gene mapping;
KW transgenic; immunogenic.
XX
XX Homo sapiens.
XX
XX US2002098505-A1.
XX
XX 25-JUL-2002.
XX
XX 28-DEC-2001; 2001US-0033246.
XX
XX 02-JUN-1999; 99WO-US12252.
XX
XX 01-DEC-1999; 99WO-US28634.
XX
XX 02-DEC-1999; 99WO-US28551.
XX
XX 11-FEB-2000; 2000WO-US03565.
XX
XX 22-FEB-2000; 2000WO-US04414.
XX
XX 02-MAR-2000; 2000WO-US05841.
XX
XX 30-MAR-2000; 2000WO-US08439.
XX
XX 02-JUN-2000; 2000WO-US14941.
XX
XX 01-DEC-2000; 2000WO-US32678.
XX
XX 16-DEC-1998; 98US-113145P.
XX
XX 22-DEC-1998; 98US-113511P.
XX
XX 12-JAN-1999; 99US-115558P.

PR 12-JAN-1999; 99US-115565P.
PR 12-JAN-1999; 99US-115733P.
PR 09-FEB-1999; 99US-119341P.
PR 10-FEB-1999; 99US-119537P.
PR 12-FEB-1999; 99US-119965P.
PR 29-OCT-1999; 99US-162506P.
XX
XX (GETH) GENENTECH INC.
XX
XX Botstein D, Desnoyers L, Ferrara N, Fong S, Gao W, Goddard A;
PI Gurney AL, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK;
XX Wood WI;
XX
XX WPI; 2002-665999/71.
DR N-PSDB; ABS67458.
XX
XX New human secreted and transmembrane (PRO) polypeptides, useful for
PT treating conditions requiring PRO polypeptides, for screening PRO
PT antagonists and agonists useful as drug candidates -
XX
XX Claim 12; Figure 10; 125pp; English.
XX
XX The invention relates to new human secreted and transmembrane proteins
CC (PRO) and nucleic acids of the invention. The polypeptides can be
CC administered therapeutically, especially by expressing encoding
CC polynucleotides, e.g. in therapeutic compositions. They can be used to
CC screen for PRO polypeptide antagonists and agonists useful to identify
CC drug candidates. They can also be used to produce antibodies, useful to
CC detect PRO polypeptides (e.g. diagnostically), purify PRO polypeptides or
CC therapeutically (e.g. as antagonists or to target and/or deliver
CC cytotoxic agents). The polynucleotides are useful therapeutically e.g. to
CC produce antisense sequences to inhibit polypeptide production. They can
CC be used to produce probes and primers useful to detect or isolate
CC sequences encoding PRO polypeptides or similar sequences e.g. variants or
CC sequences from other species. They are also useful for gene mapping and
CC to generate transgenic animals. ABG91355-ABG91363 represent human PRO
CC amino acid sequences of the invention.
XX
XX Sequence 437 AA;
SQ
Query Match 1.5%; Score 8; DB 23; Length 437;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 466 VLLALLLG 473
Db 4 VLLALLLG 11
RESULT 26
ABG92707
ID ABG92707 standard; Protein; 437 AA.
XX
XX ABG92707;
XX
XX 18-NOV-2002 (first entry)
XX
XX Human secreted protein PRO1863.
XX
XX Human; secreted and transmembrane protein; PRO1800; PRO539;
KW PRO982; PRO1434; PRO1863; PRO1917; PRO1868; PRO3434; PRO1927;
KW inflammatory disorder; immune related disease; rheumatoid arthritis;
KW systemic lupus erythematosus; systemic sclerosis; thyroiditis;
KW autoimmune haemolytic anaemia; diabetes mellitus; infectious hepatitis;
KW psoriasis; allergic disease of the lung; graft-versus host disease;
KW tumour; gene therapy.
XX
XX Homo sapiens.
XX
XX US2002098506-A1.
XX
XX 25-JUL-2002.
XX
XX

PF 27-DEC-2001; 2001US-0033301.
 XX 04-AUG-1998; 98US-095325P.
 PR 16-DEC-1998; 98US-112851P.
 PR 16-DEC-1998; 98US-113145P.
 PR 22-DEC-1998; 98US-113511P.
 PR 12-JAN-1999; 98US-115558P.
 PR 12-JAN-1999; 98US-115565P.
 PR 12-JAN-1999; 98US-115733P.
 PR 09-FEB-1999; 98US-119341P.
 PR 10-FEB-1999; 98US-119537P.
 PR 12-FEB-1999; 98US-119665P.
 PR 29-OCT-1999; 98US-162506P.
 PR 02-JUN-1999; 98WO-US12252.
 PR 01-DEC-1999; 98WO-US28634.
 PR 02-DEC-1999; 98WO-US28551.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 30-MAY-2000; 2000WO-US19411.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 01-DEC-2000; 2000WO-US32678.
 PA (GETH) GENENTECH INC.
 XX Bocstein D, Desnoyers L, Ferrara N, Feng S, Gao W, Goddard A;
 PI Gurney AL, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK;
 PI Wood WJ;
 XX MPI; 2002-690475/74.
 DR N-PSDB; ABS68390.
 XX Novel secreted and transmembrane polypeptides and polynucleotides
 PT useful for diagnosis and treatment of inflammatory disorders and
 PT immune-related diseases, and identifying modulators -
 XX
 PS Claim 12; Fig 10; 125pp; English.
 CC The invention relates to an isolated polypeptide having at least 80%
 CC amino acid sequence identity to secreted and transmembrane polypeptides
 CC PRO1800, PRO539, PRO1434, PRO1863, PRO1917, PRO1868, PRO3434 or
 CC PRO1927 and their encoding nucleic acids. Also included are vectors, host
 CC cells and antibodies against PRO polypeptides. PRO proteins are useful
 CC for identifying modulators of the polypeptide. PRO1868 useful for the
 CC diagnosis and treatment of inflammatory and immune related diseases
 CC including systemic lupus erythematosus, rheumatoid arthritis, systemic
 CC sclerosis, autoimmune haemolytic anaemia, thyroiditis, diabetes mellitus,
 CC infectious hepatitis, psoriasis, allergic diseases of the lung and
 CC graft-versus host disease and tumours. PRO nucleic acids are useful for
 CC constructing hybridisation probes for mapping the gene that encodes that
 CC PRO and for the genetic analysis of individuals with genetic disorders,
 CC and for generating transgenic animals which are useful in the development
 CC and screening of therapeutically useful reagents. PRO nucleic acids are
 CC also useful for gene therapy, chromosome identification, and tissue
 CC typing. PRO proteins are useful as molecular weight markers for protein
 CC electrophoresis purposes. The anti-PRO antibodies are useful in
 CC diagnostic assays for PRO, e.g. detecting its expression in specific
 CC cells, tissues or serum and for affinity purification of PRO.
 CC The present sequence represents a PRO protein.
 CC
 SQ Sequence 437 AA;
 Query Match 1.5%; Score 8; DB 23; Length 437;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 466 VILLALIG 473
 |||||
 |||||
 DB 4 VILLALIG 11
 RESULT 27

AAU83672
 ID AAU83672 standard; Protein: 437 AA.
 AC AAU83672;
 XX 08-MAY-2002 (first entry)
 DT
 XX Human PRO protein, Seq ID No 162.
 DE
 XX Human, secreted protein; PRO; tumour; lung cancer; colon cancer;
 KW breast cancer; prostate tumour; rectal tumour; liver tumour;
 KW pericyte cell proliferation; chondrocyte cell proliferation;
 KW tumour necrosis factor-alpha.
 XX
 CS Homo sapiens.
 XX
 EN MO200208288-A2.
 PD 31-JAN-2002.
 XX
 PF 29-JUN-2001; 2001WO-US21066.
 XX 20-JUL-2000; 2000US-219556P.
 PR 25-JUL-2000; 2000US-220585P.
 PR 25-JUL-2000; 2000US-220605P.
 PR 25-JUL-2000; 2000US-220607P.
 PR 25-JUL-2000; 2000US-220624P.
 PR 25-JUL-2000; 2000US-220638P.
 PR 25-JUL-2000; 2000US-220664P.
 PR 25-JUL-2000; 2000US-220666P.
 PR 26-JUL-2000; 2000US-220893P.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 23-AUG-2000; 2000WO-US23328.
 PR 24-AUG-2000; 2000US-000000P.
 PR 15-SEP-2000; 2000US-000000P.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 28-NOV-2000; 2000US-253646P.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000US-0747259.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 10-MAY-2001; 2001WO-US054280.
 PR 25-MAY-2001; 2001WO-US17092.
 XX
 PA (GETH) GENENTECH INC.
 XX Baker KP, Desnoyers L, Gerritsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Smith V, Stephan JF, Watanabe CK, Wood WJ;
 XX MPI; 2002-172001/22.
 DR N-PSDB; ABK33616.
 XX One hundred and twenty two nucleic acids encoding PRO polypeptides,
 PT useful for treating a PRO related disorder and for diagnosing tumours
 PT such as lung cancer, colon cancer, breast tumour, prostate tumour, rectal
 PT tumour or liver tumour -
 XX
 PS Claim 11; Figure 162; 359pp; English.
 CC The invention relates to one hundred and twenty two nucleic acids
 CC encoding PRO polypeptides. The sequences of the 122 PRO polynucleotides
 CC encode human secreted proteins. The PRO nucleic acids, polypeptides,
 CC agonists and antagonists are useful for treating a PRO related disorder.
 CC The PRO polypeptides are useful for diagnosing tumours, especially lung
 CC cancer, colon cancer, breast tumour, prostate tumour, rectal tumour or
 CC liver tumour. The PRO polypeptides are useful for stimulating the
 CC proliferation of, or gene expression, in pericyte cells, for stimulating
 CC the proliferation or differentiation of chondrocyte cells, for
 CC stimulating the release of tumour necrosis factor-alpha from human blood,
 CC for stimulating or inhibiting the proliferation of normal human dermal
 CC fibroblast cells. The PRO polypeptide may also be used as molecular
 CC weight markers and for tissue typing. The PRO nucleic acids have
 CC applications in molecular biology, including use as hybridisation probes,

CC and in chromosome and gene mapping. AAU83592-AAU83713 represent human PRO
 CC protein sequences of the invention.

SQ Sequence 437 AA;

Query Match 1.5%; Score 8; DB 23; Length 437;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 466 VLLALLLG 473
 |||||
 4 VLLALLLG 11

DB

RESULT 28
 AAG80767

ID AAG80767 standard; Protein; 437 AA.

AC AAG80767;

DT 17-APR-2002 (first entry)

DE Human granulocyte HNA-2a antigen.

KM Human; neutrophilic granulocyte; chromosome 19; HNA-2a; antigen;
 KM human neutrophil antigen-2a; NB-1 antigenic determination; diagnosis;
 KM alloantibody detection; neonatal; immunoneutropenia; iatrogenic;
 KM transplant-associated acute pulmonary insufficiency;
 KM bone marrow transplant; autoimmunoneutropenia.

OS Homo sapiens.

FX Key Location/Qualifiers
 FH 1.21
 FT Peptide /label= signal_peptide

FT Protein 22..437

FT /label= mature_peptide

FT /note= "HNA-2a (previously called NB-1)"

FN DE10028725-A1.

PD 13-DEC-2001.

PF 09-JUN-2000; 2000DE-1028725.

PR 09-JUN-2000; 2000DE-1028725.

PS (BUXJ/) BUX J.

PI Bux J, Kissel K;

DR WPI; 2002-148930/20.

N-PSDB; ABA97156.

PT Primary structure and nucleic acid of the human neutrophil antigen-2a,
 useful for antigen detection, e.g. diagnosis of various forms of
 neutropenia

PS Disclosure; Page 4-6; 8pp; German.

CC This invention describes the human neutrophil antigen-2a (HNA-2a,
 CC previously described as NB-1), expressed on neutrophilic granulocytes.
 CC The nucleic acid and amino acid sequences of HNA-2a are used in RNA- or
 CC DNA-based methods of antigen determination, e.g. polymerase chain
 CC reaction with sequence-specific primers, hybridisation with
 CC sequence-specific oligonucleotides or DNA sequencing. They are also used
 CC for recombinant production of the antigen for detection of specific
 CC alloantibodies. Allo- and auto-antibodies against HNA-2a are implicated
 CC in neonatal immunoneutropenia, transplant-associated acute pulmonary
 CC insufficiency, immunoneutropenia after bone marrow transplant, iatrogenic
 CC immunoneutropenia and autoimmunoneutropenia. Using, HNA-2a,
 CC or its nucleic acid, for diagnosis, overcomes the stability problems
 CC associated with use and transport of very unstable granulocytes. The

CC nucleic acid also allows large-scale production of the antigen. This
 CC sequence represents the human granulocyte HNA-2a (NB-1) antigen found on
 CC chromosome 19 described in the invention.

SQ Sequence 437 AA;

Query Match 1.5%; Score 8; DB 23; Length 437;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 466 VLLALLLG 473
 |||||
 4 VLLALLLG 11

DB

RESULT 29

ID ABU66802 standard; Protein; 437 AA.

AC ABU66802;

DT 23-MAY-2003 (first entry)

DE Human PRO polypeptide #233.

KM Human; PRO polypeptide; secreted and transmembrane protein;
 KM tumor necrosis factor-alpha; TNF-alpha; blood; proliferation;
 KM differentiation; chondrocyte; tumour; genetic disorder;
 KM cytosolic.

OS Homo sapiens.

PN US2003036180-A1.

PD 20-FEB-2003.

PF 09-MAY-2002; 2002US-0143114.

PR 31-MAR-1997; 97WO-US05230.

PR 12-JUN-1998; 98WO-US12456.

PR 14-JUL-1998; 98WO-US14552.

PR 28-AUG-1998; 98WO-US17888.

PR 10-SEP-1998; 98WO-US18824.

PR 14-SEP-1998; 98WO-US19093.

PR 14-SEP-1998; 98WO-US19094.

PR 14-SEP-1998; 98WO-US19177.

PR 16-SEP-1998; 98WO-US19330.

PR 17-SEP-1998; 98WO-US19437.

PR 29-OCT-1998; 98WO-US22991.

PR 29-OCT-1998; 98WO-US22992.

PR 20-NOV-1998; 98WO-US24855.

PR 01-DEC-1998; 98WO-US25108.

PR 05-JAN-1999; 99WO-US00106.

PR 08-MAR-1999; 99WO-US05028.

PR 10-MAR-1999; 99WO-US05190.

PR 20-APR-1999; 99WO-US08615.

PR 14-MAY-1999; 99WO-US10733.

PR 02-JUN-1999; 99WO-US12252.

PR 01-SEP-1999; 99WO-US20111.

PR 08-SEP-1999; 99WO-US20594.

PR 13-SEP-1999; 99WO-US20944.

PR 15-SEP-1999; 99WO-US21090.

PR 15-SEP-1999; 99WO-US21547.

PR 05-OCT-1999; 99WO-US23089.

PR 29-NOV-1999; 99WO-US28214.

PR 30-NOV-1999; 99WO-US28313.

PR 01-DEC-1999; 99WO-US28409.

PR 01-DEC-1999; 99WO-US28301.

PR 01-DEC-1999; 99WO-US28634.

PR 02-DEC-1999; 99WO-US28551.

PR 02-DEC-1999; 99WO-US28564.

PR 02-DEC-1999; 99WO-US28565.

PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 20-DEC-1999; 99WO-US30999.
 PR 22-DEC-1999; 99WO-US30720.
 PR 30-DEC-1999; 99WO-US31243.
 PR 30-DEC-1999; 99WO-US31274.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 06-JAN-2000; 2000WO-US00376.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 18-FEB-2000; 2000WO-US04342.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 02-MAR-2000; 2000WO-US05746.
 PR 10-MAR-2000; 2000WO-US06319.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 11-AUG-2000; 2000WO-US22031.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 22-JUN-2001; 2001WO-US20116.
 PR 29-JUN-2001; 2001WO-US21066.
 PR 09-JUL-2001; 2001WO-US21735.
 PR 20-DEC-2000; 2000WO-US247259.
 PR 28-FEB-2001; 2001US-0796498.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0808689.
 PR 22-MAR-2001; 2001US-0816744.
 PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 18-MAY-2001; 2001US-0860216.
 PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001US-0866034.
 PR 01-JUN-2001; 2001US-0872035.
 PR 05-JUN-2001; 2001US-0874503.
 PR 14-JUN-2001; 2001US-0882536.
 PR 19-JUN-2001; 2001US-0886342.
 PR 21-JUN-2001; 2001US-0887879.
 PR 18-JUL-2001; 2001US-0908827.
 PR 06-AUG-2001; 2001US-0924419.
 PR 09-AUG-2001; 2001US-0927796.
 PR 16-AUG-2001; 2001US-0931836.
 PR 19-DEC-2001; 2001US-0028072.
 XX
 PA (GETH) GENENTECH INC.
 XX
 PI Baker KP, Bershtei M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
 PI Ceritlsen ME, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 DR WPI; 2003-332040/31.
 DR N-PSDB; ACA03835.

XX New secreted and transmembrane PRO nucleic acids, useful for gene
 PT therapy, in chromosome and gene mapping, as chromosome markers, in
 PT tissue typing, and in chromosome identification
 PS Claim 12; Fig 466; 660pp; English.
 XX
 CC The present invention relates to the isolation of novel human PRO
 CC polypeptides, and the polynucleotide sequences encoding them. The
 CC PRO polypeptides are secreted and transmembrane proteins. The PRO
 CC polypeptides are useful for detecting other PRO polypeptides, for
 CC linking bioactive molecules to cells expressing PRO polypeptides,
 CC for modulating biological activities of cells expressing PRO
 CC polypeptides, and for identifying agonists or antagonists.
 CC The PRO polypeptides are useful for stimulating the release of
 CC tumour necrosis factor (TNF)-alpha from human blood, for stimulating
 CC the proliferation or differentiation of chondrocytes, and detecting the
 CC presence of tumours. The polynucleotide sequences encoding PRO
 CC polypeptides are useful as hybridisation probes, in chromosome and
 CC gene mapping, in the generation of antisense RNA and DNA, in the
 CC preparation of PRO polypeptides, for generating transgenic animals or
 CC knockout animals, for gene therapy. AB06570-AB06684 represent the human
 CC PRO polypeptides of the invention.
 CC Note: The sequence data for this patent was obtained in electronic
 CC format directly from the USPTO web site at
 CC segdata.uspto.gov/patseq/identry.html.
 XX
 SQ Sequence 437 AA;
 Query Match 1.5%; Score 8; DB 24; Length 437;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 466 VLLALLG 473
 Db 4 VLLALLG 11
 RESULT 30
 AB067078
 ID AB067078 standard; Protein; 437 AA.
 AC
 XX AB067078;
 XX
 DT 27-MAY-2003 (first entry)
 XX
 DE Human secreted/transmembrane, PRO, protein SEQ ID 466.
 XX
 KW Human; secreted protein; transmembrane protein; PRO;
 KW inflammatory disease; organ failure; atherosclerosis; cardiac injury;
 KW infertility; birth defects; premature aging; AIDS; biosensor;
 KW acquired immunodeficiency syndrome; cancer; diabetic complication;
 KW bioreactor; tumour.
 XX
 OS Homo sapiens.
 XX
 PN US2003032155-A1.
 XX
 PD 13-FEB-2003.
 XX
 PF 03-MAY-2002; 2002US-0137865.
 XX
 PR 31-MAR-1997; 97WO-US05230.
 PR 12-JUN-1998; 98WO-US12456.
 PR 14-JUL-1998; 98WO-US14552.
 PR 28-AUG-1998; 98WO-US17888.
 PR 10-SEP-1998; 98WO-US18824.
 PR 14-SEP-1998; 98WO-US19093.
 PR 14-SEP-1998; 98WO-US19094.
 PR 14-SEP-1998; 98WO-US19177.
 PR 16-SEP-1998; 98WO-US19330.
 PR 17-SEP-1998; 98WO-US19437.

PR 07-OCT-1998; 98WO-US21141.
 PR 29-OCT-1998; 98WO-US22991.
 PR 29-OCT-1998; 98WO-US22992.
 PR 20-NOV-1998; 98WO-US24855.
 PR 01-DEC-1998; 98WO-US25108.
 PR 05-JAN-1999; 98WO-US00106.
 PR 08-MAR-1999; 98WO-US05028.
 PR 10-MAR-1999; 98WO-US05190.
 PR 20-APR-1999; 98WO-US08615.
 PR 14-MAY-1999; 98WO-US10733.
 PR 02-JUN-1999; 98WO-US12252.
 PR 01-SEP-1999; 98WO-US20111.
 PR 08-SEP-1999; 98WO-US20594.
 PR 13-SEP-1999; 98WO-US20944.
 PR 15-SEP-1999; 98WO-US21090.
 PR 05-OCT-1999; 98WO-US21547.
 PR 29-NOV-1999; 98WO-US23089.
 PR 30-NOV-1999; 98WO-US28214.
 PR 30-NOV-1999; 98WO-US28313.
 PR 01-DEC-1999; 98WO-US28409.
 PR 01-DEC-1999; 98WO-US28301.
 PR 02-DEC-1999; 98WO-US28634.
 PR 02-DEC-1999; 98WO-US28551.
 PR 02-DEC-1999; 98WO-US28564.
 PR 16-DEC-1999; 98WO-US28565.
 PR 20-DEC-1999; 98WO-US30911.
 PR 20-DEC-1999; 98WO-US30999.
 PR 22-DEC-1999; 98WO-US30720.
 PR 30-DEC-1999; 98WO-US31243.
 PR 30-DEC-1999; 98WO-US31274.
 PR 05-JAN-2000; 2000WO-US00219.
 PR 06-JAN-2000; 2000WO-US00277.
 PR 11-FEB-2000; 2000WO-US00376.
 PR 18-FEB-2000; 2000WO-US03565.
 PR 18-FEB-2000; 2000WO-US04341.
 PR 22-FEB-2000; 2000WO-US04342.
 PR 24-FEB-2000; 2000WO-US04914.
 PR 24-FEB-2000; 2000WO-US05004.
 PR 01-MAR-2000; 2000WO-US05601.
 PR 02-MAR-2000; 2000WO-US05746.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 10-MAR-2000; 2000WO-US06319.
 PR 15-MAR-2000; 2000WO-US06884.
 PR 20-MAR-2000; 2000WO-US07377.
 PR 21-MAR-2000; 2000WO-US07532.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 11-AUG-2000; 2000WO-US22031.
 PR 23-AUG-2000; 2000WO-US23522.
 PR 24-AUG-2000; 2000WO-US23328.
 PR 08-NOV-2000; 2000WO-US30952.
 PR 10-NOV-2000; 2000WO-US30873.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 20-DEC-2000; 2000WO-US34956.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-MAR-2001; 2001WO-US06666.
 PR 25-MAY-2001; 2001WO-US17092.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 22-JUN-2001; 2001WO-US20116.
 PR 29-JUN-2001; 2001WO-US21066.
 PR 09-JUL-2001; 2001WO-US21735.
 PR 20-DEC-2000; 2000US-0747259.
 PR 28-FEB-2001; 2001US-0796498.
 PR 09-MAR-2001; 2001US-0802706.
 PR 14-MAR-2001; 2001US-0808689.
 PR 22-MAR-2001; 2001US-0816744.

PR 05-APR-2001; 2001US-0828366.
 PR 10-MAY-2001; 2001US-0854208.
 PR 10-MAY-2001; 2001US-0854280.
 PR 18-MAY-2001; 2001US-0860216.
 PR 25-MAY-2001; 2001US-0866028.
 PR 25-MAY-2001; 2001US-0866034.
 PR 01-JUN-2001; 2001US-0872035.
 PR 05-JUN-2001; 2001US-0874503.
 PR 14-JUN-2001; 2001US-0882636.
 PR 19-JUN-2001; 2001US-0886342.
 PR 21-JUN-2001; 2001US-0887879.
 PR 18-JUL-2001; 2001US-0908827.
 PR 06-AUG-2001; 2001US-0924419.
 PR 09-AUG-2001; 2001US-0927796.
 PR 16-AUG-2001; 2001US-0931836.
 PR 19-DEC-2001; 2001US-0028072.
 XX
 PA (GETH) GENENTECH INC.
 XX
 XX Baker KP, Beresini M, DeForge L, Desnoyers L, Filvaroff E, Gao W;
 PI Gerritsen MB, Goddard A, Godowski PJ, Gurney AL, Sherwood S;
 PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
 XX
 DR WPI; 2003-331925/31.
 N-PSDB; ACA04256.
 XX
 XX New secreted and transmembrane nucleic acids and polypeptides,
 PT designated as PRO, useful for treating inflammation, organ failure,
 PT atherosclerosis, cardiac injury, infertility, birth defects, premature
 PT aging, AIDS, or cancer
 XX
 XX Claim 12; Fig 466; 659pp; English.
 XX
 CC The invention relates to an isolated nucleic acid comprising, or which is
 CC at least 80% identical to, or the full-length coding sequence of, any of
 CC the 275 nucleotide sequences, encoding the corresponding PRO polypeptide
 CC (one of 275 secreted or transmembrane proteins). The nucleic acid
 CC further comprises the full-length coding sequence of the DNA deposited
 CC under American Type Culture Collection (ATCC) accession number in a list
 CC given in the specification. Also included are vectors and host
 CC cells for producing PRO proteins, PRO fusion proteins, anti-PRO
 CC antibodies, PRO extracellular domains and mature sequences, methods
 CC of detecting PRO proteins, methods for stimulating the release of
 CC TNF-alpha (tumour necrosis factor alpha) from human blood,
 CC (and the proliferation of differentiation of chondrocyte cells, the
 CC proliferation of, or gene expression in pericyte cells, the release or
 CC proteoglycans from cartilage, proliferation of inner ear utricular
 CC supporting cells, the proliferation of T-lymphocyte cells, the release
 CC of a cytokine from peripheral blood mononuclear cells (PBMC), or the
 CC proliferation of endothelial cells), a method for modulating the uptake
 CC of glucose or free fatty acid (FFA) by skeletal muscle cells,
 CC a method for inhibiting the binding of A-peptide to factor VIIA,
 CC or the differentiation of adipocyte cells, a method for detecting the
 CC presence of a tumour in a mammal and an oligonucleotide probe derived
 CC from any of the nucleic acid sequences cited above. The nucleic acids and
 CC polypeptides are useful for treating inflammatory diseases, organ
 CC failure, atherosclerosis, cardiac injury, infertility, birth defects,
 CC premature aging, AIDS (acquired immunodeficiency syndrome), cancer, or
 CC diabetic complications. The nucleic acids are useful as hybridisation
 CC probes, in chromosome and gene mapping, and in generating antisense RNA
 CC or DNA. The polypeptides are useful as pharmaceuticals, diagnostics,
 CC biosensors or bioreactors. Both are useful in tissue typing.
 CC The present sequence represents a PRO protein of the invention.
 XX
 SQ Sequence 437 AA;
 Query Match 1.5%; Score 8; DB 24; Length 437;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 466 VLLIALLG 473
 |||||
 Db 4 VLLIALLG 11

RESULT 31
ABUS9883
ID ABUS9883 standard; Protein; 437 AA.
XX
AC ABUS9883;
XX
DT 13-MAY-2003 (first entry)
XX
DE Novel secreted and transmembrane protein PRO181.
XX
KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;
KW cardiac insufficiency disorder; cancer; tumour; immune response;
KW adrenal cortical capillary endothelial growth; c-fos induction;
KW vascular endothelial growth factor inhibition; VEGF inhibition;
KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
KW retinal neurons cell survival; rod photoreceptor cell survival;
KW retinal disorder; retinitis pigmentosa; kidney disease;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
KW chondrocyte redifferentiation; sports injury; arthritis.
XX
OS Homo sapiens.
XX
PN US2003017563-A1.
XX
PD 23-JAN-2003.
XX
PF 07-MAY-2002; 2002US-0140808.
XX
XX 31-MAR-1997; 97WO-US05230.
PR 12-JUN-1998; 98WO-US12456.
PR 14-JUL-1998; 98WO-US14552.
PR 28-AUG-1998; 98WO-US17888.
PR 10-SEP-1998; 98WO-US18824.
PR 14-SEP-1998; 98WO-US19093.
PR 14-SEP-1998; 98WO-US19094.
PR 14-SEP-1998; 98WO-US19177.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
PR 07-OCT-1998; 98WO-US21141.
PR 29-OCT-1998; 98WO-US22991.
PR 29-OCT-1998; 98WO-US22992.
PR 20-NOV-1998; 98WO-US24855.
PR 01-DEC-1998; 98WO-US25108.
PR 05-JAN-1999; 99WO-US00106.
PR 08-MAR-1999; 99WO-US05028.
PR 10-MAR-1999; 99WO-US05190.
PR 20-APR-1999; 99WO-US08615.
PR 14-MAY-1999; 99WO-US10733.
PR 02-JUN-1999; 99WO-US12252.
PR 01-SEP-1999; 99WO-US20111.
PR 08-SEP-1999; 99WO-US20594.
PR 13-SEP-1999; 99WO-US20944.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 05-OCT-1999; 99WO-US23089.
PR 29-NOV-1999; 99WO-US28214.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28409.
PR 01-DEC-1999; 99WO-US28301.
PR 02-DEC-1999; 99WO-US28634.
PR 02-DEC-1999; 99WO-US28551.
PR 02-DEC-1999; 99WO-US28654.
PR 02-DEC-1999; 99WO-US28655.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 22-DEC-1999; 99WO-US30999.
PR 30-DEC-1999; 99WO-US30720.
PR 30-DEC-1999; 99WO-US31243.
PR 30-DEC-1999; 99WO-US31374.
PR 05-JAN-2000; 2000WO-US00219.

PR 06-JAN-2000; 2000WO-US00277.
PR 06-JAN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 18-FEB-2000; 2000WO-US04342.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 24-FEB-2000; 2000WO-US05004.
PR 01-MAR-2000; 2000WO-US05601.
PR 02-MAR-2000; 2000WO-US05746.
PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 21-MAR-2000; 2000WO-US07532.
PR 30-MAR-2000; 2000WO-US08439.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
PR 30-MAY-2000; 2000WO-US14941.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUL-2000; 2000WO-US20710.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 10-NOV-2000; 2000WO-US30873.
PR 01-DEC-2000; 2000WO-US32678.
PR 20-DEC-2000; 2000WO-US34956.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-MAR-2001; 2001WO-US06666.
PR 25-MAY-2001; 2001WO-US17092.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 22-JUN-2001; 2001WO-US20116.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 20-DEC-2000; 2000WO-US747259.
PR 28-FEB-2001; 2001US-0796498.
PR 09-MAR-2001; 2001US-0802705.
PR 14-MAR-2001; 2001US-0806889.
PR 22-MAR-2001; 2001US-0816744.
PR 05-APR-2001; 2001US-0826366.
PR 10-MAY-2001; 2001US-0854208.
PR 18-MAY-2001; 2001US-0860216.
PR 25-MAY-2001; 2001US-0866028.
PR 25-MAY-2001; 2001US-0866034.
PR 01-JUN-2001; 2001US-0874503.
PR 05-JUN-2001; 2001US-0874503.
PR 14-JUN-2001; 2001US-0882636.
PR 19-JUN-2001; 2001US-0886342.
PR 21-JUN-2001; 2001US-0887879.
PR 18-JUL-2001; 2001US-0908827.
PR 06-AUG-2001; 2001US-0924419.
PR 09-AUG-2001; 2001US-0927796.
PR 16-AUG-2001; 2001US-0931836.
PR 19-DEC-2001; 2001US-0028072.
XX
XX (GETH) GENENTECH INC.
PA
XX Baker KP, Beresini M, Deforge L, Desnoyers L, Filvaroff E, Gao W;
XX Gertlisen ME, Goddard A, Godowski PJ, Gunney AL, Sherwood S;
PI Smith V, Stewart TA, Tumas D, Watanabe CK, Wood WI, Zhang Z;
XX
XX WPI; 2003-148238/14.
DR N-PSDB; ABX89373.
XX
PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
PT are therapeutically useful for enhancing immune response and in cancer
PT treatments -
XX
PS Claim 12; Fig 466; 659pp; English.

XX The invention describes an isolated human PRO polypeptide. The PRO
 CC polypeptides are useful in detecting PRO polypeptides in a sample, in
 CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
 CC in modulating at least one biological activity of a cell expressing a PRO
 CC polypeptide. PRO1312 stimulates hypertrophy of neonatal heart and is thus
 CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
 CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
 CC PRO943, PRO828, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
 CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
 CC useful for treating conditions or disorders where angiogenesis would be
 CC beneficial, e.g. wound healing and antagonism of this polypeptide are
 CC useful for treating cancerous tumours. PRO812 inhibits vascular
 CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
 CC cells and is thus useful for inhibiting endothelial cell growth in
 CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
 CC PRO1068, PRO1184, PRO1366 and PRO1375 stimulate proliferation of
 CC stimulated T-lymphocytes and are therapeutically useful for enhancing
 CC immune response. PRO828, PRO1068 or PRO1132 enhance survival of
 CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
 CC rod photoreceptor cells) and therefore are useful for treating retinal
 CC disorders of injuries, e.g. retinitis pigmentum, AMD. PRO819, PRO813
 CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,
 CC and therefore are useful for treating kidney disorders associated with
 CC decreased mesangial cell function such as Berger disease or other's
 CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
 CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
 CC proliferation and/or redifferentiation of chondrocytes in culture and
 CC are thus useful for treating sports injuries, and arthritis. This
 CC is the amino acid sequence of a novel human PRO protein.

XX Sequence 437 AA;

Query Match 1.5%; Score 8; DB 24; Length 437;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 466 VLLALLLG 473
 |||||
 Db 4 VLLALLLG 11

RESULT 32
 ABU60811 standard; Protein; 437 AA.

XX AC ABU60811;

DT 06-MAY-2003 (first entry)

XX Human secreted/transmembrane protein, #5.

XX Human, PRO; secreted; transmembrane; pharmaceutical;
 KW diagnostic; biosensor; bioreactor; therapeutic; gene therapy; tumour;
 KW inflammatory disease; immune-related disease; inflammatory bowel disease;
 KW IBD; systemic lupus erythematosus; rheumatoid arthritis; thyroiditis;
 KW diabetes mellitus; glomerulonephritis; multiple sclerosis; cirrhosis;
 KW psoriasis; graft rejection; anti-inflammatory; immunosuppressive;
 KW neuroprotective; hepatotropic.

OS Homo sapiens.

XX US2002160392-A1.

XX 31-OCT-2002.

XX 27-DEC-2001; 2001US-0033245.

XX 02-JUN-1999; 99WO-US12252.

XX 01-DEC-1999; 99WO-US28634.

XX 02-DEC-1999; 99WO-US28551.

XX 11-FEB-2000; 2000WO-US03565.

XX 22-FEB-2000; 2000WO-US04414.

PR 02-MAR-2000; 2000WO-US05841.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 04-AUG-1998; 98US-095325P.
 PR 16-DEC-1998; 98US-112851P.
 PR 16-DEC-1998; 98US-113145P.
 PR 22-DEC-1998; 98US-113511P.
 PR 12-JAN-1999; 99US-115558P.
 PR 12-JAN-1999; 99US-115565P.
 PR 12-JAN-1999; 99US-115733P.
 PR 09-FEB-1999; 99US-119341P.
 PR 10-FEB-1999; 99US-119537P.
 PR 12-FEB-1999; 99US-119655P.
 PR 29-OCT-1999; 99US-162506P.
 PR 09-DEC-1999; 99US-170262P.
 PR 03-MAR-2000; 2000US-187202P.
 PR 25-MAY-2001; 2001US-0866034.

XX (GENTH) GENENTECH INC.

PI Bocstein D, Desnoyers L, Ferrara N, Fong S, Gao W, Goddard A;
 PI Gutney AL, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK;
 PI Wood WJ;

XX WPI; 2003-275292/27.
 DR N-PSDB; ABX90607.

PT New isolated PRO polypeptide, e.g. PRO1800 or PRO539, useful for
 PT diagnosing, preventing and treating tumors and inflammatory or
 PT immune-related diseases, e.g. systemic lupus erythematosus,
 PT thyroiditis, diabetes or psoriasis

XX Claim 12; Fig 10; 119pp; English.

XX The invention discloses isolated PRO secreted/transmembrane polypeptides
 CC comprising a sequence without signal peptide and the nucleic acid
 CC encoding them. The polypeptides can be used to raise antibodies that
 CC specifically bind to the PRO polypeptide, for linking a bioactive
 CC molecule to a cell expressing a PRO protein and for modulating at least
 CC one biological activity of a cell. The PRO polypeptides and the antibody
 CC are useful for diagnosing, preventing and treating tumours and
 CC inflammatory or immune-related diseases, such as inflammatory bowel
 CC disease (IBD), systemic lupus erythematosus, rheumatoid arthritis,
 CC thyroiditis, diabetes mellitus, glomerulonephritis, multiple sclerosis,
 CC cirrhosis, psoriasis or graft rejection. The proteins and the antibody
 CC may also be used in preparing medicines and medicaments for treating the
 CC above-mentioned diseases. The polynucleotide is useful in molecular
 CC biology, including uses as hybridisation probes, in chromosome and gene
 CC mapping, in generating antisense RNA and DNA, and in gene therapy. The
 CC polynucleotide may also be used in preparing PRO polypeptides by
 CC recombinant techniques, and in generating either transgenic animals or
 CC knock-out animals which, in turn, are useful in the development and
 CC screening of therapeutically useful reagents. The sequences presented in
 CC AB060807-AB060815 are the human PRO polynucleotides of the invention.

XX Sequence 437 AA;

Query Match 1.5%; Score 8; DB 24; Length 437;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 466 VLLALLLG 473
 |||||
 Db 4 VLLALLLG 11

RESULT 33

ABG73312 standard; Protein; 437 AA.

XX AC ABG73312;

XX 30-APR-2003 (first entry)
 DE Human PRO1863 polypeptide.
 XX Human; secreted and transmembrane polypeptide; PRO polypeptide;
 KW inflammatory diseases; immune-related diseases; diabetes mellitus;
 KW rheumatoid arthritis; glomerulonephritis; multiple sclerosis;
 KW immune-mediated skin disease; contact dermatitis; graft rejection;
 KW transplantation associated disease; graft-versus-host disease;
 KW tumour diagnosis; tumour cell; antiinflammatory; immunosuppressive;
 KW cytotoxic; antineoplastic; antineuritic; antiarthritic; antithyroid;
 KW antidiabetic; nephrotoxic; antipsoriatic; dermatological; haemostatic;
 KW hepatotropic; virucide; neuroprotective; PRO1863.
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT Peptide 1..15
 FT /label= Signal_peptide
 FT 16..437
 FT /label= Mature_PRO1863_polypeptide
 FT Protein
 XX
 PN US2002164646-A1.
 XX
 PD 07-NOV-2002.
 XX
 PE 27-DEC-2001; 2001US-0033223.
 XX
 PR 02-JUN-1999; 99WO-US12252.
 PR 01-DEC-1999; 99WO-US28634.
 PR 02-DEC-1999; 99WO-US28551.
 PR 11-FEB-2000; 2000WO-US03565.
 PR 22-FEB-2000; 2000WO-US04414.
 PR 02-MAR-2000; 2000WO-US05841.
 PR 30-MAR-2000; 2000WO-US08439.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 16-DEC-1998; 98US-113145P.
 PR 22-DEC-1998; 98US-113511P.
 PR 12-JAN-1999; 99US-115558P.
 PR 12-JAN-1999; 99US-115733P.
 PR 12-JAN-1999; 99US-115733P.
 PR 09-FEB-1999; 99US-119341P.
 PR 10-FEB-1999; 99US-119537P.
 PR 12-FEB-1999; 99US-119565P.
 PR 29-OCT-1999; 99US-162506P.
 XX
 PA (GENTH) GENENTECH INC.
 XX
 PI Botstein D, Desnoyers L, Ferrara N, Fong S, Gao W, Goddard A;
 PI Gurney AL, Pan J, Roy MA, Stewart TA, Tumas D, Watanabe CK;
 PI Wood WI;
 XX
 DR MPI: 2003-238305/23.
 DR N-PSDB; ABX11171.
 XX
 PT New PRO polypeptides and nucleic acid molecules, useful in diagnosing
 PT or treating inflammatory diseases or immune-related diseases, e.g.
 PT inflammatory bowel disease, systemic lupus erythematosus or rheumatoid
 PT arthritis
 XX
 PS Claim 12; Fig 10; 119pp; English.
 XX
 CC The present invention relates to the isolation of novel human
 CC secreted and transmembrane polypeptides designated PRO polypeptides
 CC (PRO1800, PRO339, PRO982, PRO1434, PRO1863, PRO1917, PRO1868, PRO3434
 CC and PRO1927), and the polynucleotide sequences encoding them. The PRO
 CC polypeptides and polynucleotide sequences of the invention are useful
 CC in diagnosing or treating inflammatory diseases or immune-related
 CC diseases (e.g. inflammatory bowel disease, systemic lupus
 CC erythematosus, rheumatoid arthritis, Sjogren's syndrome, autoimmune

CC haemolytic anaemia, autoimmune thrombocytopaenia, thyroiditis, diabetes
 CC mellitus, glomerulonephritis, multiple sclerosis, infectious hepatitis,
 CC immune-mediated skin diseases including psoriasis or contact dermatitis,
 CC and transplantation associated diseases including graft rejection or
 CC graft-versus-host disease). The PRO polypeptides are also useful for
 CC diagnosing tumours, and for inhibiting the growth of tumour cells. The
 CC PRO polynucleotide sequences may be used as hybridisation probes in
 CC chromosome and gene mapping, and in generating antisense RNA and DNA.
 CC They are also useful in preparing PRO polypeptides, in assays to
 CC identify other proteins or molecules involved in a binding reaction,
 CC to generate transgenic animals or knockout animals, which in turn are
 CC useful in the development and screening of therapeutically useful
 CC reagents, for chromosome identification, and tissue typing. The PRO
 CC polynucleotide sequences are also useful in gene therapy. Anti-PRO
 CC antibodies may be used in diagnostic assays for PRO polypeptides.
 CC The present sequence represents human PRO1863 polypeptide.
 CC
 XX
 SQ Sequence 437 AA;
 XX
 Qy 466 VLLDALG 473
 DB 4 VLLDALG 11
 XX
 Query Match 1.5%; Score 8; DB 24; Length 437;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 XX
 RESULT 34
 ABUS9153
 ID ABUS9153 standard; Protein; 437 AA.
 XX
 AC ABUS9153;
 XX
 DT 28-APR-2003 (first entry)
 XX
 DE Novel human secreted or transmembrane protein PRO181.
 XX
 KW Human; PRO: hypertrophy of neonatal heart; angiogenesis; wound healing;
 KW cardiac insufficiency disorder; cancer; tumour; immune response;
 KW adrenal cortical capillary endothelial growth; c-fos induction;
 KW vascular endothelial growth factor inhibition; VEGF inhibition;
 KW endothelial cell growth inhibitor; T-lymphocytes stimulation;
 KW retinal neurons cell survival; rod photoreceptor cell survival;
 KW retinal disorder; retinitis pigmentosa; kidney disorder;
 KW mammalian kidney mesangial cell proliferation; Berger disease;
 KW dermatitis; herpeticiformis; Cronin's disease; chondrocyte proliferation;
 KW chondrocyte redifferentiation; sports injury; arthritis.
 XX
 OS Homo sapiens.
 XX
 PN US2002132252-A1.
 XX
 PD 19-SEP-2002.
 XX
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 PR 05-NOV-1997; 97WO-US20069.
 PR 16-SEP-1998; 98WO-US19330.
 PR 17-SEP-1998; 98WO-US19437.
 PR 07-OCT-1998; 98WO-US21141.
 PR 01-DEC-1998; 98WO-US25108.
 PR 05-JAN-1999; 99WO-US00106.
 PR 08-MAR-1999; 99WO-US05028.
 PR 02-JUN-1999; 99WO-US12252.
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 PR 15-SEP-1999; 99WO-US21547.
 PR 30-NOV-1999; 99WO-US28313.
 PR 01-DEC-1999; 99WO-US28301.
 PR 01-DEC-1999; 99WO-US28634.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
 PR 06-JAN-2000; 2000WO-US00219.

PR 06-JUN-2000; 2000WO-US00376.
PR 11-FEB-2000; 2000WO-US03565.
PR 18-FEB-2000; 2000WO-US04341.
PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
PR 02-MAR-2000; 2000WO-US05004.
PR 10-MAR-2000; 2000WO-US05841.
PR 15-MAR-2000; 2000WO-US06319.
PR 20-MAR-2000; 2000WO-US06884.
PR 30-MAR-2000; 2000WO-US07377.
PR 15-MAY-2000; 2000WO-US08439.
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PR 22-MAY-2000; 2000WO-US13705.
PR 30-MAY-2000; 2000WO-US14042.
PR 02-JUN-2000; 2000WO-US15264.
PR 28-JUN-2000; 2000WO-US20710.
PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23528.
PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 28-FEB-2001; 2001WO-US06520.
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PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
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PR 07-MAY-1998; 98US-084600P.
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PR 05-JUN-1998; 98US-088167P.
PR 05-JUN-1998; 98US-088202P.
PR 05-JUN-1998; 98US-088212P.
PR 05-JUN-1998; 98US-088217P.
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PR 12-JUN-1998; 98US-088876P.
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PR 16-JUN-1998; 98US-089440P.
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PR 18-JUN-1998; 98US-089801P.
PR 18-JUN-1998; 98US-089907P.
PR 18-JUN-1998; 98US-089908P.
PR 28-AUG-2001; 2001US-0941992.

XX (GETH) GENENTECH INC.

PI Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
PI Ferrara N, Fong S, Garber H, Gerltzen ME, Goddard A, Godowski PJ;
PI Girmaidi JC, Gurney AU, Kljavin IJ, Napier MA, Pan J, Paoni NF;
PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WL;
PI Zhang Z;
XX
XX MPI; 2003-247083/24.
DR N-PSDB; ABX80352.

PT Novel isolated PRO polypeptides e.g., PRO826, PRO1068, PRO1184, PRO1346
PT and PRO1375, which stimulate proliferation of stimulated T-lymphocytes
PT are therapeutically useful for enhancing immune response and in cancer
PT treatments -
XX
XX Claim 12; Fig 250; 648pp; English.

XX The invention describes an isolated human PRO polypeptide. The PRO
CC polypeptides are useful in detecting PRO polypeptides in a sample, in
CC linking a bioactive molecule to a cell expressing a PRO polypeptide, and
CC in modulating at least one biological activity of a cell expressing a PRO
CC polypeptide. PRO1332 stimulates hypertrophy of neonatal heart and is thus
CC useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186
CC stimulate adrenal cortical capillary endothelial growth, and PRO536,
CC PRO943, PRO828, PRO1068 or PRO535, PRO826, PRO819, PRO1126,
CC PRO1360 and PRO1387 induce c-fos in endothelial cells, and are thus
CC useful for treating conditions or disorders where angiogenesis would be
CC beneficial, e.g. wound healing and antenatal of this polypeptide are
CC useful for treating cancerous tumors. PRO812 inhibits vascular
CC endothelial growth factor (VEGF) stimulated proliferation of endothelial
CC cells and is thus useful for inhibiting endothelial cell growth in
CC mammals which would be beneficial in inhibiting tumour growth. PRO826,
CC PRO1068, PRO1184, PRO1346 and PRO1375 stimulate proliferation of
CC stimulated T-lymphocytes and are therapeutically useful for enhancing
CC immune response. PRO828, PRO826, PRO1068 or PRO1132 enhance survival of
CC retinal neurons cells (PRO1132 is also enhances survival/proliferation of
CC rod photoreceptor cells) and therefore are useful for treating retinal
CC disorders of injuries, e.g. retinitis pigmentosa. AMD. PRO819, PRO813
CC and PRO1066 induce proliferation of mammalian kidney mesangial cells,
CC and therefore are useful for treating kidney disorders associated with
CC decreased mesangial cell function such as Berger disease or other
CC nephropathies associated with dermatitis, herpeticiformis or Crohn's
CC disease. PRO1310, PRO844, PRO1312, PRO1192 and PRO1387 induce the
CC proliferation and/or redifferentiation of chondrocytes in culture and
CC are thus useful for treating sports injuries, and arthritis. This
CC is the amino acid sequence of a novel human PRO protein.

XX Sequence 437 AA;

Query Match 1.5%; Score 8; DB 24; Length 437;

Best Local Similarity 100.0%; Pred. No. 71;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 466 VLLALLLG 473
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DB 4 VLLALLLG 11

RESULT 35

ABUS9300 standard; Proteins; 437 AA.

XX ABUS9300;

DT 22-APR-2003 (first entry)

XX Human secreted/transmembrane protein, #143.

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XX Human: PRO; secreted; transmembrane; pharmaceutical;
KW diagnostic; biosensor; bioreactor; tumour; therapeutic;
KW gene therapy; tumour-associated antigenic target; TAT; ADAPT;
KW antibody-dependent enzyme mediated prodrug therapy; cytostatic.
XX Homo sapiens.
XX US2003027162-A1.
XX
XX 06-FEB-2003.
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XX 15-NOV-2001; 2001US-0997428.
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XX 05-NOV-1997; 97WO-US20069.
XX 16-SEP-1998; 98WO-US19330.
XX 17-SEP-1998; 98WO-US19437.
XX 07-OCT-1998; 98WO-US21141.
XX 01-DEC-1998; 98WO-US25108.
XX 05-JAN-1999; 99WO-US00106.
XX 08-MAR-1999; 99WO-US05028.
XX 02-JUN-1999; 99WO-US12252.
XX 15-SEP-1999; 99WO-US21090.
XX 15-SEP-1999; 99WO-US21547.
XX 30-NOV-1999; 99WO-US28313.
XX 01-DEC-1999; 99WO-US28301.
XX 01-DEC-1999; 99WO-US28634.
XX 16-DEC-1999; 99WO-US30095.
XX 20-DEC-1999; 99WO-US30911.
XX 05-JAN-2000; 2000WO-US00219.
XX 06-JAN-2000; 2000WO-US00376.
XX 11-FEB-2000; 2000WO-US03565.
XX 18-FEB-2000; 2000WO-US04341.
XX 22-FEB-2000; 2000WO-US04414.
XX 24-FEB-2000; 2000WO-US04914.
XX 24-FEB-2000; 2000WO-US05004.
XX 02-MAR-2000; 2000WO-US05841.
XX 10-MAR-2000; 2000WO-US06319.
XX 15-MAR-2000; 2000WO-US06884.
XX 20-MAR-2000; 2000WO-US07377.
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XX 02-JUN-2000; 2000WO-US15264.
XX 28-JUL-2000; 2000WO-US20710.
XX 11-AUG-2000; 2000WO-US22031.
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XX 08-NOV-2000; 2000WO-US30952.
XX 01-DEC-2000; 2000WO-US32578.
XX 28-FEB-2001; 2001WO-US06520.
XX 01-JUN-2001; 2001WO-US17800.
XX 20-JUN-2001; 2001WO-US19692.
XX 29-JUN-2001; 2001WO-US21066.
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XX 17-OCT-1997; 97US-062250P.
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Query Match 1.5%; Score 8; DB 24; Length 437;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 466 VLLALLG 473
Db 4 VLLALLG 11

RESULT 36
ABUS9449

ID ABUS9449 standard; Protein; 437 AA.

AC ABUS9449;

DT 22-APR-2003 (first entry)

XX Novel human secreted or transmembrane protein PRO1182.

KW Human; PRO; hypertrophy of neonatal heart; angiogenesis; wound healing;

KW cardiac insufficiency disorder; cancer; tumour; immune response;

KW adrenal cortical capillary endothelial growth; c-fos induction;

KW vascular endothelial growth factor inhibition; VEGF inhibition;

KW endothelial cell growth inhibitor; T-lymphocytes stimulation;

KW retinal neurons cell survival; rod photoreceptor cell survival;

KW retinal disorder; retinitis pigmentosa; kidney disorder;
KW mammalian kidney mesangial cell proliferation; Berger disease;
KW dermatitis; herpeticiformis; Crohn's disease; chondrocyte proliferation;
KW chondrocyte redifferentiation; sports injury; arthritis.
OS Homo sapiens.
XX US2003027985-A1.
XX 06-FEB-2003.
XX 14-NOV-2001; 2001US-0990562.
XX 05-NOV-1997; 97WO-US20069.
PR 16-SEP-1998; 98WO-US19330.
PR 17-SEP-1998; 98WO-US19437.
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PR 01-DEC-1998; 98WO-US25108.
PR 05-JAN-1999; 99WO-US00106.
PR 08-MAR-1999; 99WO-US05028.
PR 02-JUN-1999; 99WO-US12252.
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PR 01-DEC-1999; 99WO-US28301.
PR 01-DEC-1999; 99WO-US28301.
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PR 24-FEB-2000; 2000WO-US05004.
PR 02-MAR-2000; 2000WO-US05841.
PR 10-MAR-2000; 2000WO-US06319.
PR 15-MAR-2000; 2000WO-US06884.
PR 20-MAR-2000; 2000WO-US07377.
PR 30-MAR-2000; 2000WO-US08439.
PR 15-MAY-2000; 2000WO-US13358.
PR 17-MAY-2000; 2000WO-US13705.
PR 22-MAY-2000; 2000WO-US14042.
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PR 02-JUN-2000; 2000WO-US15264.
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PR 11-AUG-2000; 2000WO-US22031.
PR 23-AUG-2000; 2000WO-US23522.
PR 24-AUG-2000; 2000WO-US23328.
PR 08-NOV-2000; 2000WO-US30952.
PR 01-DEC-2000; 2000WO-US32678.
PR 28-FEB-2001; 2001WO-US06520.
PR 01-JUN-2001; 2001WO-US17800.
PR 20-JUN-2001; 2001WO-US19692.
PR 29-JUN-2001; 2001WO-US21066.
PR 09-JUL-2001; 2001WO-US21735.
PR 16-JUN-1997; 97US-049787P.
PR 17-OCT-1997; 97US-062250P.
PR 12-NOV-1997; 97US-065186P.
PR 13-NOV-1997; 97US-065311P.
PR 24-NOV-1997; 97US-066770P.
PR 25-FEB-1998; 98US-075945P.
PR 20-MAR-1998; 98US-078910P.
PR 28-APR-1998; 98US-083322P.
PR 07-MAY-1998; 98US-084600P.
PR 28-MAY-1998; 98US-087106P.
PR 02-JUN-1998; 98US-087607P.
PR 02-JUN-1998; 98US-087609P.
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PR 04-AUG-1998; 98US-095282P.
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Query Match

Best Local Similarity 1.5%; Score 8; DB 24; Length 437;
Pred. No. 71;
Matches . 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 466 VILLALIG 473

DB 4 VILLALIG 11

RESULT 37

ID ABU60584 standard; Protein; 437 AA.

AC ABU60584;

DT 01-MAY-2003 (first entry)

DE Human secreted/transmembrane protein, #143.

KW Human; PRO; secreted; transmembrane; signal peptide;
pharmaceutical; diagnostic; therapeutic; gene therapy.

OS Homo sapiens.

PN US2002160384-A1.

PD 31-OCT-2002.

PF 14-NOV-2001; 2001US-0992598.

PR 05-NOV-1997; 97WO-US20069.

PR 16-SEP-1998; 98WO-US19330.

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PR 17-SEP-1998; 98WO-US19437.
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PR 10-MAR-2000; 2000WO-US06319.
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PR 16-JUN-1997; 97US-049787F.
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PR 10-JUN-1998; 98US-088742P.
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PR 11-JUN-1998; 98US-088876P.
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PR 18-JUN-1998; 98US-089908P.
PR 28-AUG-2001; 2001US-094192.

XX
XX
XX (GETH ) GENENTECH INC.;
XX
XX Ashkenazi AJ, Baker KP, Botstein D, Desnovers L, Eaton DL;
XX Ferrara N, Fong S, Gerber H, Gerritsen ME, Goddard A, Godowski PJ;
XX Grimaldi JC, Gurney AL, Kijavlin IJ, Napier MA, Pan J, Paoni NF;
XX Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WT;
XX Zhang Z;
XX
XX MPI. 2003-288106/28.
XX N-PSDB; ABX90330.
XX
XX
XX PT New transmembrane polypeptides and nucleic acids encoding the
XX polypeptides, useful in gene therapy, in chromosome identification, as
XX PT chromosome markers, or in generating probes -
XX
XX
XX PS Claim 12, Fig 250; 650pp; English.
XX
XX
XX CC The invention discloses isolated PRO secreted/transmembrane polypeptides
XX comprising a sequence without signal peptide and the nucleic acid
XX CC encoding them. The polypeptides can be used to raise antibodies that
XX CC specifically bind to the PRO polypeptide, for linking a bioactive
XX CC molecule to a cell expressing a PRO protein and for modulating at least
XX CC one biological activity of a cell. The PRO polypeptides or
XX CC polynucleotides are also useful in gene therapy, in chromosome
XX CC identification, as chromosome markers, or in generating probes. The PRO
XX CC polypeptides are useful as molecular markers for protein
XX CC electrophoresis, and the isolated nucleic acids may be used for
XX CC recombinantly expressing those markers. The PRO polypeptides and nucleic
XX CC acids may also be used in tissue typing. Anti-PRO antibodies are useful
XX CC in diagnostic assays for PRO, and in affinity purification of PRO from
XX CC recombinant cell culture or natural sources. The sequences presented in
XX CC ABU60478-ABU60624 are the PRO polynucleotides of the invention.
XX CC Note: The sequence data for this patent is also available in electronic
XX CC format from USPTO at seqdata.uspto.gov/sequence.html.
XX
XX
XX SQ Sequence 437 AA;
XX
XX
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XX Best Local Similarity. 100.0%; Pred. No. 71;
XX Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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XX Db 4 VLLALLLG 11
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XX ID ABUS8075 standard; Protein; 437 AA.
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XX AC ABUS8075;
XX
XX DT 14-APR-2003 (first entry)
XX

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horse; cow; dog; cat; sheep; pig; goat; rabbit; ADEPT,
antibody-dependent enzyme mediated prodrug therapy.

Homo sapiens.

US2003027163-A1.

06-FEB-2003

15-NOV-2001; 2001US-0997666

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PR	20-JUL-1998;	98US-093339P;

PR 30-JUL-1998; 98US-094651P.
PR 04-AUG-1998; 98US-095282P.
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Best Local Similarity 100.0%; Pred. No. 71;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 39

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ID ABUS9006 standard; Protein; 437 AA.

XX ABUS9006;

DT 16-APR-2003 (first entry)

DE Human secreted/transmembrane protein, #143.

KX Human; PRO; secreted; transmembrane; signal peptide;

KW pharmaceutical; diagnostic; biosensor; bioreactor; tumour; therapeutic;
colon cancer; lung cancer; breast cancer; cancer; gene therapy.

XX Homo sapiens.

XX US2002142961-A1.
XX 03-OCT-2002.
XX 19-NOV-2001; 2001US-0989721.
XX 05-NOV-1997; 97WO-US20069.
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XX 07-OCT-1998; 98WO-US21141.
PR 01-DEC-1998; 98WO-US25108.
PR 05-JAN-1999; 99WO-US00106.
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PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
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PR 16-DEC-1999; 99WO-US28634.
PR 20-DEC-1999; 99WO-US30095.
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PR 22-FEB-2000; 2000WO-US04414.
PR 24-FEB-2000; 2000WO-US04914.
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PR 10-MAR-2000; 2000WO-US05841.
PR 15-MAR-2000; 2000WO-US06319.
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 PR 17-JUN-1998; 98US-089538P.
 PR 17-JUN-1998; 98US-089599P.
 PR 17-JUN-1998; 98US-089600P.
 PR 17-JUN-1998; 98US-089653P.
 PR 18-JUN-1998; 98US-089801P.
 PR 18-JUN-1998; 98US-089907P.
 PR 18-JUN-1998; 98US-089908P.
 PR 28-AUG-2001; 2001US-0941992.
 (GENTH) GENENTECH INC.

PA Ashkenazi AJ, Baker KP, Botstein D, Deenoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gerber H, Gerriksen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gurney AL, Kijavini TJ, Napier MA, Pan J, Paoletti NF;
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
 PI Zhang Z;
 XX WPI; 2003-155950/15.

XX New secreted and transmembrane PRO polypeptides (e.g. PRO183, PRO184,
 PT PRO361 or PRO846) useful as targets for therapeutic intervention in
 PT cancers (e.g. lung or breast cancers), or for diagnosing these cancers
 PT -

XX Claim 12; Fig 250; 647pp; English.

XX The invention discloses isolated PRO secreted/transmembrane polypeptides
 CC comprising a sequence without signal peptide and the nucleic acid
 CC encoding them. The polypeptides can be used to raise antibodies that
 CC specifically bind to the PRO polypeptide, for linking a bioactive
 CC molecule to a cell expressing a PRO protein and for modulating at least
 CC one biological activity of a cell. The PRO polypeptides or
 CC polynucleotides are also useful as pharmaceuticals, diagnostics,
 CC biosensors or bioreactors, for detecting or treating e.g. tumors in
 CC mammals, e.g. humans, dogs, cats, cattle, horses, sheep, pigs, goats or
 CC rabbits as targets for therapeutic intervention in certain cancers (e.g.
 CC colon, lung or breast cancers) and diagnostic determination of the
 CC presence of these cancers. The PRO polypeptides are also useful as
 CC molecular weight markers or for chromosome identification. The PRO genes
 CC are useful as hybridization probes or for screening libraries of human
 CC cDNA, genomic DNA or mRNA. The PRO genes may also be used in gene
 CC therapy, particularly for replacing a defective gene. The sequences
 CC presented in ABUS8900-ABUS9046 are the PRO polypeptides of the invention.

XX Sequence 437 AA;

Query Match 1.5%; Score 8; DB 24; Length 437;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 466 VLLALLIG 473
 DB 4 VLLALLIG 11

RESULT 40
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 XX AC ABU13966;
 XX 26-FEB-2003 (first entry)
 DT XX
 DE Human PRO181 polypeptide.
 KW Human; PRO polypeptide; secreted protein; transmembrane protein;
 KW genetic disorder; antibacterial; immunosuppressive.
 XX Homo sapiens.
 OS US2002103125-A1.
 PN 01-AUG-2002.
 PD 20-NOV-2001; 2001US-0989731.
 XX 05-NOV-1997; 97WO-US20069.
 PR 16-SEP-1998; 98WO-US19330.
 PR 17-SEP-1998; 98WO-US19437.
 PR 07-OCT-1998; 98WO-US21141.
 PR 01-DEC-1998; 98WO-US25108.
 PR 05-JAN-1999; 99WO-US00106.
 PR 08-MAR-1999; 99WO-US05028.
 PR 02-JUN-1999; 99WO-US42252.
 PR 15-SEP-1999; 99WO-US21090.
 PR 15-SEP-1999; 99WO-US21547.
 PR 30-NOV-1999; 99WO-US28313.
 PR 01-DEC-1999; 99WO-US28301.
 PR 01-DEC-1999; 99WO-US28634.
 PR 16-DEC-1999; 99WO-US30095.
 PR 20-DEC-1999; 99WO-US30911.
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 PR 02-MAR-2000; 2000WO-US05004.
 PR 15-MAR-2000; 2000WO-US05841.
 PR 10-MAR-2000; 2000WO-US06819.
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 PR 30-MAR-2000; 2000WO-US08439.
 PR 15-MAY-2000; 2000WO-US13358.
 PR 17-MAY-2000; 2000WO-US13705.
 PR 22-MAY-2000; 2000WO-US14042.
 PR 30-MAY-2000; 2000WO-US14941.
 PR 02-JUN-2000; 2000WO-US15264.
 PR 28-JUL-2000; 2000WO-US20710.
 PR 11-AUG-2000; 2000WO-US22031.
 PR 23-AUG-2000; 2000WO-US23522.
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 PR 08-NOV-2000; 2000WO-US30952.
 PR 01-DEC-2000; 2000WO-US32678.
 PR 28-FEB-2001; 2001WO-US06520.
 PR 01-JUN-2001; 2001WO-US17800.
 PR 20-JUN-2001; 2001WO-US19692.
 PR 29-JUN-2001; 2001WO-US21066.
 PR 09-JUL-2001; 2001WO-US21735.
 PR 16-JUN-1997; 97US-049787P.
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 PR 07-MAY-1998; 98US-084600P.

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 PR 03-JUN-1998; 98US-087827P.
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 PR 17-JUN-1998; 98US-089600P.
 PR 18-JUN-1998; 98US-089653P.
 PR 18-JUN-1998; 98US-089801P.
 PR 18-JUN-1998; 98US-089907P.
 PR 18-JUN-1998; 98US-089908P.
 PR 28-AUG-2001; 2001US-0941992.

XX (GETH) GENENTECH LTD.
 PA

XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
 PI Ferrara N, Fong S, Gerber H, Gerltsen ME, Goddard A, Godowski PJ;
 PI Grimaldi JC, Gunney AL, Kijavitt IU, Napier MA, Pan J, Peoni NF;
 PI Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WI;
 PI Zhang Z;
 XX

DR MPI; 2003-102117/09.
 DR N-PSDB; ABX64176.

XX Novel secreted and transmembrane polypeptide for modulating biological
 PT activity of cell expressing the polypeptide, identifying agonists or
 PT antagonists of polypeptide, and as molecular weight markers
 XX

PS Claim 12; Fig 250; 649pp; English.

XX The present invention relates to the isolation of novel human PRO
 CC polypeptides, and the polynucleotide sequences encoding them. The
 CC PRO polypeptides are secreted and transmembrane proteins. The PRO
 CC polypeptides are useful for detecting other PRO polypeptides, for
 CC linking bioactive molecules to cells expressing PRO polypeptides,
 CC for modulating biological activities of cells expressing PRO
 CC polypeptides, and for identifying agonists or antagonists.
 CC The polynucleotide sequences encoding PRO polypeptides are useful as
 CC hybridization probes, in chromosome and gene mapping, in the generation
 CC of antisense RNA and DNA, in the preparation of PRO polypeptides, for
 CC generating transgenic animals or knockout animals, to construct
 CC hybridization probes for mapping the gene which encodes the PRO
 CC polypeptide, and for the genetic analysis of individuals with genetic
 CC disorders, in gene therapy, for chromosome identification, as

CC chromosome markers, and for generating probes for PCR, Northern
 CC analysis, Southern analysis and Western analysis. ABU13860-ABU14006
 CC represent the human PRO polypeptides of the invention.
 CC Note: The sequence data for this patent was obtained in electronic
 CC format directly from the USPTO web site at
 CC seqdata.uspto.gov/patidententry.html.
 CC

XX SQ Sequence 437 AA;

Query Match 1.5%; Score 8; DB 24; Length 437;
 Best Local Similarity 100.0%; Pred. No. 71;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 466 VLLALALG 473
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 DB 4 VLLALALG 11

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OM protein - protein search, using sw model

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(without alignments)
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Title: US-10-039-770A-1

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Searched: 328717 seqs, 42310858 residues

Word size : 0

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	8	1.5	437	4 US-09-996-243-355	Sequence 355, App
5	8	1.5	497	6 5486473-4	Patent No. 5486473
6	8	1.5	689	4 US-09-252-991A-18990	Sequence 18990, A
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8	7	1.3	100	4 US-09-205-258-1046	Sequence 1046, Ap
9	7	1.3	137	4 US-09-904-615-163	Sequence 163, Ap
10	7	1.3	146	4 US-09-252-991A-21858	Sequence 21858, A
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133	6	1.1	63	4	US-07-603-451A-3	Sequence 3, Appl1	206	6	1.1	127	1	US-08-318-193-2	Sequence 2, Appl1
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135	6	1.1	64	1	US-08-248-016-4	Sequence 4, Appl1	208	6	1.1	127	3	US-08-722-258-4	Sequence 4, Appl1
136	6	1.1	64	1	US-08-451-501-4	Sequence 4, Appl1	209	6	1.1	127	3	US-09-236-490-7	Sequence 7, Appl1
137	6	1.1	64	1	US-08-451-501-4	Sequence 4, Appl1	210	6	1.1	127	4	US-09-198-452A-464	Sequence 464, App
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139	6	1.1	64	4	US-09-228-302-5	Sequence 5, Appl1	212	6	1.1	127	5	PCT-US96-11445-7	Sequence 7, Appl1
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141	6	1.1	64	4	US-09-228-302-30	Sequence 30, Appl1	214	6	1.1	127	6	5405952-2	Parent No. 5405952
142	6	1.1	64	5	PCT-US94-05257-3	Sequence 3, Appl1	215	6	1.1	128	3	US-08-463-318-160	Sequence 160, App
143	6	1.1	64	5	PCT-US95-06761-4	Sequence 4, Appl1	216	6	1.1	128	4	US-08-468-609A-160	Sequence 160, App
144	6	1.1	65	1	US-08-248-016-12	Sequence 12, Appl1	217	6	1.1	128	4	US-08-446-872A-160	Sequence 160, App
145	6	1.1	65	1	US-08-451-501-12	Sequence 12, Appl1	218	6	1.1	128	4	US-08-762-227A-160	Sequence 160, App
146	6	1.1	65	2	US-08-117-952-770	Sequence 770, App	219	6	1.1	128	5	PCT-US95-01185-160	Sequence 160, App
147	6	1.1	65	5	PCT-US95-06761-12	Sequence 12, Appl1	220	6	1.1	129	1	US-08-049-503-1	Sequence 1, Appl1
148	6	1.1	66	4	US-09-187-999-37	Sequence 37, Appl1	221	6	1.1	129	1	US-08-225-224-2	Sequence 2, Appl1
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153	6	1.1	76	3	US-09-083-521-5	Sequence 5, Appl1	226	6	1.1	129	3	US-08-765-012A-16	Sequence 16, Appl1
154	6	1.1	77	4	US-08-311-731A-239	Sequence 239, App	227	6	1.1	129	3	US-08-765-012A-17	Sequence 17, Appl1
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163	6	1.1	90	3	US-08-912-314A-24	Sequence 24, Appl1	236	6	1.1	129	5	PCT-US95-04468-2	Sequence 2, Appl1
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166	6	1.1	95	1	US-07-928-611-2	Sequence 2, Appl1	239	6	1.1	130	3	US-08-765-012A-12	Sequence 12, Appl1
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169	6	1.1	95	4	US-09-060-694-2	Sequence 2, Appl1	242	6	1.1	130	3	US-08-765-012A-15	Sequence 15, Appl1
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171	6	1.1	95	5	PCT-US93-07370-2	Sequence 2, Appl1	244	6	1.1	131	3	US-09-033-275-10	Sequence 10, Appl1
172	6	1.1	96	1	US-08-518-878B-35	Sequence 35, Appl1	245	6	1.1	131	3	US-08-765-012A-6	Sequence 6, Appl1
173	6	1.1	96	1	US-08-294-522B-34	Sequence 34, Appl1	246	6	1.1	131	3	US-08-765-012A-7	Sequence 7, Appl1

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296	6	1.1	156	4	US-08-311-731A-164	Sequence 164, App	369	6	1.1	200	4	US-08-468-446-463	Sequence 463, App
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313	6	1.1	167	3	US-08-513-974B-363	Sequence 363, App	386	6	1.1	222	4	US-08-740-036-3	Sequence 3, Appli
314	6	1.1	167	3	US-08-513-974B-367	Sequence 367, App	387	6	1.1	222	4	US-08-740-036-3	Sequence 3, Appli
315	6	1.1	167	3	US-08-776-971-101	Sequence 101, App	388	6	1.1	222	6	5185431-4	Patent No. 5185431
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413	6	1.1	244	1	US-08-762-129-4	Sequence 4, Appli	486	6	1.1	294	2	US-08-284-465-8	Sequence 40, Appli
414	6	1.1	244	2	US-09-090-567-2	Sequence 2, Appli	487	6	1.1	294	4	US-09-372-422A-40	Sequence 8, Appli
415	6	1.1	244	2	US-09-252-991A-22858	Sequence 2, Appli	488	6	1.1	294	4	US-09-335-160D-8	Sequence 8, Appli
416	6	1.1	246	4	US-09-252-991A-27629	Sequence 22858, A	489	6	1.1	295	4	US-09-372-422A-38	Sequence 38, Appli
417	6	1.1	247	2	US-08-308-005C-2	Sequence 27629, A	490	6	1.1	295	4	US-09-252-991A-22401	Sequence 22401, A
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419	6	1.1	247	2	US-08-956-267A-2	Sequence 2, Appli	492	6	1.1	297	2	US-09-027-013-3	Sequence 3, Appli
420	6	1.1	247	2	US-08-460-529B-10	Sequence 10, Appli	493	6	1.1	297	3	US-09-244-223-3	Sequence 3, Appli
421	6	1.1	247	2	US-08-331-117A-2	Sequence 2, Appli	494	6	1.1	299	4	US-09-252-991A-17588	Sequence 17588, A
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423	6	1.1	249	4	US-09-372-422A-22	Sequence 22, Appl	496	6	1.1	300	4	US-09-252-991A-28367	Sequence 28367, A
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425	6	1.1	250	1	US-08-234-939-2	Sequence 2, Appli	498	6	1.1	301	3	US-08-468-609A-142	Sequence 142, App
426	6	1.1	250	3	US-08-558-865-2	Sequence 2, Appli	499	6	1.1	301	4	US-08-762-227A-142	Sequence 142, App
427	6	1.1	250	3	US-08-654-025-2	Sequence 2, Appli	500	6	1.1	301	4	US-08-762-227A-142	Sequence 142, App
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437	6	1.1	259	3	US-08-469-318-141	Sequence 141, App	510	6	1.1	314	3	US-09-008-271A-3	Sequence 3, Appli
438	6	1.1	259	3	US-08-468-609A-141	Sequence 141, App	511	6	1.1	314	3	US-09-023-942A-6	Sequence 6, Appli
439	6	1.1	259	4	US-08-446-872A-141	Sequence 141, App	512	6	1.1	315	4	US-08-118-270-28	Sequence 28, Appli
440	6	1.1	259	4	US-08-762-227A-141	Sequence 141, App	513	6	1.1	315	5	PCT-US93-08528-28	Sequence 28, Appli
441	6	1.1	259	5	US-09-252-991A-32989	Sequence 32989, A	514	6	1.1	316	4	US-09-134-001C-5547	Sequence 5547, Ap
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444	6	1.1	266	4	US-09-879-919-24	Sequence 24, Appl	517	6	1.1	318	4	US-09-517-739-1	Sequence 31, Appli
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453	6	1.1	268	3	US-08-871-483-11	Sequence 11, Appl	526	6	1.1	327	4	US-09-252-991A-35058	Sequence 25058, A
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459	6	1.1	274	3	US-08-468-609A-144	Sequence 144, App	532	6	1.1	329	1	US-08-309-985-7	Sequence 2, Appli
460	6	1.1	274	4	US-08-466-872A-144	Sequence 144, App	533	6	1.1	330	1	US-08-238-163-2	Sequence 2, Appli
461	6	1.1	274	4	US-08-762-227A-144	Sequence 144, App	534	6	1.1	331	3	US-08-961-083-212	Sequence 212, App
462	6	1.1	274	5	PCT-US95-01185-144	Sequence 144, App	535	6	1.1	331	4	US-09-536-788-212	Sequence 212, App
463	6	1.1	277	4	US-09-252-991A-21417	Sequence 21417, A	536	6	1.1	332	2	US-08-446-875-12	Sequence 12, Appli
464	6	1.1	278	3	US-08-663-082-4	Sequence 4, Appli	537	6	1.1	332	2	US-08-102-385G-12	Sequence 12, Appli
465	6	1.1	280	4	US-09-247-155-178	Sequence 178, App	538	6	1.1	332	4	US-09-252-991A-29873	Sequence 29873, A

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540	6	1.1	336	1	US-08-118-270-54	Sequence 54, Appl	614	6	1.1	381	4	US-09-569-804-17	Sequence 17, Appl
542	6	1.1	336	5	PCT-US93-08528-54	Sequence 54, Appl	615	6	1.1	381	4	US-09-252-991A-29970	Sequence 29970, A
543	6	1.1	339	4	US-09-690-454-66	Sequence 66, Appl	616	6	1.1	382	1	US-08-470-299-17	Sequence 7, Appl1
544	6	1.1	340	4	US-09-690-454-174	Sequence 174, App	617	6	1.1	382	1	US-08-470-299-10	Sequence 10, Appl
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546	6	1.1	341	4	US-09-252-991A-30760	Sequence 30760, A	619	6	1.1	384	1	US-08-220-958-2	Sequence 2, Appl1
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548	6	1.1	344	3	US-08-961-083-192	Sequence 192, App	621	6	1.1	385	4	US-09-587-754-2	Sequence 2, Appl1
549	6	1.1	344	4	US-09-134-001C-5004	Sequence 5004, Ap	622	6	1.1	385	4	US-08-261-293-2	Sequence 2, Appl1
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551	6	1.1	346	4	US-09-328-352-5835	Sequence 5835, Ap	624	6	1.1	387	1	US-07-626-618A-17	Sequence 17, Appl
552	6	1.1	349	3	US-09-032-523-3	Sequence 3, Appl1	625	6	1.1	387	1	US-08-123-161A-10	Sequence 10, Appl1
553	6	1.1	350	1	US-08-204-196A-1	Sequence 1, Appl1	626	6	1.1	387	1	US-08-086-439C-3	Sequence 3, Appl1
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556	6	1.1	352	1	US-08-482-577B-4	Sequence 4, Appl1	629	6	1.1	387	1	US-08-333-977-17	Sequence 17, Appl
557	6	1.1	352	3	US-09-218-176-4	Sequence 4, Appl1	630	6	1.1	387	1	US-08-483-278-10	Sequence 10, Appl1
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562	6	1.1	354	3	US-09-325-897-2	Sequence 2, Appl1	635	6	1.1	387	2	US-08-884-072-5	Sequence 5, Appl1
563	6	1.1	354	4	US-09-837-726-2	Sequence 2, Appl1	636	6	1.1	387	2	US-08-487-811A-18	Sequence 18, Appl1
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565	6	1.1	357	4	US-09-404-296B-10	Sequence 10, Appl	638	6	1.1	387	3	US-08-980-514-3	Sequence 3, Appl1
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568	6	1.1	361	3	US-09-515-039-75	Sequence 75, Appl	641	6	1.1	387	3	US-09-060-694-18	Sequence 18, Appl
569	6	1.1	361	4	US-09-339-159B-30	Sequence 30, Appl	642	6	1.1	387	4	US-09-212-168-5	Sequence 5, Appl1
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572	6	1.1	365	4	US-09-134-001C-5075	Sequence 5075, Ap	645	6	1.1	387	5	PCT-US93-07370-18	Sequence 18, Appl
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576	6	1.1	371	4	US-09-339-972-20	Sequence 20, Appl	649	6	1.1	390	4	US-09-328-352-7880	Sequence 4891, Ap
577	6	1.1	372	1	US-08-278-729A-33	Sequence 33, Appl	650	6	1.1	390	4	US-09-328-352-7880	Sequence 7880, Ap
578	6	1.1	372	1	US-08-155-343A-33	Sequence 33, Appl	651	6	1.1	396	3	US-08-208-007A-13	Sequence 13, Appl
579	6	1.1	372	1	US-08-406-672-33	Sequence 33, Appl	652	6	1.1	396	3	US-09-032-523-9	Sequence 9, Appl1
580	6	1.1	372	1	US-08-643-563A-33	Sequence 33, Appl	653	6	1.1	396	4	US-08-915-095A-13	Sequence 13, Appl
581	6	1.1	372	1	US-08-643-763A-33	Sequence 33, Appl	654	6	1.1	396	4	US-08-798-096-13	Sequence 13, Appl
582	6	1.1	372	1	US-08-462-623-33	Sequence 33, Appl	655	6	1.1	396	4	US-08-798-095A-13	Sequence 13, Appl
583	6	1.1	372	2	US-08-451-953A-33	Sequence 33, Appl	656	6	1.1	396	4	US-09-953-956-13	Sequence 13, Appl
584	6	1.1	372	2	US-08-459-346-15	Sequence 15, Appl	657	6	1.1	396	4	US-08-553-125A-13	Sequence 13, Appl
585	6	1.1	372	2	US-08-445-468A-33	Sequence 33, Appl	658	6	1.1	399	2	US-08-282-197C-54	Sequence 54, Appl
586	6	1.1	372	2	US-08-461-397A-33	Sequence 33, Appl	659	6	1.1	399	2	US-08-839-581A-2	Sequence 2, Appl1
587	6	1.1	372	2	US-08-912-088-33	Sequence 33, Appl	660	6	1.1	399	2	US-09-023-591A-2	Sequence 2, Appl1
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592	6	1.1	372	4	US-09-170-936-33	Sequence 33, Appl	665	6	1.1	407	4	US-09-569-804-21	Sequence 21, Appl
593	6	1.1	372	4	US-08-402-542-15	Sequence 15, Appl	666	6	1.1	411	4	US-09-015-188-2	Sequence 2, Appl1
594	6	1.1	372	4	US-08-461-113-33	Sequence 33, Appl	667	6	1.1	411	4	US-09-333-208-2	Sequence 2, Appl1
595	6	1.1	372	4	US-08-456-033-33	Sequence 33, Appl	668	6	1.1	416	3	US-09-183-254-2	Sequence 2, Appl1
596	6	1.1	372	4	US-08-643-321-31	Sequence 31, Appl	669	6	1.1	416	4	US-09-183-270-2	Sequence 2, Appl1
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598	6	1.1	372	5	PCT-US93-07189-15	Sequence 15, Appl	671	6	1.1	416	4	US-09-252-991A-28499	Sequence 28499, A
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601	6	1.1	372	5	PCT-US93-08742-33	Sequence 33, Appl	674	6	1.1	419	1	US-07-928-611-20	Sequence 20, Appl1
602	6	1.1	372	5	PCT-US93-08808-33	Sequence 33, Appl	675	6	1.1	419	1	US-08-385-186-2	Sequence 2, Appl1
603	6	1.1	373	5	PCT-US93-08885-33	Sequence 33, Appl	676	6	1.1	419	2	US-08-487-811A-20	Sequence 20, Appl1
604	6	1.1	373	4	US-09-996-243-503	Sequence 503, App	677	6	1.1	419	3	US-09-060-694-20	Sequence 20, Appl1
605	6	1.1	374	3	US-08-821-994-70	Sequence 70, Appl	678	6	1.1	419	3	US-08-974-691-3	Sequence 3, Appl1
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608	6	1.1	376	4	US-09-325-991A-20454	Sequence 20454, A	681	6	1.1	419	5	US-09-378-074-20	Sequence 20, Appl
609	6	1.1	378	4	US-09-325-991A-158	Sequence 158, App	682	6	1.1	419	5	PCT-US93-07370-20	Sequence 20, Appl
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685	6	1.1	423	4	US-09-252-991A-32110	Sequence 32110, A	758	6	1.1	485	4	US-09-107-532A-4797	Sequence 4797, Ap
686	6	1.1	423	4	US-09-073-009-142	Sequence 142, App	759	6	1.1	486	3	US-08-348-518C-2	Sequence 2, Appli
687	6	1.1	426	4	US-09-252-991A-20642	Sequence 20642, A	760	6	1.1	487	4	US-09-252-991A-28079	Sequence 28079, A
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691	6	1.1	431	3	US-09-381-681-3	Sequence 3, Appli	764	6	1.1	490	4	US-09-461-325-518	Sequence 518, App
692	6	1.1	433	2	US-08-919-624-1	Sequence 1, Appli	765	6	1.1	492	4	US-09-794-236-2	Sequence 2, Appl
693	6	1.1	433	2	US-08-941-532-6	Sequence 6, Appli	766	6	1.1	492	4	US-09-345-469-1	Sequence 1, Appli
694	6	1.1	433	4	US-09-051-239A-2	Sequence 2, Appli	767	6	1.1	493	4	US-09-252-991A-17194	Sequence 17194, A
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696	6	1.1	433	4	US-09-170-496B-190	Sequence 190, App	769	6	1.1	497	2	US-09-047-125-3	Sequence 3, Appli
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984 6 1.1 914 2 US-08-825-886-21 Sequence 21, Appl
985 6 1.1 914 4 US-08-989-890-21 Sequence 21, Appl
986 6 1.1 915 4 US-09-214-5558-2 Sequence 2, Appl
987 6 1.1 917 2 US-08-588-983-16 Sequence 16, Appl
988 6 1.1 917 2 US-08-588-976-16 Sequence 16, Appl
989 6 1.1 918 2 US-08-588-983-14 Sequence 14, Appl
990 6 1.1 918 2 US-08-588-976-14 Sequence 14, Appl
991 6 1.1 923 2 US-09-252-991A-28964 Sequence 28964, A
992 6 1.1 924 2 US-08-588-983-18 Sequence 18, Appl
993 6 1.1 924 2 US-08-588-976-18 Sequence 18, Appl
994 6 1.1 936 4 US-09-252-991A-30190 Sequence 30190, A
995 6 1.1 954 4 US-09-255-829-14 Sequence 14, Appl
996 6 1.1 954 4 US-09-351-150A-17 Sequence 17, Appl
997 6 1.1 956 3 US-08-772-270A-8 Sequence 8, Appl
998 6 1.1 956 4 US-09-062-126-8 Sequence 8, Appl
999 6 1.1 966 1 US-08-571-758-2 Sequence 2, Appl
1000 6 1.1 966 1 US-08-909-984A-2 Sequence 2, Appl

```

ALIGNMENTS

```

RESULT 1
US-09-485-549-3
; Sequence 3, Application US/09485549
; Patent No. 6361948
; GENERAL INFORMATION:
; APPLICANT: James Tricoli
; APPLICANT: Rachel Rhondine11
; APPLICANT: Fox Chase Cancer Center
; TITLE OF INVENTION: Prognostic Compositions for Prostate Cancer and Methods of Use
; TITLE OF INVENTION: thereof
; FILE REFERENCE: PCCC 96-13
; CURRENT APPLICATION NUMBER: US/09/485,549
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: PCT/US98/16768
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: 60/055,285
; PRIOR FILING DATE: 1997-08-13
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 3
; LENGTH: 256
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-485-549-3

Query Match 1.5%; Score 8; DB 4; Length 256;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 379 GSLSEETP 386
Db 154 GSLSEETP 161

RESULT 2
US-09-485-549-2
; Sequence 2, Application US/09485549
; Patent No. 6361948
; GENERAL INFORMATION:
; APPLICANT: James Tricoli
; APPLICANT: Rachel Rhondine11
; APPLICANT: Fox Chase Cancer Center
; TITLE OF INVENTION: Prognostic Compositions for Prostate Cancer and Methods of Use
; TITLE OF INVENTION: thereof

```

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; FILE REFERENCE: PCCC 96-13
; CURRENT APPLICATION NUMBER: US/09/485,549
; CURRENT FILING DATE: 2000-11-09
; PRIOR APPLICATION NUMBER: PCT/US98/16768
; PRIOR FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: 60/055,285
; PRIOR FILING DATE: 1997-08-13
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 276
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-485-549-2

Query Match 1.5%; Score 8; DB 4; Length 276;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 379 GSLSEETP 386
Db 174 GSLSEETP 181

RESULT 3
US-09-073-569-2
; Sequence 2, Application US/09073569
; Patent No. 6084068
; GENERAL INFORMATION:
; APPLICANT: Sheppard, Paul O.
; APPLICANT: Grossmann, Angelika
; TITLE OF INVENTION: NOVEL TUMOR ANTIGENS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/073,569
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sawislak, Deborah A
; REGISTRATION NUMBER: 37,438
; REFERENCE/DOCKET NUMBER: 97-14
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6672
; TELEFAX: 206-442-6678
; TELEX:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 437 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FRAGMENT TYPE: internal
US-09-073-569-2

Query Match 1.5%; Score 8; DB 3; Length 437;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Oy 466 VLLALLLG 473
Db 4 VLLALLLG 11

RESULT 4
US-09-996-243-355
Sequence 355, Application US/0996243
Patent No. 6478825
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Auecin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Pan, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C13
CURRENT APPLICATION NUMBER: US/09/996,243
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
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PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-04
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PRIOR FILING DATE: 1998-06-10
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PRIOR FILING DATE: 1998-06-10
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PRIOR FILING DATE: 1998-06-10
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PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
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PRIOR FILING DATE: 1998-06-17
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PRIOR FILING DATE: 1998-06-17
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PRIOR FILING DATE: 1998-06-17
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PRIOR FILING DATE: 1998-06-17
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PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089801
PRIOR FILING DATE: 1998-06-18
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PRIOR FILING DATE: 1998-06-18
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PRIOR FILING DATE: 1998-06-19
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PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/089952
PRIOR FILING DATE: 1998-06-19
PRIOR APPLICATION NUMBER: 60/090246
PRIOR FILING DATE: 1998-06-22

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PRIOR APPLICATION NUMBER: 60/090252
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090254
PRIOR FILING DATE: 1998-06-22
PRIOR APPLICATION NUMBER: 60/090349
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090355
PRIOR FILING DATE: 1998-06-23
PRIOR APPLICATION NUMBER: 60/090429
PRIOR FILING DATE: 1998-06-24
PRIOR APPLICATION NUMBER: 60/090431
PRIOR FILING DATE: 1998-06-24
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PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

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Query Match      1.5%; Score 8; DB 4; Length 437;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      466 VLLALLG 473
      |||||
DB      4 VLLALLG 11

```

RESULT 5

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5486473-4
Patent No. 5486473
APPLICANT: FUKITA, HIROYUKI, YOSHIDA, IMAO, TAKAGI, MITSUO;
MANABE, SADAJO, FUKAI, KONOSUKE
TITLE OF INVENTION: A DNA CODING FOR A FLAVIVIRUS ANTIGEN
NUMBER OF SEQUENCES: 16
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/194,049
FILING DATE: 09-FEB-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 809,255
FILING DATE: 18-DEC-1991
APPLICATION NUMBER: 279,685
FILING DATE: 05-DEC-1988
APPLICATION NUMBER: 932,419
FILING DATE: 19-NOV-1986
SEQ ID NO: 4;
LENGTH: 497

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Query Match      1.5%; Score 8; DB 6; Length 497;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      461 LAVGVLL 468
      |||||
DB      482 LAVGVLL 489

```

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RESULT 6
US-09-252-991A-18990
Sequence 18990, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 18990
LENGTH: 689
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-18990

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Query Match      1.5%; Score 8; DB 4; Length 689;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY      2 GLVGVQL 9
      |||||
DB      587 GLVGVQL 594

```

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RESULT 7
US-08-332-562A-88
Sequence 88, Application US/08332562A
Patent No. 5985599
GENERAL INFORMATION:
APPLICANT: MCKENZIE, Ian F.C.
APPLICANT: HOGARTH, Mark P.
APPLICANT: HIBBS, Margaret L.
APPLICANT: SCOTT, Bernadette M.
APPLICANT: BONADONNA, Lisa
APPLICANT: HULETT, Mark D.
TITLE OF INVENTION: FC RECEPTOR FOR IMMUNOGLOBULIN
NUMBER OF SEQUENCES: 136

```

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Foley & Lardner
;; STREET: 3000 K Street, N.W., Suite 500
;; CITY: Washington
;; STATE: D.C.
;; COUNTRY: USA
;; ZIP: 20007-5109
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patentin Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/332,562A
;; FILING DATE: 31-OCT-1994
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/896,457
;; FILING DATE: 27-MAY-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: BENT, Stephen A.
;; REGISTRATION NUMBER: 29,768
;; REFERENCE/DOCKET NUMBER: 54270/119/GRHA
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 672-5300
;; TELEFAX: (202) 672-5339
;; TELEX: 904136
;; INFORMATION FOR SEQ ID NO: 88:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 87 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; US-08-332-562A-88

Query Match 1.3%; Score 7; DB 2; Length 87;
Best Local Similarity 100.0%; Pred. No. 49;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 379 GSLSEET 385
Db 42 GSLSEET 48

RESULT 8
US-09-205-258-1046
;; Sequence 1046, Application US/09205258
;; Patent No. 6525174
;; GENERAL INFORMATION:
;; APPLICANT: Young et al.
;; TITLE OF INVENTION: 207 Human Secreted Proteins
;; FILE REFERENCE: P2007P1
;; CURRENT APPLICATION NUMBER: US/09/205,258
;; CURRENT FILING DATE: 1998-12-04
;; EARLIER APPLICATION NUMBER: PCT/US98/11422
;; EARLIER FILING DATE: 1998-06-04
;; EARLIER APPLICATION NUMBER: 60/048,885
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/049,375
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,881
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,880
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,896
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/049,020
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,876
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,895
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,884

;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,894
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,971
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,964
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,882
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,899
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,893
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,900
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,901
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,892
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,915
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/049,019
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,970
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,972
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,916
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/049,373
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,875
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/049,374
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,917
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,949
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,974
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,883
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,897
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,898
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;; EARLIER APPLICATION NUMBER: 60/048,962
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,963
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,877
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/048,878
;; EARLIER FILING DATE: 1997-06-06
;; EARLIER APPLICATION NUMBER: 60/070,923
;; EARLIER FILING DATE: 1997-12-18
;; EARLIER APPLICATION NUMBER: 60/092,921
;; EARLIER FILING DATE: 1998-07-15
;; EARLIER APPLICATION NUMBER: 60/094,657
;; EARLIER FILING DATE: 1998-07-30
;; NUMBER OF SEQ ID NOS: 1237
;; SOFTWARE: Patentin Ver. 2.0
;; SEQ ID NO 1046
;; LENGTH: 100
;; TYPE: PRT
;; ORGANISM: Homo sapiens
US-09-205-258-1046

Query Match 1.3%; Score 7; DB 4; Length 100;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 LSAITSG 41
|||||
DB 48 LSAITSG 54

RESULT 9
US-09-904-615-163
; Sequence 163, Application US/09904615
; Patent No. 6566325
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 49 Human Secreted Proteins
; FILE REFERENCE: P2032P1
; CURRENT APPLICATION NUMBER: US/09/904,615
; CURRENT FILING DATE: 2001-07-16
; PRIOR APPLICATION NUMBER: 09/511,554
; PRIOR FILING DATE: 2000-02-23
; PRIOR APPLICATION NUMBER: 60/097,917
; PRIOR FILING DATE: 1998-08-25
; PRIOR APPLICATION NUMBER: 60/098,634
; PRIOR FILING DATE: 1998-08-31
; NUMBER OF SEQ ID NOS: 170
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO: 163
; LENGTH: 137
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-904-615-163

Query Match 1.3%; Score 7; DB 4; Length 137;
Best Local Similarity 100.0%; Pred. No. 74;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 467 LLLALIG 473
|||||
DB 23 LLLALIG 29

RESULT 10
US-09-252-991A-21858
; Sequence 21858, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO: 21858
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
; FEATURE:
; NAME/KEY: UNSURE
; LOCATION: (145), (146)
; OTHER INFORMATION: Identity of amino acid at the above locations are unknown.
US-09-252-991A-21858

Query Match 1.3%; Score 7; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 78;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 468 LLLALIG 474
|||||
DB 89 LLLALIG 95

RESULT 11
US-09-252-991A-31557
; Sequence 31557, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO: 31557
; LENGTH: 147
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31557

Query Match 1.3%; Score 7; DB 4; Length 147;
Best Local Similarity 100.0%; Pred. No. 79;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 469 LLLALIG 475
|||||
DB 93 LLLALIG 99

RESULT 12
US-08-756-387B-13
; Sequence 13, Application US/08756387B
; Patent No. 5945294
; GENERAL INFORMATION:
; APPLICANT: Frank, Glenn R.
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wasson, Donald L.
; TITLE OF INVENTION: Method to Detect IGE
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Carol Talkington Verser, Ph.D.
; ADDRESSEE: Heeka Corporation
; STREET: 1825 Sharp Point Drive
; CITY: Fort Collins
; STATE: Colorado
; COUNTRY: USA
; ZIP: 80525
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: Windows 95
; SOFTWARE: WordPerfect for Windows, Version 7.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/756,387B
; FILING DATE: No. 5945294ember 26, 1996
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Verser, Carol Talkington
; REGISTRATION NUMBER: 37,459
; REFERENCE/DOCKET NUMBER: DI-1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 970/493-7272
; TELEFAX: 970/484-9505
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 172 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-756-387B-13

Query Match 1.3%; Score 7; DB 2; Length 172;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 379 GSLSEET 385
Db 43 GSLSEET 49

RESULT 13

US-09-285-873-13
Sequence 13, Application US/09285873
Patent No. 6309832
GENERAL INFORMATION:
APPLICANT: Frank, Glenn R.
APPLICANT: Porter, James P.
APPLICANT: Rushlow, Keith E.
APPLICANT: Wassom, Donald L.
TITLE OF INVENTION: Method to Detect IGE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heeka Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: WordPerfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/285,873
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/756,387
FILING DATE: No. 6309832ember 26, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: DI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 172 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein

US-09-285-873-13
Query Match 1.3%; Score 7; DB 4; Length 172;
Best Local Similarity 100.0%; Pred. No. 90;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 379 GSLSEET 385
Db 43 GSLSEET 49

RESULT 14
US-09-252-991A-26925
Sequence 26925, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS

FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 26925
LENGTH: 176
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-26925

Query Match 1.3%; Score 7; DB 4; Length 176;
Best Local Similarity 100.0%; Pred. No. 92;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 460 GLAVGV 466
Db 57 GLAVGV 63

RESULT 15
US-08-469-260A-52
Sequence 52, Application US/08469260A
Patent No. 6451578
GENERAL INFORMATION:
APPLICANT: JOHN N. SIMONS
APPLICANT: TAMI J. PILOT-MATIAS
APPLICANT: GEORGE J. DAMSON
APPLICANT: GEORGE G. SCHLAUDER
APPLICANT: SURESH M. DESAI
APPLICANT: THOMAS P. LEARY
APPLICANT: ANTHONY SCOTT MUEHROFF
APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUIJK
APPLICANT: ISA K. MUSHAWAR

TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
ADDRESSEE: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,260A
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 177 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear

MOLECULE TYPE: protein
US-08-469-260A-52

Query Match 1.3%; Score 7; DB 4; Length 177;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 461 LAVGVVL 467
| | | | |
DB 30 LAVGVVL 36

RESULT 16
US-08-488-446-52

Sequence 52, Application US/08488446
Patent No. 6558898

GENERAL INFORMATION:
APPLICANT: JOHN N. SIMONS
APPLICANT: TAMU J. PILOT-MATIAS
APPLICANT: GEORGE J. DAMSON
APPLICANT: GEORGE G. SCHLAUDER
APPLICANT: SURESH M. DESAI
APPLICANT: THOMAS P. LEARY
APPLICANT: ANTHONY SCOTT MUEHROFF
APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUTIK
APPLICANT: ISA K. MUSHAMMAR
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
ADDRESSER: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,446
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/424,550
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 177 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein

US-08-488-446-52

Query Match 1.3%; Score 7; DB 4; Length 177;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 461 LAVGVVL 467
| | | | |
DB 30 LAVGVVL 36

RESULT 17
US-08-467-344A-52

Sequence 52, Application US/08467344A
Patent No. 6586568

GENERAL INFORMATION:
APPLICANT: JOHN N. SIMONS
APPLICANT: TAMU J. PILOT-MATIAS
APPLICANT: GEORGE J. DAMSON
APPLICANT: GEORGE G. SCHLAUDER
APPLICANT: SURESH M. DESAI
APPLICANT: THOMAS P. LEARY
APPLICANT: ANTHONY SCOTT MUEHROFF
APPLICANT: JAMES C. ERKER
APPLICANT: SHERI L. BUTIK
APPLICANT: ISA K. MUSHAMMAR
TITLE OF INVENTION: NON-A, NON-B, NON-C, NON-D, NON-E HEPATITIS
TITLE OF INVENTION: REAGENTS AND METHODS FOR THEIR USE
NUMBER OF SEQUENCES: 716
CORRESPONDENCE ADDRESS:
ADDRESSER: ABBOTT LABORATORIES D377/AP6D
STREET: 100 ABBOTT PARK ROAD
CITY: ABBOTT PARK
STATE: IL
COUNTRY: USA
ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/467,344A
FILING DATE: 07-Jun-1995
CLASSIFICATION: <unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/424,550
FILING DATE: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: FOREMSKI, PRISCILLA E.
REGISTRATION NUMBER: 33,207
REFERENCE/DOCKET NUMBER: 5527.PC.01
TELECOMMUNICATION INFORMATION:
TELEPHONE: 708-937-6365
TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO: 52:
SEQUENCE CHARACTERISTICS:
LENGTH: 177 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 52:

US-08-467-344A-52

Query Match 1.3%; Score 7; DB 4; Length 177;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 461 LAVGVVL 467
| | | | |
DB 30 LAVGVVL 36

RESULT 18

US-09-252-991A-30129
Sequence 30129, Application US/09252991A
Patent No. 6551795

GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.136

;; CURRENT APPLICATION NUMBER: US/09/252,991A
;; CURRENT FILING DATE: 1999-02-18
;; PRIOR APPLICATION NUMBER: US 60/074,788
;; PRIOR FILING DATE: 1998-02-18
;; PRIOR APPLICATION NUMBER: US 60/094,130
;; PRIOR FILING DATE: 1998-07-27
;; NUMBER OF SEQ ID NOS: 33142
;; SEQ ID NO 30129
;; LENGTH: 191
;; TYPE: PRT
;; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-30129

Query Match 1.3%; Score 7; DB 4; Length 191;
Best Local Similarity 100.0%; Pred. No. 99;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 466 VLLALL 472
DB 53 VLLALL 59

RESULT 19
US-08-765-536-1
; Sequence 1, Application US/08765536
; Patent No. 5962634
; GENERAL INFORMATION:
; APPLICANT: Jameson, Bradford A.
; APPLICANT: Sutton, Brian J. M.
; APPLICANT: McDonnell, James M.
; APPLICANT: Gould, Hannah J.
; APPLICANT: Korgold, Robert
; APPLICANT: Beavill, Andrew J.
; TITLE OF INVENTION: Ige Antagonists
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz & No. 5962634rls
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/765,536
; FILING DATE: April 30, 1997
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/271,943
; FILING DATE: 08-JUL-1994
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1619
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3439
; TELEFAX: 215-568-3100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-765-536-1

Query Match 1.3%; Score 7; DB 2; Length 193;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 379 GSLSEET 385
DB 63 GSLSEET 69

RESULT 20
PCT-US95-08401-1
; Sequence 1, Application PC/TUS9508401
; GENERAL INFORMATION:
; APPLICANT: Jameson, Bradford A.
; APPLICANT: Sutton, Brian J. M.
; APPLICANT: McDonnell, James M.
; APPLICANT: Gould, Hannah J.
; APPLICANT: Korgold, Robert
; APPLICANT: Beavill, Andrew J.
; TITLE OF INVENTION: Ige Antagonists
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
; ADDRESSEE: Norris
; STREET: One Liberty Place, 46th Floor
; CITY: Philadelphia
; STATE: PA
; COUNTRY: USA
; ZIP: 19103
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Wordperfect
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08401
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/271,943
; FILING DATE: 08-JUL-1994
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Deluca, Mark
; REGISTRATION NUMBER: 33,229
; REFERENCE/DOCKET NUMBER: TJU-1597
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 215-568-3439
; TELEFAX: 215-568-3100
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 193 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-08401-1

Query Match 1.3%; Score 7; DB 5; Length 193;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 379 GSLSEET 385
DB 63 GSLSEET 69

RESULT 21
US-08-756-387B-11
; Sequence 11, Application US/08756387B
; Patent No. 5945294
; GENERAL INFORMATION:
; APPLICANT: Porter, James P.
; APPLICANT: Rushlow, Keith E.
; APPLICANT: Wassom, Donald L.
; TITLE OF INVENTION: Method to Detect Ige

NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heeka Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordperfect for Windows, Version 7.0
CURRENT APPLICATION DATA: US/08/756,387B
APPLICATION NUMBER: US/08/756,387B
FILING DATE: No. 5945294ember 26, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: DI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 197 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-756-387B-11

Query Match 1.3%; Score 7; DB 2; Length 197;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 379 GSISET 385
DB 68 GSISET 74

RESULT 22
US-08-788-954-2
Sequence 2, Application US/08788954
Patent No. 6090384
GENERAL INFORMATION:
APPLICANT: RA, CHISEI
APPLICANT: NAITO, KOJI
APPLICANT: HIRAMA, MINORU
APPLICANT: OKUMURA, KO
TITLE OF INVENTION: ANTIALLERGIC COMPOSITION
NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK, & SEAS
STREET: 2100 PENNSYLVANIA AVE., N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: U.S.A
ZIP: 20037
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/788,954
FILING DATE: 24-JAN-1997
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/474,168
FILING DATE:
APPLICATION NUMBER: US 08/023,912

FILING DATE: 26-FEB-1993
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
TELEFAX: (202)293-7660
TELEX: 6491103
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 197 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-788-954-2

Query Match 1.3%; Score 7; DB 3; Length 197;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 379 GSISET 385
DB 68 GSISET 74

RESULT 23
US-09-285-873-11
Sequence 11, Application US/09285873
Patent No. 6309832
GENERAL INFORMATION:
APPLICANT: Frank, Glenn R.
APPLICANT: Porter, James P.
APPLICANT: Rushlow, Keith E.
APPLICANT: Massom, Donald L.
TITLE OF INVENTION: Method to Detect IGE
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
ADDRESSEE: Heeka Corporation
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordperfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/285,873
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/756,387
FILING DATE: No. 6309832ember 26, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: DI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 197 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-285-873-11

Query Match 1.3%; Score 7; DB 4; Length 197;
Best Local Similarity 100.0%; Pred. No. 1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 379 GSISET 385

Db 68 GSLSEET 74

RESULT 24

US-09-252-991A-18239
 ; Sequence 18239, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfeld et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 18239
 ; LENGTH: 205
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-18239

Query Match 1.3%; Score 7; DB 4; Length 205;

Best Local Similarity 100.0%; Pred. No. 1.1e+02; Mismatches 0; Indels 0; Gaps 0;

QY 20 ASGLSSS 26
 Db 84 ASGLSSS 90

RESULT 25

US-09-252-991A-32491
 ; Sequence 32491, Application US/09252991A
 ; Patent No. 6551795
 ; GENERAL INFORMATION:
 ; APPLICANT: Marc J. Rubenfeld et al.
 ; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
 ; FILE REFERENCE: 107196.136
 ; CURRENT APPLICATION NUMBER: US/09/252,991A
 ; CURRENT FILING DATE: 1999-02-18
 ; PRIOR APPLICATION NUMBER: US 60/074,788
 ; PRIOR FILING DATE: 1998-02-18
 ; PRIOR APPLICATION NUMBER: US 60/094,190
 ; PRIOR FILING DATE: 1998-07-27
 ; NUMBER OF SEQ ID NOS: 33142
 ; SEQ ID NO 32491
 ; LENGTH: 212
 ; TYPE: PRT
 ; ORGANISM: Pseudomonas aeruginosa
 US-09-252-991A-32491

Query Match 1.3%; Score 7; DB 4; Length 212;

Best Local Similarity 100.0%; Pred. No. 1.1e+02; Mismatches 0; Indels 0; Gaps 0;

QY 370 SAAVSYT 376
 Db 101 SAAVSYT 107

RESULT 26

US-08-107-684B-9
 ; Sequence 9, Application US/08107684B
 ; Patent No. 5552273
 ; GENERAL INFORMATION:
 ; APPLICANT: CLEUZAT, Philippe L.
 ; APPLICANT: AMADE, Abalo

APPLICANT: ROBERT-BAUDOUY, Jeanine

APPLICANT: GAYRAL, Jean-Pierre

TITLE OF INVENTION: POLYPEPTIDES CONTAINING SEQUENCES

TITLE OF INVENTION: CHARACTERISTIC OF PYRROLIDONE CARBOXYLYL PEPTIDASES.

TITLE OF INVENTION: POLYNUCLEOTIDES CONTAINING A SEQUENCE CODING FOR SUCH

TITLE OF INVENTION: POLYPEPTIDES, AND THEIR USE, IN PARTICULAR FOR DIAGNOSTIC

NUMBER OF SEQUENCES: 43

CORRESPONDENCE ADDRESS:

ADDRESSEE: OLIEF & BERRIDGE

STREET: P. O. Box 19928

CITY: Alexandria

STATE: VA

COUNTRY: USA

ZIP: 22320

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/107,684B

FILING DATE: 17-AUG-1993

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Berridge, William P.

REGISTRATION NUMBER: 30,024

REFERENCE/DOCKET NUMBER: WPB 26478

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 836-6400

TELEFAX: (703) 836-2787

INFORMATION FOR SEQ ID NO: 9:

SEQUENCE CHARACTERISTICS:

LENGTH: 215 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: peptide

US-08-107-684B-9

Query Match 1.3%; Score 7; DB 1; Length 215;

Best Local Similarity 100.0%; Pred. No. 1.1e+02; Mismatches 0; Indels 0; Gaps 0;

QY 371 AAVSYTA 377
 Db 133 AAVSYTA 139

RESULT 27

US-08-107-684B-13
 ; Sequence 13, Application US/08107684B
 ; Patent No. 5552273
 ; GENERAL INFORMATION:
 ; APPLICANT: CLEUZAT, Philippe L.
 ; APPLICANT: AMADE, Abalo
 ; APPLICANT: ROBERT-BAUDOUY, Jeanine
 ; APPLICANT: GAYRAL, Jean-Pierre
 ; TITLE OF INVENTION: POLYPEPTIDES CONTAINING SEQUENCES
 ; TITLE OF INVENTION: CHARACTERISTIC OF PYRROLIDONE CARBOXYLYL PEPTIDASES.
 ; TITLE OF INVENTION: POLYNUCLEOTIDES CONTAINING A SEQUENCE CODING FOR SUCH
 ; TITLE OF INVENTION: POLYPEPTIDES, AND THEIR USE, IN PARTICULAR FOR DIAGNOSTIC
 ; NUMBER OF SEQUENCES: 43
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: OLIEF & BERRIDGE
 ; STREET: P. O. Box 19928
 ; CITY: Alexandria
 ; STATE: VA
 ; COUNTRY: USA
 ; ZIP: 22320
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25

```

; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/107,684B
; FILING DATE: 17-AUG-1993
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Beridge, William P.
; REGISTRATION NUMBER: 30,024
; REFERENCE/DOCKET NUMBER: WPP 28478
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 836-6400
; TELEFAX: (703) 836-2787
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 215 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-107-684B-13

Query Match      1.3%; Score 7; DB 1; Length 215;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      371 AAVSYTA 377
DB      133 AAVSYTA 139

RESULT 28
US-09-205-258-1044
; Sequence 1044, Application US/09205258
; Patent No. 6525174
; GENERAL INFORMATION:
; APPLICANT: Young et al.
; TITLE OF INVENTION: 207 Human Secreted Proteins
; FILE REFERENCE: P2007P1
; CURRENT APPLICATION NUMBER: US/09/205,258
; CURRENT FILING DATE: 1998-12-04
; EARLIER APPLICATION NUMBER: PCT/US98/11422
; EARLIER FILING DATE: 1998-06-04
; EARLIER APPLICATION NUMBER: 60/048,885
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,375
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,881
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,880
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,896
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,020
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,876
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,895
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,884
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,894
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,971
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,882
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,899
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,893
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,900
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,901
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; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,892
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,915
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,019
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,970
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,972
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,916
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,373
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,875
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/049,374
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,917
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,949
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,974
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,883
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,897
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,898
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,962
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,963
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,877
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/048,878
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/070,923
; EARLIER FILING DATE: 1997-12-18
; EARLIER APPLICATION NUMBER: 60/092,921
; EARLIER FILING DATE: 1998-07-15
; EARLIER APPLICATION NUMBER: 60/094,657
; EARLIER FILING DATE: 1998-07-30
; NUMBER OF SEQ ID NOS: 1227
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 1044
; LENGTH: 216
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-205-258-1044

Query Match      1.3%; Score 7; DB 4; Length 216;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      35 LSASTSG 41
DB      96 LSASTSG 102

RESULT 29
US-09-252-991A-23837
; Sequence 23837, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
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PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 23837
LENGTH: 228
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-23837

Query Match 1.3%; Score 7; DB 4; Length 228;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 465 GVLALL 471
Db 213 GVLALL 219

RESULT 30
US-07-869-933-13
Sequence 13, Application US/07869933
Patent No. 5770396
GENERAL INFORMATION:
APPLICANT: KINET, Jean-Pierre
TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF
TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/869,933
FILING DATE: 19920416
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/154 NTHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
ORIGINAL SOURCE:
ORGANISM: homo sapien
STRAIN: FCRI alpha subunit
US-07-869-933-13

Query Match 1.3%; Score 7; DB 1; Length 232;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 379 GSLSEET 385
Db 43 GSLSEET 49

RESULT 31
US-08-756-387B-6
Sequence 6, Application US/08756387B
Patent No. 5945294
GENERAL INFORMATION:
APPLICANT: Frank, Glenn R.
APPLICANT: Porter, James P.
APPLICANT: Rushlow, Keith E.
APPLICANT: Wasson, Donald L.
TITLE OF INVENTION: Method to Detect Ige
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordperfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/756,387B
FILING DATE: No. 5945294ember 26, 1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: DI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-756-387B-6

Query Match 1.3%; Score 7; DB 2; Length 232;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 379 GSLSEET 385
Db 43 GSLSEET 49

RESULT 32
US-09-103-663-13
Sequence 13, Application US/09103663D
Patent No. 6171803
GENERAL INFORMATION:
APPLICANT: Kinet et al.
TITLE OF INVENTION: Isolation, characterization, and use of the human beta
TITLE OF INVENTION: subunit of the high affinity receptor for
TITLE OF INVENTION: immunoglobulin E.
FILE REFERENCE: 50490
CURRENT APPLICATION NUMBER: US/09/103,663D
CURRENT FILING DATE: 1998-06-23
EARLIER APPLICATION NUMBER: 07/869,933
EARLIER FILING DATE: 1992-04-16
NUMBER OF SEQ ID NOS: 35
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
LENGTH: 232
TYPE: PRT
ORGANISM: Homo sapiens

US-09-103-663-13

Query Match 1.3%; Score 7; DB 3; Length 232;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 379 GSLSEET 385
DB 43 GSLSEET 49

RESULT 33

US-09-285-873-6
Sequence 6, Application US/09285873
Patent No. 6309832
GENERAL INFORMATION:
APPLICANT: Frank, Glenn R.
APPLICANT: Porter, James P.
APPLICANT: Rushlow, Keith E.
APPLICANT: Masson, Donald L.
TITLE OF INVENTION: Method to Detect Igs
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: Carol Talkington Verser, Ph.D.
STREET: 1825 Sharp Point Drive
CITY: Fort Collins
STATE: Colorado
COUNTRY: USA
ZIP: 80525
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: Windows 95
SOFTWARE: Wordperfect for Windows, Version 7.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/285,873
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/756,387
FILING DATE: No. 6309832ember 26, 1996
ATTORNEY/AGENT INFORMATION:
NAME: Verser, Carol Talkington
REGISTRATION NUMBER: 37,459
REFERENCE/DOCKET NUMBER: DI-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 970/493-7272
TELEFAX: 970/484-9505
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 232 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-285-873-6

Query Match 1.3%; Score 7; DB 4; Length 232;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 379 GSLSEET 385
DB 43 GSLSEET 49

RESULT 34

US-09-364-230-10
Sequence 10, Application US/09364230
Patent No. 6348339
GENERAL INFORMATION:
APPLICANT: Cahoon, Rebecca E.
APPLICANT: Hltz, William D.

APPLICANT: Kinney, Anthony J.
APPLICANT: Rafalski, J. Antoni
TITLE OF INVENTION: Enzymes Involved in Degradation of Branched-Chain Amino Acids
FILE REFERENCE: BB-1178
CURRENT APPLICATION NUMBER: US/09/364,230
CURRENT FILING DATE: 1999-07-29
EARLIER APPLICATION NUMBER: 60/094,990
EARLIER FILING DATE: July 31, 1998
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Microsoft Office 97
SEQ ID NO 10
LENGTH: 234
TYPE: PRT
ORGANISM: Glycine max
US-09-364-230-10

Query Match 1.3%; Score 7; DB 4; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.2e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 314 YPLTQA 320
DB 194 YPLTQA 200

RESULT 35

US-07-869-933-11
Sequence 11, Application US/07869933
Patent No. 5770396
GENERAL INFORMATION:
APPLICANT: KINET, Jean-Pierre
TITLE OF INVENTION: ISOLATION, CHARACTERIZATION, AND USE OF
TITLE OF INVENTION: THE HUMAN B SUBUNIT OF THE HIGH AFFINITY RECEPTOR FOR
NUMBER OF SEQUENCES: 34
CORRESPONDENCE ADDRESS:
ADDRESSEE: Foley & Lardner
STREET: 1800 Diagonal Road, Suite 500
CITY: Alexandria
STATE: VA
COUNTRY: USA
ZIP: 22313-0299
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/869,933
FILING DATE: 19920416
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 40399/154 NIND
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703)836-9300
TELEFAX: (703)683-4109
TELEX: 899149
INFORMATION FOR SEQ ID NO: 11:
SEQUENCE CHARACTERISTICS:
LENGTH: 257 amino acids
TYPE: AMINO ACID
TOPOLOGY: linear
MOLECULE TYPE: protein
US-07-869-933-11

Query Match 1.3%; Score 7; DB 1; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 379 GSLSEET 385
DB 43 GSLSEET 49

Db 68 GSLSEET 74

RESULT 36

US-08-756-387B-2
; Sequence 2, Application US/08756387B

; Patent No. 5945294

; GENERAL INFORMATION:

; APPLICANT: Frank, Glenn R.

; APPLICANT: Porter, James P.

; APPLICANT: Rushlow, Keith E.

; APPLICANT: Wassom, Donald L.

; TITLE OF INVENTION: Method to Detect IGE

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Carol Talkington Verser, Ph.D.

; STREET: 1825 Sharp Point Drive

; CITY: Fort Collins

; STATE: Colorado

; COUNTRY: USA

; ZIP: 80525

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Windows 95

; SOFTWARE: WordPerfect for Windows, Version 7.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/756,387B

; FILING DATE: No. 5945294ember 26, 1996

; CLASSIFICATION: 435

; ATTORNEY/AGENT INFORMATION:

; NAME: Verser, Carol Talkington

; REGISTRATION NUMBER: 37,459

; REFERENCE/DOCKET NUMBER: DI-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 970/493-7272

; TELEFAX: 970/484-9505

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 257 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-756-387B-2

Query Match 1.3%; Score 7; DB 2; Length 257;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 379 GSLSEET 385

Db 68 GSLSEET 74

RESULT 37

US-09-103-663-11

; Sequence 11, Application US/09103663D

; Patent No. 6171803

; GENERAL INFORMATION:

; APPLICANT: Kinet et al.

; TITLE OF INVENTION: Isolation, characterization, and use of the human beta

; TITLE OF INVENTION: subunit of the high affinity receptor for

; TITLE OF INVENTION: immunoglobulin E.

; FILE REFERENCE: 50490

; CURRENT APPLICATION NUMBER: US/09/103,663D

; CURRENT FILING DATE: 1998-06-23

; EARLIER APPLICATION NUMBER: 07/869,933

; EARLIER FILING DATE: 1992-04-16

; NUMBER OF SEQ ID NOS: 35

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 11

; LENGTH: 257

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-103-663-11

Query Match 1.3%; Score 7; DB 3; Length 257;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 379 GSLSEET 385

Db 68 GSLSEET 74

RESULT 38

US-09-285-873-2

; Sequence 2, Application US/09285873

; Patent No. 6309832

; GENERAL INFORMATION:

; APPLICANT: Frank, Glenn R.

; APPLICANT: Porter, James P.

; APPLICANT: Rushlow, Keith E.

; APPLICANT: Wassom, Donald L.

; TITLE OF INVENTION: Method to Detect IGE

; NUMBER OF SEQUENCES: 13

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Carol Talkington Verser, Ph.D.

; STREET: 1825 Sharp Point Drive

; CITY: Fort Collins

; STATE: Colorado

; COUNTRY: USA

; ZIP: 80525

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: Windows 95

; SOFTWARE: WordPerfect for Windows, Version 7.0

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/285,873

; FILING DATE:

; CLASSIFICATION:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US/08/756,387

; FILING DATE: No. 6309832ember 26, 1996

; ATTORNEY/AGENT INFORMATION:

; NAME: Verser, Carol Talkington

; REGISTRATION NUMBER: 37,459

; REFERENCE/DOCKET NUMBER: DI-1

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 970/493-7272

; TELEFAX: 970/484-9505

; INFORMATION FOR SEQ ID NO: 2:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 257 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-09-285-873-2

Query Match 1.3%; Score 7; DB 4; Length 257;

Best Local Similarity 100.0%; Pred. No. 1.3e+02;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 379 GSLSEET 385

Db 68 GSLSEET 74

RESULT 39

US-08-897-956A-1

; Sequence 1, Application US/08897956A

; Patent No. 6423512

; GENERAL INFORMATION:

APPLICANT: Mary Ellen Digan
APPLICANT: Philip Lake
APPLICANT: Hermann Gram
TITLE OF INVENTION: Fusion Polypeptides
FILE REFERENCE: 600-7244/CPA
CURRENT APPLICATION NUMBER: US/08/897,956A
CURRENT FILING DATE: 1997-07-21
PRIOR APPLICATION NUMBER: 60/022,689
PRIOR FILING DATE: 1996-07-26
NUMBER OF SEQ ID NOS: 38
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO: 1
LENGTH: 257
TYPE: PRT
ORGANISM: Homo Sapiens
US-08-897-956A-1

Query Match 1.3%: Score 7; DB 4; Length 257;
Best Local Similarity 100.0%; Pred. No. 1.3e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 379 GSI:SEET 385
DB 68 GSI:SEET 74

RESULT 40
US-09-252-991A-17952
Sequence 17952, Application US/09252991A
Patent No. 6551795
GENERAL INFORMATION:
APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
NUMBER OF SEQ ID NOS: 33142
SEQ ID NO 17952
LENGTH: 302
TYPE: PRT
ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-17952

Query Match 1.3%: Score 7; DB 4; Length 302;
Best Local Similarity 100.0%; Pred. No. 1.5e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 124 GNP:PGG 130
DB 242 GNP:PGG 248

Search completed: October 2, 2003, 16:06:59
Job time: 43 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: October 2, 2003, 16:06:00 ; Search time 68 Seconds
(without alignments)
1258.724 Million cell updates/sec

Title: US-10-039-770A-1

Perfect score: 541
Sequence: 1 MGVLGVQLVLVLVADCTIFA.....EAEENIQDGETHWVEGDY 541

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 587654 seqs, 158212981 residues

Word size : 0

Total number of hits satisfying chosen parameters: 587654

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 1000 summaries

Database :

Published Applications_AA:*

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- 2: /cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep:*
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- 5: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubppaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubppaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubppaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubppaa/US10C_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9	1.7	218	US-10-156-761-10882	Sequence 10882, A
2	9	1.7	280	US-10-156-424A-13	Sequence 13, App1
3	8	1.5	106	US-09-950-933A-70	Sequence 70, App1
4	8	1.5	200	US-10-080-170-438	Sequence 438, App
5	8	1.5	238	US-10-102-806-499	Sequence 499, App
6	8	1.5	255	US-10-106-698-5043	Sequence 5043, App
7	8	1.5	437	US-09-989-723-355	Sequence 355, App
8	8	1.5	437	US-09-989-723-355	Sequence 355, App
9	8	1.5	437	US-09-989-727-355	Sequence 355, App
10	8	1.5	437	US-09-989-731-355	Sequence 355, App
11	8	1.5	437	US-09-989-732-355	Sequence 355, App
12	8	1.5	437	US-09-991-073-355	Sequence 355, App
13	8	1.5	437	US-09-990-442-355	Sequence 355, App
14	8	1.5	437	US-09-991-163-355	Sequence 355, App
15	8	1.5	437	US-09-991-163-355	Sequence 355, App

16	8	1.5	437	US-09-993-604-355	Sequence 355, App
17	8	1.5	437	US-09-990-456-355	Sequence 355, App
18	8	1.5	437	US-09-989-721-355	Sequence 355, App
19	8	1.5	437	US-09-992-598-355	Sequence 355, App
20	8	1.5	437	US-09-989-292A-355	Sequence 355, App
21	8	1.5	437	US-09-989-735-355	Sequence 355, App
22	8	1.5	437	US-09-990-444-355	Sequence 355, App
23	8	1.5	437	US-09-991-181-355	Sequence 355, App
24	8	1.5	437	US-09-989-730-355	Sequence 355, App
25	8	1.5	437	US-09-990-436-355	Sequence 355, App
26	8	1.5	437	US-09-993-687-355	Sequence 355, App
27	8	1.5	437	US-09-989-734-355	Sequence 355, App
28	8	1.5	437	US-09-997-653-355	Sequence 355, App
29	8	1.5	437	US-09-993-667-355	Sequence 355, App
30	8	1.5	437	US-09-997-428-355	Sequence 355, App
31	8	1.5	437	US-09-997-666-355	Sequence 355, App
32	8	1.5	437	US-09-990-438-355	Sequence 355, App
33	8	1.5	437	US-09-990-562-355	Sequence 355, App
34	8	1.5	437	US-09-990-711-355	Sequence 355, App
35	8	1.5	437	US-09-989-726-355	Sequence 355, App
36	8	1.5	437	US-09-998-156-355	Sequence 355, App
37	8	1.5	437	US-09-990-437-355	Sequence 355, App
38	8	1.5	437	US-09-991-157-355	Sequence 355, App
39	8	1.5	437	US-09-997-514-355	Sequence 355, App
40	8	1.5	437	US-09-997-573-355	Sequence 355, App
41	8	1.5	437	US-09-991-172-355	Sequence 355, App
42	8	1.5	437	US-09-990-726-355	Sequence 355, App
43	8	1.5	437	US-09-997-559-355	Sequence 355, App
44	8	1.5	437	US-09-997-601-355	Sequence 355, App
45	8	1.5	437	US-09-990-443-355	Sequence 355, App
46	8	1.5	437	US-09-991-854-355	Sequence 355, App
47	8	1.5	437	US-09-997-628-355	Sequence 355, App
48	8	1.5	437	US-09-997-683-355	Sequence 355, App
49	8	1.5	437	US-09-989-728A-355	Sequence 355, App
50	8	1.5	437	US-09-997-349-355	Sequence 355, App
51	8	1.5	437	US-09-997-440-355	Sequence 355, App
52	8	1.5	437	US-09-990-440-355	Sequence 355, App
53	8	1.5	437	US-09-993-469-355	Sequence 355, App
54	8	1.5	437	US-09-997-542-355	Sequence 355, App
55	8	1.5	437	US-09-993-748-355	Sequence 355, App
56	8	1.5	437	US-09-990-429-355	Sequence 355, App
57	8	1.5	437	US-09-990-427-355	Sequence 355, App
58	8	1.5	437	US-09-990-427-355	Sequence 355, App
59	8	1.5	437	US-09-989-328-355	Sequence 355, App
60	8	1.5	437	US-09-993-583-355	Sequence 355, App
61	8	1.5	437	US-09-991-992-355	Sequence 355, App
62	8	1.5	437	US-09-997-531-355	Sequence 355, App
63	8	1.5	437	US-09-997-384-355	Sequence 355, App
64	8	1.5	437	US-09-998-041-355	Sequence 355, App
65	8	1.5	437	US-09-997-585-355	Sequence 355, App
66	8	1.5	437	US-09-997-614-355	Sequence 355, App
67	8	1.5	437	US-09-989-862-355	Sequence 355, App
68	8	1.5	437	US-09-989-725-355	Sequence 355, App
69	8	1.5	437	US-09-997-529-355	Sequence 355, App
70	8	1.5	437	US-10-137-870-466	Sequence 466, App
71	8	1.5	437	US-10-140-018-466	Sequence 466, App
72	8	1.5	437	US-10-140-021-466	Sequence 466, App
73	8	1.5	437	US-10-140-274-466	Sequence 466, App
74	8	1.5	437	US-10-140-471-466	Sequence 466, App
75	8	1.5	437	US-10-140-807-466	Sequence 466, App
76	8	1.5	437	US-10-140-922-466	Sequence 466, App
77	8	1.5	437	US-10-140-924-466	Sequence 466, App
78	8	1.5	437	US-10-140-924-466	Sequence 466, App
79	8	1.5	437	US-10-141-698-466	Sequence 466, App
80	8	1.5	437	US-10-141-702-466	Sequence 466, App
81	8	1.5	437	US-10-141-704-466	Sequence 466, App
82	8	1.5	437	US-10-142-421-466	Sequence 466, App
83	8	1.5	437	US-10-142-432-466	Sequence 466, App
84	8	1.5	437	US-10-142-767-466	Sequence 466, App
85	8	1.5	437	US-10-143-093-466	Sequence 466, App
86	8	1.5	437	US-10-144-994-466	Sequence 466, App
87	8	1.5	437	US-10-145-628-466	Sequence 466, App
88	8	1.5	437	US-10-145-631-466	Sequence 466, App

89	8	1.5	437	12	US-10-145-633-466	Sequence 466, App	162	8	1.5	437	12	US-10-145-751-466	Sequence 466, App
90	8	1.5	437	12	US-10-145-746-466	Sequence 466, App	163	8	1.5	437	12	US-10-145-821-466	Sequence 466, App
91	8	1.5	437	12	US-10-145-748-466	Sequence 466, App	164	8	1.5	437	12	US-10-145-824-466	Sequence 466, App
92	8	1.5	437	12	US-10-145-823-466	Sequence 466, App	165	8	1.5	437	12	US-10-145-827-466	Sequence 466, App
93	8	1.5	437	12	US-10-145-826-466	Sequence 466, App	166	8	1.5	437	12	US-10-145-861-466	Sequence 466, App
94	8	1.5	437	12	US-10-145-870-466	Sequence 466, App	167	8	1.5	437	12	US-10-145-875-466	Sequence 466, App
95	8	1.5	437	12	US-10-145-876-466	Sequence 466, App	168	8	1.5	437	12	US-10-145-877-466	Sequence 466, App
96	8	1.5	437	12	US-10-145-959-466	Sequence 466, App	169	8	1.5	437	12	US-10-145-959-466	Sequence 466, App
97	8	1.5	437	12	US-10-146-724-466	Sequence 466, App	170	8	1.5	437	12	US-10-146-781-466	Sequence 466, App
98	8	1.5	437	12	US-10-146-725-466	Sequence 466, App	171	8	1.5	437	12	US-10-146-790-466	Sequence 466, App
99	8	1.5	437	12	US-10-146-795-466	Sequence 466, App	172	8	1.5	437	12	US-10-146-793-466	Sequence 466, App
100	8	1.5	437	12	US-10-147-495-466	Sequence 466, App	173	8	1.5	437	12	US-10-147-498-466	Sequence 466, App
101	8	1.5	437	12	US-10-147-501-466	Sequence 466, App	174	8	1.5	437	12	US-10-147-488-466	Sequence 466, App
102	8	1.5	437	12	US-10-147-504-466	Sequence 466, App	175	8	1.5	437	12	US-10-147-487-466	Sequence 466, App
103	8	1.5	437	12	US-10-147-506-466	Sequence 466, App	176	8	1.5	437	12	US-10-147-490-466	Sequence 466, App
104	8	1.5	437	12	US-10-147-509-466	Sequence 466, App	177	8	1.5	437	12	US-10-147-494-466	Sequence 466, App
105	8	1.5	437	12	US-10-147-510-466	Sequence 466, App	178	8	1.5	437	12	US-10-147-499-466	Sequence 466, App
106	8	1.5	437	12	US-10-147-511-466	Sequence 466, App	179	8	1.5	437	12	US-10-147-514-466	Sequence 466, App
107	8	1.5	437	12	US-10-147-529-466	Sequence 466, App	180	8	1.5	437	12	US-10-147-524-466	Sequence 466, App
108	8	1.5	437	12	US-10-152-397-466	Sequence 466, App	181	8	1.5	437	12	US-10-152-379-466	Sequence 466, App
109	8	1.5	437	12	US-10-153-586-466	Sequence 466, App	182	8	1.5	437	12	US-10-152-394-466	Sequence 466, App
110	8	1.5	437	12	US-10-158-783-466	Sequence 466, App	183	8	1.5	437	12	US-10-152-394-466	Sequence 466, App
111	8	1.5	437	12	US-10-158-786-466	Sequence 466, App	184	8	1.5	437	12	US-10-152-408-466	Sequence 466, App
112	8	1.5	437	12	US-10-140-019-466	Sequence 466, App	185	8	1.5	437	12	US-10-156-847-466	Sequence 466, App
113	8	1.5	437	12	US-10-140-022-466	Sequence 466, App	186	8	1.5	437	12	US-10-157-779-466	Sequence 466, App
114	8	1.5	437	12	US-10-140-861-466	Sequence 466, App	187	8	1.5	437	12	US-10-160-504-466	Sequence 466, App
115	8	1.5	437	12	US-10-140-862-466	Sequence 466, App	188	8	1.5	437	12	US-09-866-034-16	Sequence 16, App1
116	8	1.5	437	12	US-10-141-697-466	Sequence 466, App	189	8	1.5	437	12	US-10-152-392-466	Sequence 466, App
117	8	1.5	437	12	US-10-141-700-466	Sequence 466, App	190	8	1.5	437	12	US-10-152-392-466	Sequence 466, App
118	8	1.5	437	12	US-10-141-705-466	Sequence 466, App	191	8	1.5	437	12	US-10-157-781-466	Sequence 466, App
119	8	1.5	437	12	US-10-141-753-466	Sequence 466, App	192	8	1.5	437	12	US-10-157-781-466	Sequence 466, App
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121	8	1.5	437	12	US-10-142-418-466	Sequence 466, App	194	8	1.5	437	12	US-10-147-491-466	Sequence 466, App
122	8	1.5	437	12	US-10-142-420-466	Sequence 466, App	195	8	1.5	437	12	US-10-152-382-466	Sequence 466, App
123	8	1.5	437	12	US-10-142-422-466	Sequence 466, App	196	8	1.5	437	12	US-10-152-382-466	Sequence 466, App
124	8	1.5	437	12	US-10-142-427-466	Sequence 466, App	197	8	1.5	437	12	US-10-152-388-466	Sequence 466, App
125	8	1.5	437	12	US-10-142-760-466	Sequence 466, App	198	8	1.5	437	12	US-10-152-387-466	Sequence 466, App
126	8	1.5	437	12	US-10-145-821-466	Sequence 466, App	199	8	1.5	437	12	US-10-152-388-466	Sequence 466, App
127	8	1.5	437	12	US-10-152-531-466	Sequence 466, App	200	8	1.5	437	12	US-10-152-392-466	Sequence 466, App
128	8	1.5	437	12	US-10-152-531-466	Sequence 466, App	201	8	1.5	437	12	US-10-152-392-466	Sequence 466, App
129	8	1.5	437	12	US-10-127-8640A-466	Sequence 466, App	202	8	1.5	437	12	US-10-153-756-466	Sequence 466, App
130	8	1.5	437	12	US-10-142-424-466	Sequence 466, App	203	8	1.5	437	12	US-10-157-784-466	Sequence 466, App
131	8	1.5	437	12	US-10-142-761-466	Sequence 466, App	204	8	1.5	437	12	US-10-157-797-466	Sequence 466, App
132	8	1.5	437	12	US-10-142-763-466	Sequence 466, App	205	8	1.5	437	12	US-10-145-625-466	Sequence 466, App
133	8	1.5	437	12	US-10-142-765-466	Sequence 466, App	206	8	1.5	437	12	US-10-145-627-466	Sequence 466, App
134	8	1.5	437	12	US-10-142-887-466	Sequence 466, App	207	8	1.5	437	12	US-10-139-980-466	Sequence 466, App
135	8	1.5	437	12	US-10-143-034-466	Sequence 466, App	208	8	1.5	437	12	US-10-142-762-466	Sequence 466, App
136	8	1.5	437	12	US-10-143-116-466	Sequence 466, App	209	8	1.5	437	12	US-10-142-764-466	Sequence 466, App
137	8	1.5	437	12	US-10-143-116-466	Sequence 466, App	210	8	1.5	437	12	US-10-142-764-466	Sequence 466, App
138	8	1.5	437	12	US-10-144-957-466	Sequence 466, App	211	8	1.5	437	12	US-10-145-960-466	Sequence 466, App
139	8	1.5	437	12	US-10-144-992-466	Sequence 466, App	212	8	1.5	437	12	US-10-145-962-466	Sequence 466, App
140	8	1.5	437	12	US-10-145-015-466	Sequence 466, App	213	8	1.5	437	12	US-10-145-962-466	Sequence 466, App
141	8	1.5	437	12	US-10-145-090-466	Sequence 466, App	214	8	1.5	437	12	US-10-145-962-466	Sequence 466, App
142	8	1.5	437	12	US-10-145-091-466	Sequence 466, App	215	8	1.5	437	12	US-10-145-962-466	Sequence 466, App
143	8	1.5	437	12	US-10-145-629-466	Sequence 466, App	216	8	1.5	437	12	US-10-147-496-466	Sequence 466, App
144	8	1.5	437	12	US-10-145-630-466	Sequence 466, App	217	8	1.5	437	12	US-10-147-505-466	Sequence 466, App
145	8	1.5	437	12	US-10-145-747-466	Sequence 466, App	218	8	1.5	437	12	US-10-147-516-466	Sequence 466, App
146	8	1.5	437	12	US-10-145-752-466	Sequence 466, App	219	8	1.5	437	12	US-10-147-516-466	Sequence 466, App
147	8	1.5	437	12	US-10-145-754-466	Sequence 466, App	220	8	1.5	437	12	US-10-152-398-466	Sequence 466, App
148	8	1.5	437	12	US-10-145-755-466	Sequence 466, App	221	8	1.5	437	12	US-10-152-398-466	Sequence 466, App
149	8	1.5	437	12	US-10-145-818-466	Sequence 466, App	222	8	1.5	437	12	US-10-152-398-466	Sequence 466, App
150	8	1.5	437	12	US-10-145-820-466	Sequence 466, App	223	8	1.5	437	12	US-10-033-223-16	Sequence 16, App1
151	8	1.5	437	12	US-10-145-822-466	Sequence 466, App	224	8	1.5	437	12	US-10-033-223-16	Sequence 16, App1
152	8	1.5	437	12	US-10-145-873-466	Sequence 466, App	225	8	1.5	437	12	US-10-033-167-16	Sequence 16, App1
153	8	1.5	437	12	US-10-147-481-466	Sequence 466, App	226	8	1.5	437	12	US-10-033-167-16	Sequence 16, App1
154	8	1.5	437	12	US-10-147-482-466	Sequence 466, App	227	8	1.5	437	12	US-10-033-244-16	Sequence 16, App1
155	8	1.5	437	12	US-10-147-503-466	Sequence 466, App	228	8	1.5	437	12	US-10-028-072-466	Sequence 466, App
156	8	1.5	437	12	US-10-147-522-466	Sequence 466, App	229	8	1.5	437	12	US-10-121-049-466	Sequence 466, App
157	8	1.5	437	12	US-10-152-401-466	Sequence 466, App	230	8	1.5	437	12	US-10-123-904-466	Sequence 466, App
158	8	1.5	437	12	US-10-157-793-466	Sequence 466, App	231	8	1.5	437	12	US-10-140-470-466	Sequence 466, App
159	8	1.5	437	12	US-10-158-462-466	Sequence 466, App	232	8	1.5	437	12	US-10-033-435-16	Sequence 16, App1
160	8	1.5	437	12	US-10-158-792-466	Sequence 466, App	233	8	1.5	437	12	US-10-175-746-466	Sequence 466, App
161	8	1.5	437	12	US-10-143-035-466	Sequence 466, App	234	8	1.5	437	12	US-10-176-918-466	Sequence 466, App

235	8	1.5	437	15	US-10-176-921-466	Sequence 466, App	308	8	1.5	437	15	US-10-219-076-162	Sequence 162, App
236	8	1.5	437	15	US-10-227-884-162	Sequence 162, App	309	8	1.5	437	15	US-10-230-434-162	Sequence 162, App
237	8	1.5	437	15	US-10-032-990-16	Sequence 16, Appl	310	8	1.5	437	15	US-10-125-926A-466	Sequence 466, App
238	8	1.5	437	15	US-10-137-865-466	Sequence 466, App	311	8	1.5	437	15	US-10-125-930A-466	Sequence 466, App
239	8	1.5	437	15	US-10-140-474-466	Sequence 466, App	312	8	1.5	437	15	US-10-127-831A-466	Sequence 466, App
240	8	1.5	437	15	US-10-142-431-466	Sequence 466, App	313	8	1.5	437	15	US-10-127-837A-466	Sequence 466, App
241	8	1.5	437	15	US-10-143-114-466	Sequence 466, App	314	8	1.5	437	15	US-10-127-838A-466	Sequence 466, App
242	8	1.5	437	15	US-10-230-163-162	Sequence 162, App	315	8	1.5	437	15	US-10-127-842A-466	Sequence 466, App
243	8	1.5	437	15	US-10-140-002-466	Sequence 466, App	316	8	1.5	437	15	US-10-127-843A-466	Sequence 466, App
244	8	1.5	437	15	US-10-230-338-162	Sequence 162, App	317	8	1.5	437	15	US-10-127-845A-466	Sequence 466, App
245	8	1.5	437	15	US-10-142-419-466	Sequence 466, App	318	8	1.5	437	15	US-10-127-846A-466	Sequence 466, App
246	8	1.5	437	15	US-10-218-631-162	Sequence 162, App	319	8	1.5	437	15	US-10-127-848A-466	Sequence 466, App
247	8	1.5	437	15	US-10-123-262-466	Sequence 466, App	320	8	1.5	437	15	US-10-127-849A-466	Sequence 466, App
248	8	1.5	437	15	US-10-142-423-466	Sequence 466, App	321	8	1.5	437	15	US-10-127-850A-466	Sequence 466, App
249	8	1.5	437	15	US-10-230-414-162	Sequence 162, App	322	8	1.5	437	15	US-10-127-851A-466	Sequence 466, App
250	8	1.5	437	15	US-10-032-996-16	Sequence 16, Appl	323	8	1.5	437	15	US-10-128-684A-466	Sequence 466, App
251	8	1.5	437	15	US-10-121-050-466	Sequence 466, App	324	8	1.5	437	15	US-10-128-686A-466	Sequence 466, App
252	8	1.5	437	15	US-10-141-755-466	Sequence 466, App	325	8	1.5	437	15	US-10-128-690A-466	Sequence 466, App
253	8	1.5	437	15	US-10-143-032-466	Sequence 466, App	326	8	1.5	437	15	US-10-128-691A-466	Sequence 466, App
254	8	1.5	437	15	US-10-123-108-466	Sequence 466, App	327	8	1.5	437	15	US-10-131-819A-466	Sequence 466, App
255	8	1.5	437	15	US-10-123-236-466	Sequence 466, App	328	8	1.5	437	15	US-10-131-829A-466	Sequence 466, App
256	8	1.5	437	15	US-10-123-261-466	Sequence 466, App	329	8	1.5	437	15	US-10-131-836A-466	Sequence 466, App
257	8	1.5	437	15	US-10-140-521-466	Sequence 466, App	330	8	1.5	437	15	US-10-146-729-466	Sequence 466, App
258	8	1.5	437	15	US-10-140-528-466	Sequence 466, App	331	8	1.5	437	15	US-10-146-791-466	Sequence 466, App
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261	8	1.5	437	15	US-10-123-292-466	Sequence 466, App	334	8	1.5	437	15	US-10-147-884A-466	Sequence 466, App
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267	8	1.5	437	15	US-10-218-849-162	Sequence 162, App	340	8	1.5	437	15	US-10-124-818-466	Sequence 466, App
268	8	1.5	437	15	US-10-227-873-162	Sequence 162, App	341	8	1.5	437	15	US-10-137-868-466	Sequence 466, App
269	8	1.5	437	15	US-10-227-883-162	Sequence 162, App	342	8	1.5	437	15	US-10-147-92-466	Sequence 466, App
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272	8	1.5	437	15	US-10-127-825A-466	Sequence 466, App	345	8	1.5	437	15	US-10-123-907-466	Sequence 466, App
273	8	1.5	437	15	US-10-127-829A-466	Sequence 466, App	346	8	1.5	437	15	US-10-124-815-466	Sequence 466, App
274	8	1.5	437	15	US-10-127-835A-466	Sequence 466, App	347	8	1.5	437	15	US-10-125-921A-466	Sequence 466, App
275	8	1.5	437	15	US-10-127-839A-466	Sequence 466, App	348	8	1.5	437	15	US-10-125-928A-466	Sequence 466, App
276	8	1.5	437	15	US-10-127-901A-466	Sequence 466, App	349	8	1.5	437	15	US-10-127-821A-466	Sequence 466, App
277	8	1.5	437	15	US-10-128-693A-466	Sequence 466, App	350	8	1.5	437	15	US-10-127-822A-466	Sequence 466, App
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279	8	1.5	437	15	US-10-131-818A-466	Sequence 466, App	352	8	1.5	437	15	US-10-127-826A-466	Sequence 466, App
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281	8	1.5	437	15	US-10-131-824A-466	Sequence 466, App	354	8	1.5	437	15	US-10-127-828A-466	Sequence 466, App
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284	8	1.5	437	15	US-10-137-872A-466	Sequence 466, App	357	8	1.5	437	15	US-10-127-833A-466	Sequence 466, App
285	8	1.5	437	15	US-10-147-500-466	Sequence 466, App	358	8	1.5	437	15	US-10-127-834A-466	Sequence 466, App
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287	8	1.5	437	15	US-10-147-515-466	Sequence 466, App	360	8	1.5	437	15	US-10-127-841A-466	Sequence 466, App
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289	8	1.5	437	15	US-10-147-526-466	Sequence 466, App	362	8	1.5	437	15	US-10-128-687A-466	Sequence 466, App
290	8	1.5	437	15	US-10-147-527-466	Sequence 466, App	363	8	1.5	437	15	US-10-128-688A-466	Sequence 466, App
291	8	1.5	437	15	US-10-121-041-466	Sequence 466, App	364	8	1.5	437	15	US-10-128-689A-466	Sequence 466, App
292	8	1.5	437	15	US-10-121-043-466	Sequence 466, App	365	8	1.5	437	15	US-10-128-694A-466	Sequence 466, App
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294	8	1.5	437	15	US-10-123-915-466	Sequence 466, App	367	8	1.5	437	15	US-10-219-017-466	Sequence 466, App
295	8	1.5	437	15	US-10-123-902-466	Sequence 466, App	368	8	1.5	437	15	US-10-219-013-162	Sequence 162, App
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298	8	1.5	437	15	US-10-123-910-466	Sequence 466, App	371	8	1.5	437	15	US-10-219-466-162	Sequence 162, App
299	8	1.5	437	15	US-10-124-813-466	Sequence 466, App	372	8	1.5	437	15	US-10-219-479-162	Sequence 162, App
300	8	1.5	437	15	US-10-124-817-466	Sequence 466, App	373	8	1.5	437	15	US-10-219-481-162	Sequence 162, App
301	8	1.5	437	15	US-10-125-922-466	Sequence 466, App	374	8	1.5	437	15	US-10-230-260-162	Sequence 162, App
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305	8	1.5	437	15	US-10-147-519-466	Sequence 466, App	378	8	1.5	437	15	US-10-131-817A-466	Sequence 466, App
306	8	1.5	437	15	US-10-157-782-466	Sequence 466, App	379	8	1.5	437	15	US-10-131-821A-466	Sequence 466, App
307	8	1.5	437	15	US-10-152-395-466	Sequence 466, App	380	8	1.5	437	15	US-10-131-822A-466	Sequence 466, App

381	8	1.5	437	15	US-10-131-828A-466	Sequence 466, App	454	8	1.5	437	16	US-10-146-727-466	Sequence 466, App
382	8	1.5	437	15	US-10-131-835A-466	Sequence 466, App	455	8	1.5	437	16	US-10-146-788-466	Sequence 466, App
383	8	1.5	437	15	US-10-137-864A-466	Sequence 466, App	456	8	1.5	437	16	US-10-152-380-466	Sequence 466, App
384	8	1.5	437	15	US-10-137-869A-466	Sequence 466, App	457	8	1.5	437	16	US-10-153-834-466	Sequence 466, App
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388	8	1.5	437	15	US-10-216-165-162	Sequence 162, App	461	8	1.5	616	12	US-10-006-130A-24	Sequence 24, App1
389	8	1.5	437	15	US-10-218-956-162	Sequence 162, App	462	8	1.5	616	12	US-10-199-672-158	Sequence 158, App
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391	8	1.5	437	15	US-10-219-478-162	Sequence 162, App	464	8	1.5	616	12	US-10-187-749-158	Sequence 158, App
392	8	1.5	437	15	US-10-219-536-162	Sequence 162, App	465	8	1.5	616	12	US-10-194-657-158	Sequence 158, App
393	8	1.5	437	15	US-10-233-205-162	Sequence 162, App	466	8	1.5	616	12	US-10-184-452-158	Sequence 158, App
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397	8	1.5	437	15	US-10-219-474-162	Sequence 162, App	470	8	1.5	616	12	US-10-173-689-158	Sequence 158, App
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399	8	1.5	437	15	US-10-219-528-162	Sequence 162, App	472	8	1.5	616	12	US-10-173-691-158	Sequence 158, App
400	8	1.5	437	15	US-10-227-880-162	Sequence 162, App	473	8	1.5	616	12	US-10-173-692-158	Sequence 158, App
401	8	1.5	437	15	US-10-227-881-162	Sequence 162, App	474	8	1.5	616	12	US-10-173-694-158	Sequence 158, App
402	8	1.5	437	15	US-10-227-882-162	Sequence 162, App	475	8	1.5	616	12	US-10-173-698-158	Sequence 158, App
403	8	1.5	437	15	US-10-230-436-162	Sequence 162, App	476	8	1.5	616	12	US-10-173-699-158	Sequence 158, App
404	8	1.5	437	15	US-10-233-223-162	Sequence 162, App	477	8	1.5	616	12	US-10-173-707-158	Sequence 158, App
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406	8	1.5	437	15	US-10-233-227-162	Sequence 162, App	479	8	1.5	616	12	US-10-174-583-158	Sequence 158, App
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408	8	1.5	437	15	US-10-233-234-162	Sequence 162, App	481	8	1.5	616	12	US-10-174-589-158	Sequence 158, App
409	8	1.5	437	15	US-10-219-060-162	Sequence 162, App	482	8	1.5	616	12	US-10-175-36-158	Sequence 158, App
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412	8	1.5	437	15	US-10-216-162-162	Sequence 162, App	485	8	1.5	616	12	US-10-175-745-158	Sequence 158, App
413	8	1.5	437	15	US-10-216-164-162	Sequence 162, App	486	8	1.5	616	12	US-10-175-748-158	Sequence 158, App
414	8	1.5	437	15	US-10-216-167-162	Sequence 162, App	487	8	1.5	616	12	US-10-175-751-158	Sequence 158, App
415	8	1.5	437	15	US-10-216-168-162	Sequence 162, App	488	8	1.5	616	12	US-10-175-754-158	Sequence 158, App
416	8	1.5	437	15	US-10-219-065-162	Sequence 162, App	489	8	1.5	616	12	US-10-176-80-158	Sequence 158, App
417	8	1.5	437	15	US-10-219-071-162	Sequence 162, App	490	8	1.5	616	12	US-10-176-80-158	Sequence 158, App
418	8	1.5	437	15	US-10-219-074-162	Sequence 162, App	491	8	1.5	616	12	US-10-176-489-158	Sequence 158, App
419	8	1.5	437	15	US-10-219-077-162	Sequence 162, App	492	8	1.5	616	12	US-10-176-754-158	Sequence 158, App
420	8	1.5	437	15	US-10-219-465-162	Sequence 162, App	493	8	1.5	616	12	US-10-176-755-158	Sequence 158, App
421	8	1.5	437	15	US-10-219-467-162	Sequence 162, App	494	8	1.5	616	12	US-10-176-759-158	Sequence 158, App
422	8	1.5	437	15	US-10-219-468-162	Sequence 162, App	495	8	1.5	616	12	US-10-176-820-158	Sequence 158, App
423	8	1.5	437	15	US-10-219-471-162	Sequence 162, App	496	8	1.5	616	12	US-10-176-922-158	Sequence 158, App
424	8	1.5	437	15	US-10-219-473-162	Sequence 162, App	497	8	1.5	616	12	US-10-176-924-158	Sequence 158, App
425	8	1.5	437	15	US-10-219-476-162	Sequence 162, App	498	8	1.5	616	12	US-10-176-984-158	Sequence 158, App
426	8	1.5	437	15	US-10-219-482-162	Sequence 162, App	499	8	1.5	616	12	US-10-179-508-158	Sequence 158, App
427	8	1.5	437	15	US-10-227-874-162	Sequence 162, App	500	8	1.5	616	12	US-10-179-512-158	Sequence 158, App
428	8	1.5	437	15	US-10-227-876-162	Sequence 162, App	501	8	1.5	616	12	US-10-179-515-158	Sequence 158, App
429	8	1.5	437	15	US-10-227-878-162	Sequence 162, App	502	8	1.5	616	12	US-10-179-515-158	Sequence 158, App
430	8	1.5	437	15	US-10-229-974-162	Sequence 162, App	503	8	1.5	616	12	US-10-173-702-158	Sequence 158, App
431	8	1.5	437	15	US-10-230-024-162	Sequence 162, App	504	8	1.5	616	12	US-10-173-703-158	Sequence 158, App
432	8	1.5	437	15	US-10-230-113-162	Sequence 162, App	505	8	1.5	616	12	US-10-174-704-158	Sequence 158, App
433	8	1.5	437	15	US-10-230-183-162	Sequence 162, App	506	8	1.5	616	12	US-10-174-574-158	Sequence 158, App
434	8	1.5	437	15	US-10-230-438-162	Sequence 162, App	507	8	1.5	616	12	US-10-176-486-158	Sequence 158, App
440	8	1.5	437	15	US-10-232-222-162	Sequence 162, App	513	8	1.5	616	12	US-10-179-517-158	Sequence 158, App
441	8	1.5	437	15	US-10-232-223-162	Sequence 162, App	514	8	1.5	616	12	US-10-179-521-158	Sequence 158, App
442	8	1.5	437	15	US-10-192-007-466	Sequence 466, App	515	8	1.5	616	12	US-10-012-064A-24	Sequence 24, App1
443	8	1.5	437	15	US-10-194-359-466	Sequence 466, App	516	8	1.5	616	12	US-10-017-867A-24	Sequence 24, App1
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445	8	1.5	437	15	US-10-219-472-162	Sequence 162, App	518	8	1.5	616	14	US-10-032-586-158	Sequence 158, App
446	8	1.5	437	15	US-10-219-527-162	Sequence 162, App	519	8	1.5	616	15	US-10-174-590-158	Sequence 158, App
447	8	1.5	437	15	US-10-227-877-162	Sequence 162, App	520	8	1.5	616	15	US-10-176-758-158	Sequence 158, App
448	8	1.5	437	15	US-10-127-847A-466	Sequence 466, App	521	8	1.5	616	15	US-10-175-737-158	Sequence 158, App
449	8	1.5	437	15	US-10-216-166-162	Sequence 162, App	522	8	1.5	616	15	US-10-173-706-158	Sequence 158, App
450	8	1.5	437	15	US-10-218-612-162	Sequence 162, App	523	8	1.5	616	15	US-10-175-728-158	Sequence 158, App
451	8	1.5	437	15	US-10-175-590-466	Sequence 466, App	524	8	1.5	616	15	US-10-175-752-158	Sequence 158, App
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527	8	1.5	616	15	US-10-176-913-158	Sequence 158, App	600	8	1.5	616	15	US-10-184-616-158	Sequence 158, App
528	8	1.5	616	15	US-10-180-552-158	Sequence 158, App	601	8	1.5	616	15	US-10-184-617-158	Sequence 158, App
529	8	1.5	616	15	US-10-180-557-158	Sequence 158, App	602	8	1.5	616	15	US-10-184-622-158	Sequence 158, App
530	8	1.5	616	15	US-10-173-700-158	Sequence 158, App	603	8	1.5	616	15	US-10-184-628-158	Sequence 158, App
531	8	1.5	616	15	US-10-174-572-158	Sequence 158, App	604	8	1.5	616	15	US-10-184-629-158	Sequence 158, App
532	8	1.5	616	15	US-10-174-579-158	Sequence 158, App	605	8	1.5	616	15	US-10-184-630-158	Sequence 158, App
533	8	1.5	616	15	US-10-174-582-158	Sequence 158, App	606	8	1.5	616	15	US-10-184-631-158	Sequence 158, App
534	8	1.5	616	15	US-10-174-588-158	Sequence 158, App	607	8	1.5	616	15	US-10-184-632-158	Sequence 158, App
535	8	1.5	616	15	US-10-175-739-158	Sequence 158, App	608	8	1.5	616	15	US-10-184-636-158	Sequence 158, App
536	8	1.5	616	15	US-10-175-740-158	Sequence 158, App	609	8	1.5	616	15	US-10-184-640-158	Sequence 158, App
537	8	1.5	616	15	US-10-175-743-158	Sequence 158, App	610	8	1.5	616	15	US-10-184-650-158	Sequence 158, App
538	8	1.5	616	15	US-10-176-488-158	Sequence 158, App	611	8	1.5	616	15	US-10-184-651-158	Sequence 158, App
539	8	1.5	616	15	US-10-176-492-158	Sequence 158, App	612	8	1.5	616	15	US-10-187-588-158	Sequence 158, App
540	8	1.5	616	15	US-10-176-750-158	Sequence 158, App	613	8	1.5	616	15	US-10-187-597-158	Sequence 158, App
541	8	1.5	616	15	US-10-176-757-158	Sequence 158, App	614	8	1.5	616	15	US-10-187-598-158	Sequence 158, App
542	8	1.5	616	15	US-10-176-985-158	Sequence 158, App	615	8	1.5	616	15	US-10-187-743-158	Sequence 158, App
543	8	1.5	616	15	US-10-176-987-158	Sequence 158, App	616	8	1.5	616	15	US-10-187-600-158	Sequence 158, App
544	8	1.5	616	15	US-10-176-992-158	Sequence 158, App	617	8	1.5	616	15	US-10-187-602-158	Sequence 158, App
545	8	1.5	616	15	US-10-176-993-158	Sequence 158, App	618	8	1.5	616	15	US-10-187-603-158	Sequence 158, App
546	8	1.5	616	15	US-10-184-658-158	Sequence 158, App	619	8	1.5	616	15	US-10-187-741-158	Sequence 158, App
547	8	1.5	616	15	US-10-176-691-158	Sequence 158, App	620	8	1.5	616	15	US-10-187-743-158	Sequence 158, App
548	8	1.5	616	15	US-10-176-695-158	Sequence 158, App	621	8	1.5	616	15	US-10-187-746-158	Sequence 158, App
549	8	1.5	616	15	US-10-173-697-158	Sequence 158, App	622	8	1.5	616	15	US-10-187-747-158	Sequence 158, App
550	8	1.5	616	15	US-10-173-705-158	Sequence 158, App	623	8	1.5	616	15	US-10-187-751-158	Sequence 158, App
551	8	1.5	616	15	US-10-174-576-158	Sequence 158, App	624	8	1.5	616	15	US-10-187-753-158	Sequence 158, App
552	8	1.5	616	15	US-10-174-585-158	Sequence 158, App	625	8	1.5	616	15	US-10-187-754-158	Sequence 158, App
553	8	1.5	616	15	US-10-174-586-158	Sequence 158, App	626	8	1.5	616	15	US-10-187-757-158	Sequence 158, App
554	8	1.5	616	15	US-10-175-747-158	Sequence 158, App	627	8	1.5	616	15	US-10-187-884-158	Sequence 158, App
555	8	1.5	616	15	US-10-176-481-158	Sequence 158, App	628	8	1.5	616	15	US-10-188-767-158	Sequence 158, App
556	8	1.5	616	15	US-10-176-485-158	Sequence 158, App	629	8	1.5	616	15	US-10-188-769-158	Sequence 158, App
557	8	1.5	616	15	US-10-176-487-158	Sequence 158, App	630	8	1.5	616	15	US-10-188-770-158	Sequence 158, App
558	8	1.5	616	15	US-10-176-493-158	Sequence 158, App	631	8	1.5	616	15	US-10-188-773-158	Sequence 158, App
559	8	1.5	616	15	US-10-176-756-158	Sequence 158, App	632	8	1.5	616	15	US-10-188-781-158	Sequence 158, App
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561	8	1.5	616	15	US-10-176-919-158	Sequence 158, App	634	8	1.5	616	15	US-10-194-423-158	Sequence 158, App
562	8	1.5	616	15	US-10-176-925-158	Sequence 158, App	635	8	1.5	616	15	US-10-195-887-158	Sequence 158, App
563	8	1.5	616	15	US-10-176-978-158	Sequence 158, App	636	8	1.5	616	15	US-10-195-901-158	Sequence 158, App
564	8	1.5	616	15	US-10-179-510-158	Sequence 158, App	637	8	1.5	616	15	US-10-195-902-158	Sequence 158, App
565	8	1.5	616	15	US-10-180-543-158	Sequence 158, App	638	8	1.5	616	15	US-10-196-743-158	Sequence 158, App
566	8	1.5	616	15	US-10-180-544-158	Sequence 158, App	639	8	1.5	616	15	US-10-196-760-158	Sequence 158, App
567	8	1.5	616	15	US-10-180-546-158	Sequence 158, App	640	8	1.5	616	15	US-10-197-708-158	Sequence 158, App
568	8	1.5	616	15	US-10-180-547-158	Sequence 158, App	641	8	1.5	616	15	US-10-176-479-158	Sequence 158, App
569	8	1.5	616	15	US-10-180-549-158	Sequence 158, App	642	8	1.5	616	15	US-10-176-748-158	Sequence 158, App
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571	8	1.5	616	15	US-10-180-559-158	Sequence 158, App	644	8	1.5	616	15	US-10-179-507-158	Sequence 158, App
572	8	1.5	616	15	US-10-181-000-158	Sequence 158, App	645	8	1.5	616	15	US-10-179-516-158	Sequence 158, App
573	8	1.5	616	15	US-10-183-010-158	Sequence 158, App	646	8	1.5	616	15	US-10-179-519-158	Sequence 158, App
574	8	1.5	616	15	US-10-183-012-158	Sequence 158, App	647	8	1.5	616	15	US-10-179-525-158	Sequence 158, App
575	8	1.5	616	15	US-10-184-614-158	Sequence 158, App	648	8	1.5	616	15	US-10-180-540-158	Sequence 158, App
576	8	1.5	616	15	US-10-184-623-158	Sequence 158, App	649	8	1.5	616	15	US-10-180-545-158	Sequence 158, App
577	8	1.5	616	15	US-10-184-635-158	Sequence 158, App	650	8	1.5	616	15	US-10-183-006-158	Sequence 158, App
578	8	1.5	616	15	US-10-184-637-158	Sequence 158, App	651	8	1.5	616	15	US-10-183-008-158	Sequence 158, App
579	8	1.5	616	15	US-10-184-646-158	Sequence 158, App	652	8	1.5	616	15	US-10-183-017-158	Sequence 158, App
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581	8	1.5	616	15	US-10-184-652-158	Sequence 158, App	654	8	1.5	616	15	US-10-184-618-158	Sequence 158, App
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584	8	1.5	616	15	US-10-187-745-158	Sequence 158, App	657	8	1.5	616	15	US-10-184-627-158	Sequence 158, App
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586	8	1.5	616	15	US-10-187-886-158	Sequence 158, App	659	8	1.5	616	15	US-10-184-654-158	Sequence 158, App
587	8	1.5	616	15	US-10-199-464-158	Sequence 158, App	660	8	1.5	616	15	US-10-184-655-158	Sequence 158, App
588	8	1.5	616	15	US-10-196-756-158	Sequence 158, App	661	8	1.5	616	15	US-10-188-774-158	Sequence 158, App
589	8	1.5	616	15	US-10-176-751-158	Sequence 158, App	662	8	1.5	616	15	US-10-188-775-158	Sequence 158, App
590	8	1.5	616	15	US-10-176-760-158	Sequence 158, App	663	8	1.5	616	15	US-10-194-462-158	Sequence 158, App
591	8	1.5	616	15	US-10-176-990-158	Sequence 158, App	664	8	1.5	616	15	US-10-194-745-158	Sequence 158, App
592	8	1.5	616	15	US-10-180-541-158	Sequence 158, App	665	8	1.5	616	15	US-10-196-762-158	Sequence 158, App
593	8	1.5	616	15	US-10-180-542-158	Sequence 158, App	666	8	1.5	616	15	US-10-197-695-158	Sequence 158, App
594	8	1.5	616	15	US-10-180-548-158	Sequence 158, App	667	8	1.5	616	15	US-10-195-894-158	Sequence 158, App
595	8	1.5	616	15	US-10-180-551-158	Sequence 158, App	668	8	1.5	616	15	US-10-006-886A-24	Sequence 24, App1
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598	8	1.5	616	15	US-10-183-013-158	Sequence 158, App	671	8	1.5	616	15	US-10-176-917-158	Sequence 158, App
599	8	1.5	616	15	US-10-184-612-158	Sequence 158, App	672	8	1.5	616	15	US-10-176-982-158	Sequence 158, App

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676	8	1.5	616	15	US-10-179-522-158	Sequence 158, App	749	8	1.5	616	15	US-10-199-462-158	Sequence 158, App
677	8	1.5	616	15	US-10-180-556-158	Sequence 158, App	750	8	1.5	616	15	US-10-201-324-158	Sequence 158, App
678	8	1.5	616	15	US-10-180-560-158	Sequence 158, App	751	8	1.5	616	15	US-10-201-328-158	Sequence 158, App
679	8	1.5	616	15	US-10-183-015-158	Sequence 158, App	752	8	1.5	616	15	US-10-201-528-158	Sequence 158, App
680	8	1.5	616	15	US-10-184-615-158	Sequence 158, App	753	8	1.5	616	15	US-10-201-530-158	Sequence 158, App
681	8	1.5	616	15	US-10-184-620-158	Sequence 158, App	754	8	1.5	616	15	US-10-201-530-158	Sequence 158, App
682	8	1.5	616	15	US-10-184-643-158	Sequence 158, App	755	8	1.5	616	15	US-10-202-408-158	Sequence 158, App
683	8	1.5	616	15	US-10-184-655-158	Sequence 158, App	756	8	1.5	616	15	US-10-202-409-158	Sequence 158, App
684	8	1.5	616	15	US-10-192-010-158	Sequence 158, App	757	8	1.5	616	15	US-10-202-411-158	Sequence 158, App
685	8	1.5	616	15	US-10-203-908-158	Sequence 158, App	758	8	1.5	616	15	US-10-202-472-158	Sequence 158, App
686	8	1.5	616	15	US-10-186-855-158	Sequence 158, App	759	8	1.5	616	15	US-10-203-502-158	Sequence 158, App
687	8	1.5	616	15	US-10-186-855-158	Sequence 158, App	760	8	1.5	616	15	US-10-203-507-158	Sequence 158, App
688	8	1.5	616	15	US-10-184-619-158	Sequence 158, App	761	8	1.5	616	15	US-10-205-507-158	Sequence 158, App
689	8	1.5	616	15	US-10-187-559-158	Sequence 158, App	762	8	1.5	616	15	US-10-205-511-158	Sequence 158, App
690	8	1.5	616	15	US-10-187-750-158	Sequence 158, App	763	8	1.5	616	15	US-10-205-902-158	Sequence 158, App
691	8	1.5	616	15	US-10-188-780-158	Sequence 158, App	764	8	1.5	616	15	US-10-205-907-158	Sequence 158, App
692	8	1.5	616	15	US-10-192-015-158	Sequence 158, App	765	8	1.5	616	15	US-10-194-456-158	Sequence 158, App
693	8	1.5	616	15	US-10-194-394-158	Sequence 158, App	766	8	1.5	616	15	US-10-196-758-158	Sequence 158, App
694	8	1.5	616	15	US-10-194-425-158	Sequence 158, App	767	8	1.5	616	15	US-10-198-770-158	Sequence 158, App
695	8	1.5	616	15	US-10-194-485-158	Sequence 158, App	768	8	1.5	616	15	US-10-199-308-158	Sequence 158, App
696	8	1.5	616	15	US-10-195-885-158	Sequence 158, App	769	8	1.5	616	15	US-10-200-617-158	Sequence 158, App
697	8	1.5	616	15	US-10-195-899-158	Sequence 158, App	770	8	1.5	616	15	US-10-205-893-158	Sequence 158, App
698	8	1.5	616	15	US-10-196-748-158	Sequence 158, App	771	8	1.5	616	15	US-10-205-897-158	Sequence 158, App
699	8	1.5	616	15	US-10-196-750-158	Sequence 158, App	772	8	1.5	616	15	US-10-196-754-158	Sequence 158, App
700	8	1.5	616	15	US-10-197-699-158	Sequence 158, App	773	8	1.5	616	15	US-10-174-571-158	Sequence 158, App
701	8	1.5	616	15	US-10-197-700-158	Sequence 158, App	774	8	1.5	616	15	US-10-176-746-158	Sequence 158, App
702	8	1.5	616	15	US-10-197-705-158	Sequence 158, App	775	8	1.5	616	15	US-10-176-923-158	Sequence 158, App
703	8	1.5	616	15	US-10-197-708-158	Sequence 158, App	776	8	1.5	616	15	US-10-183-021-158	Sequence 158, App
704	8	1.5	616	15	US-10-198-764-158	Sequence 158, App	777	8	1.5	616	15	US-10-184-633-158	Sequence 158, App
705	8	1.5	616	15	US-10-198-765-158	Sequence 158, App	778	8	1.5	616	15	US-10-184-639-158	Sequence 158, App
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707	8	1.5	616	15	US-10-198-769-158	Sequence 158, App	780	8	1.5	616	15	US-10-187-748-158	Sequence 158, App
708	8	1.5	616	15	US-10-199-305-158	Sequence 158, App	781	8	1.5	616	15	US-10-188-766-158	Sequence 158, App
709	8	1.5	616	15	US-10-199-306-158	Sequence 158, App	782	8	1.5	616	15	US-10-188-771-158	Sequence 158, App
710	8	1.5	616	15	US-10-199-310-158	Sequence 158, App	783	8	1.5	616	15	US-10-192-006-158	Sequence 158, App
711	8	1.5	616	15	US-10-199-311-158	Sequence 158, App	784	8	1.5	616	15	US-10-192-008-158	Sequence 158, App
712	8	1.5	616	15	US-10-199-314-158	Sequence 158, App	785	8	1.5	616	15	US-10-192-009-158	Sequence 158, App
713	8	1.5	616	15	US-10-199-317-158	Sequence 158, App	786	8	1.5	616	15	US-10-192-012-158	Sequence 158, App
714	8	1.5	616	15	US-10-199-665-158	Sequence 158, App	787	8	1.5	616	15	US-10-192-014-158	Sequence 158, App
715	8	1.5	616	15	US-10-199-666-158	Sequence 158, App	788	8	1.5	616	15	US-10-192-016-158	Sequence 158, App
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717	8	1.5	616	15	US-10-201-534-158	Sequence 158, App	790	8	1.5	616	15	US-10-194-364-158	Sequence 158, App
718	8	1.5	616	15	US-10-201-770-158	Sequence 158, App	791	8	1.5	616	15	US-10-194-395-158	Sequence 158, App
719	8	1.5	616	15	US-10-201-855-158	Sequence 158, App	792	8	1.5	616	15	US-10-194-424-158	Sequence 158, App
720	8	1.5	616	15	US-10-201-856-158	Sequence 158, App	793	8	1.5	616	15	US-10-194-458-158	Sequence 158, App
721	8	1.5	616	15	US-10-202-469-158	Sequence 158, App	794	8	1.5	616	15	US-10-194-459-158	Sequence 158, App
722	8	1.5	616	15	US-10-202-470-158	Sequence 158, App	795	8	1.5	616	15	US-10-194-486-158	Sequence 158, App
723	8	1.5	616	15	US-10-202-476-158	Sequence 158, App	796	8	1.5	616	15	US-10-195-888-158	Sequence 158, App
724	8	1.5	616	15	US-10-202-934-158	Sequence 158, App	797	8	1.5	616	15	US-10-195-892-158	Sequence 158, App
725	8	1.5	616	15	US-10-202-935-158	Sequence 158, App	798	8	1.5	616	15	US-10-195-746-158	Sequence 158, App
726	8	1.5	616	15	US-10-202-936-158	Sequence 158, App	799	8	1.5	616	15	US-10-197-696-158	Sequence 158, App
727	8	1.5	616	15	US-10-202-939-158	Sequence 158, App	800	8	1.5	616	15	US-10-196-753-158	Sequence 158, App
728	8	1.5	616	15	US-10-205-504-158	Sequence 158, App	801	8	1.5	616	15	US-10-196-761-158	Sequence 158, App
729	8	1.5	616	15	US-10-205-509-158	Sequence 158, App	802	8	1.5	616	15	US-10-197-693-158	Sequence 158, App
730	8	1.5	616	15	US-10-205-895-158	Sequence 158, App	803	8	1.5	616	15	US-10-197-693-158	Sequence 158, App
731	8	1.5	616	15	US-10-205-899-158	Sequence 158, App	804	8	1.5	616	15	US-10-197-696-158	Sequence 158, App
732	8	1.5	616	15	US-10-205-899-158	Sequence 158, App	805	8	1.5	616	15	US-10-197-698-158	Sequence 158, App
733	8	1.5	616	15	US-10-205-899-158	Sequence 158, App	806	8	1.5	616	15	US-10-197-703-158	Sequence 158, App
734	8	1.5	616	15	US-10-205-899-158	Sequence 158, App	807	8	1.5	616	15	US-10-197-711-158	Sequence 158, App
735	8	1.5	616	15	US-10-206-818A-24	Sequence 24, Appl	808	8	1.5	616	15	US-10-198-757-158	Sequence 158, App
736	8	1.5	616	15	US-10-183-002-158	Sequence 158, App	809	8	1.5	616	15	US-10-198-761-158	Sequence 158, App
737	8	1.5	616	15	US-10-184-621-158	Sequence 158, App	810	8	1.5	616	15	US-10-198-763-158	Sequence 158, App
738	8	1.5	616	15	US-10-184-638-158	Sequence 158, App	811	8	1.5	616	15	US-10-198-763-158	Sequence 158, App
739	8	1.5	616	15	US-10-187-752-158	Sequence 158, App	812	8	1.5	616	15	US-10-198-767-158	Sequence 158, App
740	8	1.5	616	15	US-10-187-887-158	Sequence 158, App	813	8	1.5	616	15	US-10-199-301-158	Sequence 158, App
741	8	1.5	616	15	US-10-194-461-158	Sequence 158, App	814	8	1.5	616	15	US-10-199-307-158	Sequence 158, App
742	8	1.5	616	15	US-10-195-892-158	Sequence 158, App	815	8	1.5	616	15	US-10-199-312-158	Sequence 158, App
743	8	1.5	616	15	US-10-195-892-158	Sequence 158, App	816	8	1.5	616	15	US-10-199-315-158	Sequence 158, App
744	8	1.5	616	15	US-10-197-694-158	Sequence 158, App	817	8	1.5	616	15	US-10-199-315-158	Sequence 158, App
745	8	1.5	616	15	US-10-197-697-158	Sequence 158, App	818	8	1.5	616	15	US-10-199-315-158	Sequence 158, App

819	8	1.5	616	15	US-10-199-459-158	Sequence 158, App	892	8	1.5	616	15	US-10-205-904-158	Sequence 158, App
820	8	1.5	616	15	US-10-199-460-158	Sequence 158, App	893	8	1.5	616	15	US-10-175-553-158	Sequence 158, App
821	8	1.5	616	15	US-10-199-461-158	Sequence 158, App	894	8	1.5	616	15	US-10-180-553-158	Sequence 158, App
822	8	1.5	616	15	US-10-199-667-158	Sequence 158, App	895	8	1.5	616	15	US-10-201-327-158	Sequence 158, App
823	8	1.5	616	15	US-10-199-673-158	Sequence 158, App	896	8	1.5	616	15	US-10-121-062-158	Sequence 158, App
824	8	1.5	616	15	US-10-201-921-158	Sequence 158, App	897	8	1.5	616	15	US-10-006-116A-24	Sequence 24, App1
825	8	1.5	616	15	US-10-201-922-158	Sequence 158, App	898	8	1.5	616	15	US-10-017-527A-24	Sequence 24, App1
826	8	1.5	616	15	US-10-201-926-158	Sequence 158, App	899	8	1.5	616	15	US-10-183-003-158	Sequence 158, App
827	8	1.5	616	15	US-10-201-532-158	Sequence 158, App	900	8	1.5	616	15	US-10-183-006-158	Sequence 158, App
828	8	1.5	616	15	US-10-201-533-158	Sequence 158, App	901	8	1.5	616	15	US-10-173-696-158	Sequence 158, App
829	8	1.5	616	15	US-10-201-535-158	Sequence 158, App	902	8	1.5	616	15	US-10-125-923A-158	Sequence 158, App
830	8	1.5	616	15	US-10-201-769-158	Sequence 158, App	903	8	1.5	616	15	US-10-176-491-158	Sequence 158, App
831	8	1.5	616	15	US-10-201-771-158	Sequence 158, App	904	8	1.5	616	15	US-10-176-491-158	Sequence 158, App
832	8	1.5	616	15	US-10-202-410-158	Sequence 158, App	905	8	1.5	616	15	US-10-176-491-158	Sequence 158, App
833	8	1.5	616	15	US-10-202-410-158	Sequence 158, App	906	8	1.5	616	15	US-10-176-491-158	Sequence 158, App
834	8	1.5	616	15	US-10-202-473-158	Sequence 158, App	907	8	1.5	616	15	US-10-187-592-158	Sequence 158, App
835	8	1.5	616	15	US-10-202-474-158	Sequence 158, App	908	8	1.5	616	15	US-10-197-691-158	Sequence 158, App
836	8	1.5	616	15	US-10-205-503-158	Sequence 158, App	909	8	1.5	616	15	US-10-197-691-158	Sequence 158, App
837	8	1.5	616	15	US-10-205-512-158	Sequence 158, App	910	8	1.5	616	15	US-10-198-771-158	Sequence 158, App
838	8	1.5	616	15	US-10-205-512-158	Sequence 158, App	911	8	1.5	616	15	US-10-013-430A-24	Sequence 24, App1
839	8	1.5	616	15	US-10-205-894-158	Sequence 158, App	912	8	1.5	616	15	US-10-174-575A-158	Sequence 158, App
840	8	1.5	616	15	US-10-205-896-158	Sequence 158, App	913	8	1.5	616	15	US-10-179-520-158	Sequence 158, App
841	8	1.5	616	15	US-10-205-898-158	Sequence 158, App	914	8	1.5	616	15	US-10-201-325-158	Sequence 158, App
842	8	1.5	616	15	US-10-205-901-158	Sequence 158, App	915	8	1.5	616	15	US-10-202-941-158	Sequence 158, App
843	8	1.5	616	15	US-10-205-903-158	Sequence 158, App	916	8	1.5	616	15	US-10-205-910-158	Sequence 158, App
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887	8	1.5	616	15	US-10-206-917-158	Sequence 158, App	960	7	1.3	70	9	US-09-864-761-46021	Sequence 46021, A
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965 7 1.3 112 10 US-09-893-737-322 Sequence 322, App
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970 7 1.3 148 9 US-09-864-761-41723 Sequence 41723, A
971 7 1.3 148 9 US-09-864-761-46739 Sequence 46739, A
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973 7 1.3 172 10 US-09-245-764-9 Sequence 9, Appl
974 7 1.3 176 11 US-09-809-715-2 Sequence 2, Appl
975 7 1.3 176 11 US-09-809-715-4 Sequence 4, Appl
976 7 1.3 177 8 US-08-424-550B-52 Sequence 52, Appl
977 7 1.3 193 9 US-09-815-242-4983 Sequence 4983, Ap
978 7 1.3 197 9 US-09-944-277A-11 Sequence 11, Appl
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980 7 1.3 216 15 US-10-023-282-1044 Sequence 1044, Ap
981 7 1.3 221 15 US-10-156-761-13675 Sequence 13675, A
982 7 1.3 222 11 US-09-986-480-330 Sequence 330, App
983 7 1.3 232 9 US-09-944-277A-6 Sequence 6, Appl
984 7 1.3 240 15 US-10-156-761-9337 Sequence 9337, Ap
985 7 1.3 247 15 US-10-128-714-3316 Sequence 3316, Ap
986 7 1.3 256 10 US-09-738-626-6299 Sequence 6299, Ap
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989 7 1.3 257 12 US-10-384-850-45 Sequence 45, Appl
990 7 1.3 258 15 US-10-128-714-8316 Sequence 8316, Ap
991 7 1.3 271 12 US-09-479-040-2316 Sequence 23, Appl
992 7 1.3 317 12 US-10-017-161-2428 Sequence 2428, Ap
993 7 1.3 324 12 US-10-214-519-19 Sequence 19, Appl
994 7 1.3 324 15 US-10-071-338-19 Sequence 19, Appl
995 7 1.3 324 15 US-10-288-985-19 Sequence 19, Appl
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997 7 1.3 377 14 US-10-091-628-2 Sequence 2, Appl
998 7 1.3 426 15 US-10-127-032-94 Sequence 94, Appl
999 7 1.3 426 15 US-10-156-761-8581 Sequence 8581, Ap
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ALIGNMENTS

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RESULT 1
US-10-156-761-10882
; Sequence 10882, Application US/10156761
; Publication No. US20030119018A1
; GENERAL INFORMATION:
; APPLICANT: OMURA, SATOSHI
; APPLICANT: IKEDA, HARUO
; APPLICANT: ISHIKAWA, JUN
; APPLICANT: HORIKAWA, HIROSHI
; APPLICANT: SHIBA, TADAYOSHI
; APPLICANT: SAKAKI, YOSHIYUKI
; APPLICANT: HATTORI, MASAHIRA
; TITLE OF INVENTION: NOVEL POLYNUCLEOTIDES
; FILE REFERENCE: 249-262
; CURRENT APPLICATION NUMBER: US/10/156,761
; PRIOR FILING DATE: 2002-05-29
; PRIOR APPLICATION NUMBER: JP 2001-204089
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: JP 2001-272697
; PRIOR FILING DATE: 2001-08-02
; NUMBER OF SEQ ID NOS: 15109
; SEQ ID NO 10882
; LENGTH: 218
; TYPE: PRT
; ORGANISM: Streptomyces avermitilis
US-10-156-761-10882

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Query Match 1.7%; Score 9; DB 15; Length 218;
Best Local Similarity 100.0%; Pred. No. 2.3;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 463 VGVVLLALL 471

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Db 35 VGVVLLALL 43
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RESULT 2
US-10-156-424A-13
; Sequence 13, Application US/10156424A
; Publication No. US2003003999A1
; GENERAL INFORMATION:
; APPLICANT: Yoshinaga, Steve Kiyoshi
; APPLICANT: Sun, Woong-Kyung
; APPLICANT: Mak, Tak W.
; TITLE OF INVENTION: B7 Related Protein-2 Molecules and Uses Thereof
; FILE REFERENCE: 01-384-A
; CURRENT APPLICATION NUMBER: US/10/156,424A
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: 60/293,629
; PRIOR FILING DATE: 2001-05-25
; NUMBER OF SEQ ID NOS: 32
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 13
; LENGTH: 280
; TYPE: PRT
; ORGANISM: Grus americana
US-10-156-424A-13

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Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 4 VGVVLLALL 12
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RESULT 3
US-09-950-933A-70
; Sequence 70, Application US/09950933A
; Patent No. US20020166141A1
; GENERAL INFORMATION:
; APPLICANT: Simmons, Carl R.
; APPLICANT: Navarro, Pedro
; TITLE OF INVENTION: Antimicrobial Peptides and Methods of
; TITLE OF INVENTION: Use
; FILE REFERENCE: 35718/238472
; CURRENT APPLICATION NUMBER: US/09/950,933A
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: 60/232,569
; PRIOR FILING DATE: 2000-09-13
; NUMBER OF SEQ ID NOS: 99
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 70
; LENGTH: 106
; TYPE: PRT
; ORGANISM: Glycine max
US-09-950-933A-70

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Query Match 1.5%; Score 8; DB 10; Length 106;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 466 VLLVLLALL 473
Db 9 VLLVLLALL 16

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RESULT 4
US-10-080-170-438
; Sequence 438, Application US/10080170
; Publication No. US20030129601A1
; GENERAL INFORMATION:
; APPLICANT: Cole, S.T.
; TITLE OF INVENTION: COMPARATIVE MYCOBACTERIAL GENOMICS AS A TOOL FOR

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TITLE OF INVENTION: IDENTIFYING TARGETS FOR THE DIAGNOSIS, PROPHYLAXIS OR
TREATMENT OF MYCOBACTERIOSES
FILE REFERENCE: 03495.0218
CURRENT APPLICATION NUMBER: US/10/080,170
CURRENT FILING DATE: 2002-06-10
PRIOR APPLICATION NUMBER: 60/270,123
PRIOR FILING DATE: 2001-02-22
NUMBER OF SEQ ID NOS: 652
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 438
LENGTH: 200
TYPE: PRT
ORGANISM: Mycobacterium tuberculosis
US-10-080-170-438

Query Match 1.5%; Score 8; DB 16; Length 200;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 467 LLLALLGG 474
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Db 88 LLLALLGG 95

RESULT 5
US-10-102-806-499
Sequence 499, Application US/10102806
Publication No. US20030054421A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA103P1C1
CURRENT APPLICATION NUMBER: US/10/102,806
CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: 09/925,298
PRIOR FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05881
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 846
SOFTWARE: PatentIn Ver. 2.10
SEQ ID NO 499
LENGTH: 238
TYPE: PRT
ORGANISM: Homo sapiens
US-10-102-806-499

Query Match 1.5%; Score 8; DB 15; Length 238;
Best Local Similarity 100.0%; Pred. No. 24;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 379 GSLSEETP 386
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Db 136 GSLSEETP 143

RESULT 6
US-10-106-698-5043
Sequence 5043, Application US/10106698
Publication No. US20030109690A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Colon and Colon Cancer Associated Polynucleotides and Polypeptide
FILE REFERENCE: PA005P1
CURRENT APPLICATION NUMBER: US/10/106,698
CURRENT FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: PCT/US00/26524
PRIOR FILING DATE: 2000-09-28
PRIOR APPLICATION NUMBER: US 60/157,137
PRIOR FILING DATE: 1999-09-29
PRIOR APPLICATION NUMBER: US 60/163,280
PRIOR FILING DATE: 1999-11-03

NUMBER OF SEQ ID NOS: 8564
SOFTWARE: PatentIn Ver. 3.0
SEQ ID NO 5043
LENGTH: 255
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: MISC FEATURE
LOCATION: (242)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: MISC FEATURE
LOCATION: (249)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-10-106-698-5043

Query Match 1.5%; Score 8; DB 15; Length 255;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 466 VLLALLGG 473
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Db 6 VLLALLGG 13

RESULT 7
US-09-989-722-355
Sequence 355, Application US/09989722
Patent No. US20020072067A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Bostein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottlieb, Mary E.
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavitt, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2730P1C3
CURRENT APPLICATION NUMBER: US/09/989,722
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25

PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/089559
PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/089600
PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/089653
PRIOR FILING DATE:	1998-06-17
PRIOR APPLICATION NUMBER:	60/089801
PRIOR FILING DATE:	1998-06-18
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PRIOR FILING DATE:	1998-06-18
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PRIOR FILING DATE:	1998-06-18
PRIOR APPLICATION NUMBER:	60/089947
PRIOR FILING DATE:	1998-06-19
PRIOR APPLICATION NUMBER:	60/089948
PRIOR FILING DATE:	1998-06-19
PRIOR APPLICATION NUMBER:	60/089952
PRIOR FILING DATE:	1998-06-19
PRIOR APPLICATION NUMBER:	60/090246
PRIOR FILING DATE:	1998-06-22
PRIOR APPLICATION NUMBER:	60/090252
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PRIOR APPLICATION NUMBER:	60/090254
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PRIOR FILING DATE:	1998-06-23
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PRIOR FILING DATE:	1998-06-24
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PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090535
PRIOR FILING DATE:	1998-06-24
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PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090542
PRIOR FILING DATE:	1998-06-24
PRIOR APPLICATION NUMBER:	60/090557
PRIOR FILING DATE:	1998-06-24
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PRIOR FILING DATE:	1998-06-25
PRIOR APPLICATION NUMBER:	60/090678
PRIOR FILING DATE:	1998-06-25
PRIOR APPLICATION NUMBER:	60/090650
PRIOR FILING DATE:	1998-06-25
PRIOR APPLICATION NUMBER:	60/090654
PRIOR FILING DATE:	1998-06-25
PRIOR APPLICATION NUMBER:	60/090655
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PRIOR FILING DATE:	1998-07-01
PRIOR APPLICATION NUMBER:	60/091478
PRIOR FILING DATE:	1998-07-02
PRIOR APPLICATION NUMBER:	60/091544
PRIOR FILING DATE:	1998-07-01
PRIOR APPLICATION NUMBER:	60/091519
PRIOR FILING DATE:	1998-07-02

PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 8; DB 9; Length 437;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 466 VLLALLG 473
Db 4 VLLALLG 11

RESULT 8
US-09-989-723-355
Sequence 355, Application US/09989723
Patent No. US20020072092A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C62
CURRENT APPLICATION NUMBER: US/09/989,723
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
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QY 466 VLLALLG 473
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US-09-989-279-355
Sequence 355, Application US/09989279
Patent No. US20020072496A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C56
CURRENT APPLICATION NUMBER: US/09/989,279
CURRENT FILING DATE: 2001-11-19
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GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnuyers, Luc
APPLICANT: Eaton, Dan L.
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APPLICANT: Gerber, Hanspeter
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APPLICANT: Pan, Nicholas F.
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P27301C65
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Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Bostein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
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; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730P1C70
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 8; DB 10; Length 437;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 466 VLLALLLG 473
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Db 4 VLLALLLG 11

RESULT 12
US-09-989-732-355
Sequence 355, Application US/09989732
Patent No. US20020123463A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David

APPLICANT: Deenoyers, Luc
APPLICANT: Batron, Dan L.
APPLICANT: Ferrera, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OR INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730FIC57
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
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PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 8; DB 10; Length 437;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 466 VLLALLG 473
DB 4 VLLALLG 11

RESULT 13
US-09-991-073-355
Sequence 355, Application US/09991073
Patent No. US20020127576A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltsen, Mary E.
APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
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APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
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APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Collin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC15
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 PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 8; DB 10; Length 437;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 466 VLLALLIG 473
 Db 4 VLLALLIG 11

RESULT 14
 US-09-990-442-355
 Sequence 355; Application US/09990442
 Patent No. US20020132252A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnoyers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gottlieb, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
 APPLICANT: Kijavits, Ivar J.
 APPLICANT: Napier, Mary A.
 APPLICANT: Pan, James
 APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC8
CURRENT FILING DATE: 2001-11-14
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
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PRIOR APPLICATION NUMBER: 60/090696
PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090862
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
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PRIOR APPLICATION NUMBER: 60/091626
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 8; DB 10; Length 437;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 466 VLLALALG 473
Db 4 VLLALALG 11

RESULT 15
US-09-391-163-355
Sequence 355: Application US/09991163
Patent No. US20020132253A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Kurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC17
CURRENT APPLICATION NUMBER: US/09/991,163
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 8; DB 10; Length 437;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 466 VLLALLG 473
Db 4 VLLALLG 11

RESULT 16
US-09-993-604-355
Sequence 355, Application US/09993604
Patent No. US20020137075A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Matanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC25
CURRENT APPLICATION NUMBER: US/09/993,604
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16

PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512.1
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
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PRIOR FILING DATE: 1998-06-26
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PRIOR FILING DATE: 1998-07-01
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PRIOR FILING DATE: 1998-07-02
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PRIOR FILING DATE: 1998-07-01
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 8; DB 10; Length 437;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 466 VLLALLG 473
DB 4 VLLALLG 11

RESULT 17

US-09-990-456-355
Sequence 355, Application US/09990456
Patent No. US20020137890A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C22
CURRENT APPLICATION NUMBER: US/09/990,456
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770

PRIOR FILING DATE: 1997-11-24
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PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
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PRIOR FILING DATE: 1998-05-07
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PRIOR APPLICATION NUMBER: 60/091544

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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query March 1.5% Score 8; DB 10; Length 437;
Best local similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 466 VLLALALG 473
DB 4 VLLALALG 11

RESULT 18
US-09-989-721-355
Sequence 355, Application US/09989721
Patent No. US20020142961A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tamas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P27301C55
CURRENT APPLICATION NUMBER: US/09/989,721
PRIOR FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR APPLICATION NUMBER: 60/065186
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;; PRIOR FILING DATE: 1998-07-09

Query Match .1.5%; Score 8; DB 10; Length 437;
Best Local Similarity 100.0%; Pred. No. 41;
Matches . 8; Conservative .0; Mismatches . 0; Indels . 0; Gaps . 0;

OY 466 VLLALLLG 473
Db 4 VLLALLLG 11

RESULT 19
US-09-992-598-355
; Sequence 355, Application US/09992598
; Patent No. US20020160384A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Boctstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eacott, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gottlieb, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OR INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C20
; CURRENT APPLICATION NUMBER: US/09/992,598
; CURRENT FILING DATE: 2001-11-14
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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Query Match 1.5%; Score 8; DB 10; Length 437;
Best Local Similarity 100.0%; Pred. No. 41;
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RESULT 20
US-09-989-293A-355
Sequence 355, Application US/09989293A
Patent No. US20020177164A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerder, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
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APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
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APPLICANT: Wacanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PLC6
CURRENT FILING DATE: 2001-11-20
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Query Match 1.5%; Score 8; DB 10; Length 437;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 4 VLLIALLG 11

RESULT 21
US-09-989-735-355
Sequence 355, Application US/09989735
Publication No. US20020193299A1
GENERAL INFORMATION:
APPLICANT: Aekhenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerltzen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
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APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730PIC61
CURRENT APPLICATION NUMBER: US/09/989,735
PRIOR FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
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PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 8; DB 10; Length 437;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 466 VLLALLG 473
Db 4 VLLALLG 11

RESULT 22
US-09-990-444-355
Sequence 355, Application US/09990444
Publication No. US20020193300A1
GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deonyshe, Luc
APPLICANT: Baton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C19
CURRENT APPLICATION NUMBER: US/09/990,444
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 8; DB 10; Length 437;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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RESULT 23
US-09-991-181-355
Sequence 355, Application US/09991181
Publication No. US20020197615A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijaviri, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC53
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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PRIOR APPLICATION NUMBER: 60/090444
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; PRIOR FILING DATE: 1998-06-24
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; PRIOR FILING DATE: 1998-06-24
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; PRIOR APPLICATION NUMBER: 60/092182
; PRIOR FILING DATE: 1998-07-09

Query Match      1.5%; Score 8; DB 10; Length 437;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      466 VLLALLG 473
DB      4 VLLALLG 11

RESULT 24
US-09-989-730-355
; Sequence 355, Application US/099898730
; Publication No. US20020197674A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Desnoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltzen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kijavini, Ivar J.

; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; TITLE OF INVENTION: Acids Encoding the Same
; FILE REFERENCE: P2730P1C69
; CURRENT APPLICATION NUMBER: US/09/989,730
; PRIOR FILING DATE: 2001-11-20
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
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;; PRIOR APPLICATION NUMBER: 60/091360
;; PRIOR FILING DATE: 1998-07-01
;; PRIOR APPLICATION NUMBER: 60/091478
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;; PRIOR APPLICATION NUMBER: 60/091544
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;; PRIOR APPLICATION NUMBER: 60/091978
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/091982
;; PRIOR FILING DATE: 1998-07-07
;; PRIOR APPLICATION NUMBER: 60/092182
;; PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 8; DB 10; Length 437;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 466 VLLALLAG 473
Db 4 VLLALLAG 11

RESULT 25
US-09-990-436-355
;; Publication No. US20020198146A1
;; GENERAL INFORMATION:
;; APPLICANT: Ashkenazi, Avi J.
;; APPLICANT: Baker, Kevin P.
;; APPLICANT: Botstein, David
;; APPLICANT: Desnoyers, Luc
;; APPLICANT: Baton, Dan L.
;; APPLICANT: Ferrara, Napoleone
;; APPLICANT: Fong, Sherman
;; APPLICANT: Gerber, Hanspeter
;; APPLICANT: Gerlitsen, Mary E.
;; APPLICANT: Goddard, Audrey
;; APPLICANT: Grimaldi, Paul J.
;; APPLICANT: Gurney, Austin L.
;; APPLICANT: Kijavini, Ivar J.
;; APPLICANT: Napier, Mary A.
;; APPLICANT: Pan, James
;; APPLICANT: Pao, Nicholas F.
;; APPLICANT: Roy, Margaret Ann
;; APPLICANT: Stewart, Timothy A.
;; APPLICANT: Tumas, Daniel
;; APPLICANT: Matanabe, Colin K.

APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P.C14
CURRENT APPLICATION NUMBER: US/09/990,436
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/067770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
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PRIOR APPLICATION NUMBER: 60/083322
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PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
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PRIOR FILING DATE: 1998-07-07
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 8; DB 10; Length 437;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 466 VLLALLG 473
Db 4 VLLALLG 11

RESULT 26
US-09-993-687-355
Sequence 355, Application US/09993687
Publication No. US20020198149A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Goddard, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavini, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Pao, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
Acids Encoding the Same
FILE REFERENCE: P2730P1C11
CURRENT APPLICATION NUMBER: US/09/993,687

CURRENT FILING DATE: 2002-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
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PRIOR APPLICATION NUMBER: 60/090694
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PRIOR FILING DATE: 1998-06-25
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PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/090863
PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
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PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091519
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 8; DB 10; Length 437;
Best Local Similarity 100.0%; Pred.No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 466 VLLALLG 4/73
DB 4 VLLALLG 11

RESULT 27
US-09-989-734-355
Sequence 355, Application US/09989734
Publication No. US20030003531A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Boctstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PLC64
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12

[illegible]

PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
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PRIOR FILING DATE: 1998-07-07
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PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 8; DB 11; Length 437;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 466 VLLALLG 473
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Db 4 VLLALLG 11

RESULT 28
US-09-997-653-355
Sequence 355, Application US/09997653
Publication No. US20030008297A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
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APPLICANT: Napier, Mary A.
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APPLICANT: Stewart, Timothy A.
APPLICANT: Thomas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C38
CURRENT APPLICATION NUMBER: US/09/997, 653
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR APPLICATION NUMBER: 60/065186
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PRIOR APPLICATION NUMBER: 60/075945
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PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 8; DB 11; Length 437;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 466 VLLALAG 473
Db 4 VLLALAG 11

RESULT 29
US-09-993-667-355
Sequence: 355, Application US/09993667
Publication No. US20030022187A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730Pic4
CURRENT APPLICATION NUMBER: US/09/993.667
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
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PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28

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69	PRIOR FILING DATE: 1998-07-02
70	PRIOR APPLICATION NUMBER: 60/091978
71	PRIOR FILING DATE: 1998-07-07
72	PRIOR APPLICATION NUMBER: 60/091982
73	PRIOR FILING DATE: 1998-07-07

PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 1.5% Score 8; DB 11; Length 437;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 466 VLLALLLG 473
Db 4 VLLALLLG 11

RESULT 30

US-09-997-428-355
Sequence 355, Application US/09997428
Publication No. US20030027162A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Auerin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC44
CURRENT APPLICATION NUMBER: US/09/997,428
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
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PRIOR APPLICATION NUMBER: 60/065311
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PRIOR FILING DATE: 1998-07-07
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PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 8; DB 11; Length 437;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 466 VLLALLG 473
Db 4 VLLALLG 11
RESULT 31
US-09-997-666-355
; Sequence 355, Application US/09997666
; Publication No. US20030027163A1
; GENERAL INFORMATION:
; APPLICANT: Ashkenazi, Avi J.
; APPLICANT: Baker, Kevin P.
; APPLICANT: Botstein, David
; APPLICANT: Deenoyers, Luc
; APPLICANT: Eaton, Dan L.
; APPLICANT: Ferrara, Napoleone
; APPLICANT: Fong, Sherman
; APPLICANT: Gerber, Hanspeter
; APPLICANT: Gerltsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Kljavin, Ivar J.
; APPLICANT: Napier, Mary A.
; APPLICANT: Pan, James
; APPLICANT: Paoni, Nicholas F.
; APPLICANT: Roy, Margaret Ann
; APPLICANT: Stewart, Timothy A.
; APPLICANT: Tumas, Daniel
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Williams, P. Mickey
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
; FILE REFERENCE: P2730PIC42
; CURRENT APPLICATION NUMBER: US/09/997,666
; PRIOR FILING DATE: 2001-11-15
; PRIOR APPLICATION NUMBER: 60/049787
; PRIOR FILING DATE: 1997-06-16
; PRIOR APPLICATION NUMBER: 60/062250
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PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 8; DB 11; Length 437;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 466 VLLALLAG 473
|||||
Db 4 VLLALLAG 11

RESULT 32
US-09-990-438-355

Sequence 355, Application US/09990438
Publication No. US20030027754A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerlitsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guirney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PLC3
CURRENT APPLICATION NUMBER: US/09/990,438
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR APPLICATION NUMBER: 60/065186
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PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 8; DB 11; Length 437;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 466 VLLALLG 473
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Db 4 VLLALLG 11

RESULT 33
US-09-990-562-355
Sequence 355, Application US/09990562
Publication No. US20030027985A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deemeyer, Luc

APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C18
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: US/09/990,562
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PRIOR APPLICATION NUMBER: 60/090444

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PRIOR FILING DATE: 1998-06-24
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PRIOR APPLICATION NUMBER: 60/090695
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PRIOR APPLICATION NUMBER: 60/091519
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PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 1.5% Score 8; DB 11; Length 437;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 466 VILLALG 473
DB 4 VILLALG 11

RESULT 34
US-09-990-711-355
Sequence 355, Application US/09990711
Publication No. US20030032023A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gerritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Auelin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC2
CURRENT APPLICATION NUMBER: US/09/990,711
PRIOR FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
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PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 8; DB 11; Length 437;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 466 VLLALLG 473
Db 4 VLLALLG 11

RESULT 35
US-09-989-726-355

Sequence 355, Application US/09989726
Publication No. US2003040473A1

GENERAL INFORMATION:

APPLICANT: Aehkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Geritsen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Guirney, Austin J.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P2730P1C60
CURRENT APPLICATION NUMBER: US/09/989,726
CURRENT FILING DATE: 2001-11-19
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
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 PRIOR APPLICATION NUMBER: 60/092182
 PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 8; DB 11; Length 437;
 Best Local Similarity 100.0%; Pred. No. 41;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 466 VLLALLG 473
 Db 4 VLLALLG 11

RESULT 36
 US-09-998-156-355
 Sequence 355, Application US/09998156
 Publication No. US20030044806A1
 GENERAL INFORMATION:
 APPLICANT: Ashkenazi, Avi J.
 APPLICANT: Baker, Kevin P.
 APPLICANT: Botstein, David
 APPLICANT: Desnovers, Luc
 APPLICANT: Eaton, Dan L.
 APPLICANT: Ferrara, Napoleone
 APPLICANT: Fong, Sherman
 APPLICANT: Gerber, Hanspeter
 APPLICANT: Gertlisen, Mary E.
 APPLICANT: Goddard, Audrey
 APPLICANT: Godowski, Paul J.
 APPLICANT: Grimaldi, J. Christopher
 APPLICANT: Gurney, Austin L.
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 APPLICANT: Napier, Mary A.
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 APPLICANT: Stewart, Timothy A.
 APPLICANT: Tumas, Daniel
 APPLICANT: Watanabe, Colin K.
 APPLICANT: Williams, P. Mickey
 APPLICANT: Wood, William I.
 APPLICANT: Zhang, Zemin
 TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same
FILE REFERENCE: P27301C28
CURRENT APPLICATION NUMBER: US/09/998,156
CURRENT FILING DATE: 2001-11-15
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Tue Oct 7 10:37:58 2003

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PRIOR APPLICATION NUMBER: 60/090695
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Query Match 1.5% Score 8; DB 11; Length 437;

Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 466 VLLALLG 473
|||||
Db 4 VLLALLG 11

RESULT 37
US-09-990-437-355

Sequence 355, Application US/0990437
Publication No. US20030045463A1

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Batton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottlieb, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, U. Christopher
APPLICANT: Gurney, Auelin L.
APPLICANT: Klavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumes, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C49
CURRENT APPLICATION NUMBER: US/09/990,437
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/049787
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PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
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PRIOR APPLICATION NUMBER: 60/088742
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PRIOR FILING DATE: 1998-06-11
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PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088876
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16

PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
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PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089600
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PRIOR FILING DATE: 1998-06-18
PRIOR APPLICATION NUMBER: 60/089907
PRIOR FILING DATE: 1998-06-18
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PRIOR FILING DATE: 1998-06-25
PRIOR APPLICATION NUMBER: 60/090696
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PRIOR FILING DATE: 1998-06-26
PRIOR APPLICATION NUMBER: 60/091360
PRIOR FILING DATE: 1998-07-01
PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
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PRIOR APPLICATION NUMBER: 60/091519
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PRIOR APPLICATION NUMBER: 60/091626
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 8; DB 11; Length 437;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 466 VLLALLG 473
|||||
Db 4 VLLALLG 11

RESULT 38
US-09-991-157-355
Sequence 355, Application US/09991157
Publication No. US20030049638A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnovers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlesen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Aubelin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730PIC51
CURRENT APPLICATION NUMBER: US/09/991.157
CURRENT FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24

1	PRIOR APPLICATION NUMBER: 60/075945
2	PRIOR FILING DATE: 1998-02-25
3	PRIOR APPLICATION NUMBER: 60/078910
4	PRIOR FILING DATE: 1998-03-20
5	PRIOR APPLICATION NUMBER: 60/080322
6	PRIOR FILING DATE: 1998-04-28
7	PRIOR APPLICATION NUMBER: 60/084600
8	PRIOR FILING DATE: 1998-05-07
9	PRIOR APPLICATION NUMBER: 60/087106
10	PRIOR FILING DATE: 1998-05-28
11	PRIOR APPLICATION NUMBER: 60/087607
12	PRIOR FILING DATE: 1998-06-02
13	PRIOR APPLICATION NUMBER: 60/087609
14	PRIOR FILING DATE: 1998-06-02
15	PRIOR APPLICATION NUMBER: 60/088028
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29	PRIOR APPLICATION NUMBER: 60/088202
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31	PRIOR APPLICATION NUMBER: 60/088212
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33	PRIOR APPLICATION NUMBER: 60/088217
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38	PRIOR FILING DATE: 1998-06-10
39	PRIOR APPLICATION NUMBER: 60/088738
40	PRIOR FILING DATE: 1998-06-10
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51	PRIOR APPLICATION NUMBER: 60/088861
52	PRIOR FILING DATE: 1998-06-11
53	PRIOR APPLICATION NUMBER: 60/088876
54	PRIOR FILING DATE: 1998-06-11
55	PRIOR APPLICATION NUMBER: 60/089105
56	PRIOR FILING DATE: 1998-06-12
57	PRIOR APPLICATION NUMBER: 60/089440
58	PRIOR FILING DATE: 1998-06-16
59	PRIOR APPLICATION NUMBER: 60/089512
60	PRIOR FILING DATE: 1998-06-16
61	PRIOR APPLICATION NUMBER: 60/089514
62	PRIOR FILING DATE: 1998-06-16
63	PRIOR APPLICATION NUMBER: 60/089532
64	PRIOR FILING DATE: 1998-06-17
65	PRIOR APPLICATION NUMBER: 60/089538

[illegible]

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PRIOR APPLICATION NUMBER: 60/091978
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match      1.5%  Score 8;  DB 11;  Length 437;
Best Local Similarity 100.0%;  Fred. No. 41;
Matches      8;  Conservative      0;  Mismatches      0;  Gaps      0;

Qy      466 VLLALLG 473
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Db      4 VLLALLG 11

RESULT 39
US-09-997-514-355
Sequence 355, Application US/09997514
Publication No. US20030049681A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gertlisen, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, U. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tuma, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C46
CURRENT APPLICATION NUMBER: US/09/997,514
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
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PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
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PRIOR FILING DATE: 1998-05-28
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PRIOR FILING DATE: 1998-06-02
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PRIOR FILING DATE: 1998-06-17
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PRIOR APPLICATION NUMBER: 60/091478
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091544
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PRIOR FILING DATE: 1998-07-02
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PRIOR APPLICATION NUMBER: 60/091633
PRIOR FILING DATE: 1998-07-02
PRIOR APPLICATION NUMBER: 60/091978

PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/091982
PRIOR FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: 60/092182
PRIOR FILING DATE: 1998-07-09

Query Match 1.5%; Score 8; DB 11; Length 437;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 466 VLLIALLG 473
Db 4 VLLIALLG 11

RESULT 40
US-09-997-573-355
Sequence 355, Application US/09997573
Publication No. US20030049682A1
GENERAL INFORMATION:
APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Botstein, David
APPLICANT: Deenoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter
APPLICANT: Gottlieb, Mary E.
APPLICANT: Goddard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kijavlin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Pan, James
APPLICANT: Paoni, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zemin
TITLE OR INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C45
CURRENT APPLICATION NUMBER: US/09/997,573
CURRENT FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25
PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
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PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02

Query Match . 4.5%; Score 8; DB 11; Length 437;

Best Local Similarity 100.0%; Pred. No. 41;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 466 VLLALLG 473
|||||
Db 4 VLLALLG 11

Search completed: October 2, 2003, 16:15:26
Job time : 80 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: October 2, 2003, 15:46:24 ; Search time 104 Seconds
(without alignments)
1342.370 Million cell updates/sec

Title: US-10-039-770A-1

Perfect score: 2922

Sequence: 1 MGLVGVQVLVLVADCTIFA.....EAEENIDQGETHVEGDY 541

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

SPTREMBL_23:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_protent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacterioph:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2922	100.0	541	5	O15681 toxoplasma
2	434	14.9	622	5	O94661 plasmodium
3	433	14.8	622	5	O967K3 plasmodium
4	432.5	14.8	592	5	O25745 plasmodium
5	431	14.8	622	5	O967K2 plasmodium
6	431	14.8	622	5	O96Z05 plasmodium
7	431	14.8	622	5	O967K1 plasmodium
8	426	14.6	622	5	O967J3 plasmodium
9	425	14.5	622	5	O967K0 plasmodium
10	422.5	14.5	558	5	O25687 plasmodium
11	422	14.4	562	5	O61130 plasmodium
12	420.5	14.4	555	5	O26162 plasmodium
13	420.5	14.4	563	5	O96413 plasmodium
14	419.5	14.4	604	5	O25747 plasmodium
15	419	14.3	557	5	O26225 plasmodium
16	419	14.3	622	5	O96712 plasmodium

17	418	14.3	622	5	O967J4 plasmodium
18	416.5	14.3	555	5	O26163 plasmodium
19	415.5	14.2	605	5	O9NFW9 plasmodium
20	413	14.1	526	5	O9N9G0 plasmodium
21	413	14.1	526	5	O96738 plasmodium
22	413	14.1	622	5	O96735 plasmodium
23	412.5	14.1	621	5	O9TY48 plasmodium
24	412	14.1	557	5	O26224 plasmodium
25	412	14.1	622	5	O95N21 plasmodium
26	412	14.1	622	5	O96739 plasmodium
27	410.5	14.0	620	5	O00784 plasmodium
28	410	14.0	556	5	O25657 plasmodium
29	410	14.0	622	5	O95N02 plasmodium
30	410	14.0	622	5	O96736 plasmodium
31	407	13.9	526	5	O9N9E4 plasmodium
32	407	13.9	622	5	O9N9E4 plasmodium
33	406.5	13.9	605	5	O9GV27 plasmodium
34	406	13.9	622	5	O96718 plasmodium
35	405	13.9	526	5	O9N9E2 plasmodium
36	405	13.9	622	5	O9N9E2 plasmodium
37	404	13.8	526	5	O9N9E4 plasmodium
38	404	13.8	562	5	O25667 plasmodium
39	404	13.8	622	5	O96719 plasmodium
40	403	13.8	526	5	O9N9E6 plasmodium
41	402	13.8	622	5	O95N04 plasmodium
42	401	13.7	622	5	O96732 plasmodium
43	400	13.7	526	5	O9N9D9 plasmodium
44	398.5	13.6	592	5	O25749 plasmodium
45	398.5	13.6	604	5	O25746 plasmodium

ALIGNMENTS

RESULT 1

ID	Accession	Database	Length	Score	DB 5	Length	Score	DB 5
AC	O15681	PRELIMINARY	541	AA.				
DT	01-JAN-1998	(TREMUREL. 05, Created)						
DT	01-JAN-1998	(TREMUREL. 05, Last sequence update)						
DT	01-MAR-2003	(TREMUREL. 23, Last annotation update)						
DE	Apical membrane antigen 1 homolog.							
GN	AMA1G.							
OS	Toxoplasma gondii.							
OC	Eukaryota; Alveolata; Apicomplexa; Coccidia; Eimeriida; Sarcocystidae;							
OC	Toxoplasma.							
OX	NCBI_TaxID=5811;							
RN	[1]							
RP	SEQUENCE FROM N.A.							
RC	STRAIN=ME49;							
RX	MEDLINE=20516458; PubMed=11083833;							
RA	Hohl A.B., Lekutis C., Grigg M.E., Bradley P.J., Dubremetz J.F.,							
RA	Ortega-Barria E., Boothroyd J.C.,							
RT	"Toxoplasma gondii: Homologue of Plasmodium Apical Membrane Antigen 1							
RT	is involved in invasion of Host Cells."							
RL	Infect. Immun. 68:7078-7086(2000).							
DR	EMBL: AF010264; AAB65410.1; -							
DR	InterPro: IPR003298; Apmem_Agl.							
DR	Pfam: PF02430; AMA-1; 1.							
DR	PRINTS: PRO1361; MEROZOITESA.							
DR	SEQUENCE 541 AA; 59978 MW; DD38BF3A0F258E27 CRC64;							

Query Match 100.0%; Score 2922; DB 5: Length 541;
Best Local Similarity 100.0%; Pred. No. 1.2e-245; Indels 0; Gaps 0;
Matches 541; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy	1	MGLVGVQVLVLVADCTIFASGLSSSTRSBSQTLASSTSGNPFQAVNEMKTFERNLTL	60
Db	1	MGLVGVQVLVLVADCTIFASGLSSSTRSBSQTLASSTSGNPFQAVNEMKTFERNLTL	60
Oy	61	HHHOSGIYVDIGQKEVDGTLTYREPAGLCPIWGRIELQOPDRLPYRNPFLEVDVTEKEY	120
Db	61	HHHOSGIYVDIGQKEVDGTLTYREPAGLCPIWGRIELQOPDRLPYRNPFLEVDVTEKEY	120

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QY 121 KOSGNPLPGCFNLNFTVTPSGGRIISPPMELLEKNISIKASTLDGRCARFAFTVAMDKN 180
DB 121 KOSGNPLPGCFNLNFTVTPSGGRIISPPMELLEKNISIKASTLDGRCARFAFTVAMDKN 180
QY 181 KATKRRYPVYVSKKRLCHILVYSQMLMEGKKYCSVKGEPDLYWCYCFKRSVTENHNL 240
DB 181 KATKRRYPVYVSKKRLCHILVYSQMLMEGKKYCSVKGEPDLYWCYCFKRSVTENHNL 240
QY 241 IYGSAYVGENPDPAFISKCPNOLRGFRGVWKKGRCLDYTELTDYVIERVESKACQWKT 300
DB 241 IYGSAYVGENPDPAFISKCPNOLRGFRGVWKKGRCLDYTELTDYVIERVESKACQWKT 300
QY 301 FENDGVAASQPHHTYPLTTSQASNDMDWPHLQSDQPHSGGVRGVRGYVDTTTEGCALSD 360
DB 301 FENDGVAASQPHHTYPLTTSQASNDMDWPHLQSDQPHSGGVRGVRGYVDTTTEGCALSD 360
QY 361 QVPDCLVSDSAVSYTAAGSLSEETPNFIIPSNPSVTPTPTALQCTADKPPDSFGACD 420
DB 361 QVPDCLVSDSAVSYTAAGSLSEETPNFIIPSNPSVTPTPTALQCTADKPPDSFGACD 420
QY 421 VQACRKQKTSVGVGQIQTSTVDTADDEQNEGCSNTALLIAGLAVGVLLALLGGGCFYAK 480
DB 421 VQACRKQKTSVGVGQIQTSTVDTADDEQNEGCSNTALLIAGLAVGVLLALLGGGCFYAK 480
QY 481 RLDNRKGVQAAHHEHFQSDRGARKRPSDLMQEAEPFWDABEENIEDDGETHWVEGD 540
DB 481 RLDNRKGVQAAHHEHFQSDRGARKRPSDLMQEAEPFWDABEENIEDDGETHWVEGD 540
QY 541 Y 541
DB 541 Y 541

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RESULT 2

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QY 094661 PRELIMINARY; PRT; 622 AA.
DB 094661, Q25744, 02, Created
QY 01-FEB-1997 (Tremblrel. 02, Last sequence update)
DB 01-FEB-1997 (Tremblrel. 02, Last sequence update)
QY 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DB 01-MAR-2003 (Tremblrel. 23, Last annotation update)
QY AMA-1 OR PPI 0344.
DB AMA-1 OR PPI 0344.
QY Plasmodium falciparum (isolate 3D7).
DB Plasmodium falciparum (isolate 3D7).
QY Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
DB Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
QY NCB1_Taxid=36329;
DB NCB1_Taxid=36329;
QY SEQUENCE FROM N.A.
DB SEQUENCE FROM N.A.
QY STRAIN=3D7;
DB STRAIN=3D7;
QY tme J.A., Lauer D.E., Smith D.M., Wellde B.T., Schultzeis P.,
DB tme J.A., Lauer D.E., Smith D.M., Wellde B.T., Schultzeis P.,
QY Ware L.A., Kaufman E.B., Wirtz R.A., de Taisne C., Hui G.S.N.,
DB Ware L.A., Kaufman E.B., Wirtz R.A., de Taisne C., Hui G.S.N.,
QY Chang S.P., Church P., Hollingdale M.R., Kaslow D.C., Hoffman S.,
DB Chang S.P., Church P., Hollingdale M.R., Kaslow D.C., Hoffman S.,
QY Guico K.P., Bailou W.R., Sadoff J.C., Paolietti E.;
DB Guico K.P., Bailou W.R., Sadoff J.C., Paolietti E.;
QY Infect. Immun. 64:0-0(0).
DB Infect. Immun. 64:0-0(0).
QY SEQUENCE OF 9-604 FROM N.A.
DB SEQUENCE OF 9-604 FROM N.A.
QY STRAIN=3D7;
DB STRAIN=3D7;
QY MEDLINE=2225705; PubMed=12368864;
DB MEDLINE=2225705; PubMed=12368864;
QY Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
DB Gardner M.J., Hall N., Fung E., White O., Berriman M., Hyman R.W.,
QY Elisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyse S.,
DB Elisen J.A., Rutherford K., Salzberg S.L., Craig A., Kyse S.,
QY Chan M.-S., Nene V., Shallow S.J., Sun B., Peterson J., Angiolini S.,
DB Chan M.-S., Nene V., Shallow S.J., Sun B., Peterson J., Angiolini S.,
QY Perera M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
DB Perera M., Allen J., Selengut J., Haft D., Mather M.W., Vaidya A.B.,
QY Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
DB Martin D.M.A., Fairlamb A.H., Fraunholz M.J., Roos D.S., Ralph S.A.,
QY McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
DB McFadden G.I., Cummings L.M., Subramanian G.M., Mungall C.,
QY Venner J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,
DB Venner J.C., Carucci D.J., Hoffman S.L., Newbold C., Davis R.W.,

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RA Fraser C.M., Barrell B.;
RT "Genome sequence of the human malaria parasite Plasmodium
RT falciparum.";
RL Nature 419:498-511(2002).
DR EMBL; U65407; AAB36701.1; -
DR EMBL; U33274; AAC47104.1; -
DR EMBL; AE014841; AAN35928.1; -
DR InterPro; IPR003298; Apmem_Agl.
DR Pfam; PF02430; AMA-1; 1.
DR PRINTS; PRO1361; MERKOZITESA.
SQ SEQUENCE 622 AA; 72041 MW; 60FE442074C38E94 CRC64;

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Query Match 14.9%; Score 434; DB 5; Length 622;
Best Local Similarity 26.4%; Pred. No. 6.6e-29;
Matches 150; Conservative 84; Mismatches 213; Indels 122; Gaps 24;

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QY 41 GNPFOANVEMKTFMERFNLTHHOSGIYVDIGQDEVDGTLRYEBAGLCPIWKGHIELOQ 100
DB 107 GNPW-----TEYMAKYDIEEVHSGSIRVDIGDAEAVAGTQYRLPSGCKPVGKGIILEN 160
QY 101 PDRLRYNNFEDPTEKEYQSGNPLPGCFNLNFTVTPSGGRIISPPME-----LLEKSN 156
DB 161 SN-----TFTLTPVATGNQYLKD-----GGFAF--PTEPLMSPMTLDEMRHFYKDKY 207
QY 157 IKASTDLGRCAEFKFTVAMDKNNKATKRYRPFVYDSKKRLCHILVYSQMLMEGKKYCSV 216
DB 208 VKNDELTLCSRHAGNMT--PDNDKSNYKTPAYVDDKDKCHILYIAQENNGRNYCN- 264
QY 217 KGEPPDLTWYCFKPKSVTENHNLVYSAYVGEN-PDAFISKCPNOLRGFRGVWKKGR 275
DB 265 KDESRRNSMFCFRPAKDISFONY-----TYLSKVVDWMEKVCPRKNLQNNKFKGLVMDGN 319
QY 276 CLDYTELTD-VYIERVESKACQWKTFFENDGVAASQPHHTP--LTSQASNDMDWPF----- 327
DB 320 CEDIPHNEFPALIDFE---CNKLVFELS--ASDPKPYQOHLDYKIEKGFNKRNAS 373
QY 328 -----LHSDQPHSGGVRGVRGYVDTTTEGCALSDQVPDCLVSDSAVSYTA 377
DB 374 MKSAFLPTGAFCADRYSHGKGYWGNYNETQ---KCELFNVKPTLLINSSYIATTA 430
QY 378 AGSLSEETPNFIIPSN-----PSYTPPTPTAL 405
DB 431 LSHPIEVENNPF--PCLYKDEIMKEIERESKRIKINDNDGNNKIIAPRIFISDDKSL 488
QY 406 OCTAPKFPDROACQVQACRKQKTSVGVGQIQTSTVDTA-----DEQNEGCSN----- 454
DB 489 KCPCDPEMVSNTGCFEVCK-----CVERRAVTSNNVNVVKEEYKDYADIPHEKPTTD 543
QY 455 --TALIAGLAVGVLLALLGGGCFYAKRLDNRKGVQAAHHEHFQSDRGARKRPSDLM 512
DB 544 KKKIILASSAAVAVLATILM---VLYYKR-----KONAKYDKMDERPODYGKNSNR-NDEN 595
QY 513 OEAPSPFWDABEENIEDDGETHWVEGDY 541
DB 596 LDPEASFWGEER---RASHTPVLMEMKPY 621

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RESULT 3

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QY 0967K3 PRELIMINARY; PRT; 622 AA.
DB 0967K3, Q25744, 02, Created
QY 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DB 01-DEC-2001 (Tremblrel. 19, Last sequence update)
QY 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DB 01-MAR-2003 (Tremblrel. 23, Last annotation update)
QY Apical membrane antigen-1 (Fragment).
DB Apical membrane antigen-1 (Fragment).
QY AMA-1.
DB AMA-1.
QY Plasmodium falciparum.
DB Plasmodium falciparum.
QY Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
DB Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
QY NCB1_Taxid=5833;
DB NCB1_Taxid=5833;
QY SEQUENCE FROM N.A.
DB SEQUENCE FROM N.A.
QY STRAIN=VEN760;
DB STRAIN=VEN760;
QY MEDLINE=21192561; PubMed=11295182;
DB MEDLINE=21192561; PubMed=11295182;

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RA Escalante A.A., Grebert H.M., Chaiyaraj S.C., Magris M., Biswas S.,
 RA Nahlen B.L., Lal A.A.;
 RT "Polymorphism in the gene encoding the apical membrane antigen-1 (AMA-
 RT 1) of Plasmodium falciparum. X. Asembo Bay Cohort Project.";
 RL Mol. Biochem. Parasitol. 113:279-287(2001).
 RN [2]
 RC SEQUENCE FROM N.A.
 RC STRAIN=VEN760;
 RA Ananias E.A., Grebert H.M., Chaiyaraj S.C., Magris M., Biswas S.,
 RA Nahlen B.L., Lal A.A.;
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY016412; AAGS0119.1; -
 DR InterPro: IPR003298; Apmem_Ag1.
 DR Pfam: PF02430; AMA-1; 1.
 DR PRINTS: PR01361; MEROZOITESA.
 DR NON TER 622 622
 FT SEQUENCE 622 AA; 72016 MW; AFCA807826A9CBA CRC64;
 SQ
 Query March 14.8%; Score 433; DB 5; Length 622;
 Best Local Similarity 25.9%; Pred. No. 8e-29;
 Matches 147; Conservative 86; Mismatches 215; Indels 120; Gaps 23;
 QY 41 GNPFQAVNEMKTFMERFNLTHHOSGIYVDLGODKEVDGTLYRBPAGLCPIWGHIELOQ 100
 DB 107 GNPF-----TEWAKVDIEVHSGIRVDLGEDEAVAGTQRLPSGKCPVFGKGIILEN 160
 QY 101 PDRLPYRNPFLEDPVTEKEYGKSGNPLPGFNLNVTPSGQRISPPME-----LLEKSN 156
 DB 161 SN-----TFLTPATGNOQLKD-----GGRFAP--PTEPHMSPTLIDENRHFYKDKY 207
 QY 157 IKASTDLGRCAEFAFKTVAMDKNKATKYRYPVYDSKKRLCHILYVSMQMEGKKYCSV 216
 DB 208 VKNDDELTLCSRHAGNM--PDNDKSNYKYPAYVDKDKKCHILYIAQENNGPRYCN- 264
 QY 217 KGEPPDLTWYCFKPKSKVTENHNLIGSAVYGEN-PDAFISKCPNOLRGYRFGYWKGR 275
 DB 265 KDQSIIRNSMFCFRPAKDISFQNY-----TYSKNNVDMWEKCPKRNLENNAKFGIWDGN 319
 QY 276 CLDYTELDTVIERVESKACQCVKTFENDGVAVDQHTYP--LTSQASNDMP----- 327
 DB 320 CEDLPDVEF---SANDLFECKNLVFEIS--ASDQPKQYEQHLDYEKIKEGFKNKNASM 374
 QY 328 -----LHSDQPHSGVGRNNGFYVDITGEGKCALSDQVPCLVSDSAVSYTA 378
 DB 375 IKSAFLPTGAKADRYKSHGKGMGNVNTET--HKCEIFNVKPTCLINNSYIATATL 431
 QY 379 GSLSSEETNFIIPSN-----PSTPPTPETALQ 406
 DB 432 SHPTEVENNF--PCSLYKDEIMKEIERESKRILKNDNDGKIKLIAPRIEISDDKSLK 489
 QY 407 CTADKFPDSFGACDVQACRQKTSVGGQIQSTSVDTA-----DEQNEGGSN----- 454
 DB 490 CPCDPEWVNSSTCRPFVCK-----CVERRAEVTSSNNEVVVKEBYKDEYADIPHKPTPD 544
 QY 455 -TALIAGLVGVLALLLGGCYFAKRLDRNKGVQAAHHEHFEFOSDRGAKKPPSDLMQ 513
 DB 545 MKIIIASAANAVALATILM---VYLKRR---KGAKEKYDKMDERODYGSNSR-NDENL 596
 QY 514 EAPSPFMDAEENIBODEGTHVMVEGDY 541
 DB 597 DPEASFVGEER--RASHTTFLVMEKPY 621
 RESULT 4
 Q25745 PRELIMINARY; PRT; 592 AA.
 AC Q25745;
 DT 01-NOV-1996 (Tremblrel. 01. Created)
 DT 01-NOV-1996 (Tremblrel. 01. Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23. Last annotation update)
 DE Apical membrane antigen-1 (fragment).
 GN AMA-1.
 OS Plasmodium falciparum.

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 RN NCB1_TaxID=5833;
 RX [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CMPI;
 RC MEDLINE=96147889; PubMed=8556798;
 RX Zhang L.X., Zhan B., Wang J., Feng X.;
 RT "Sequence analysis of apical membrane antigen 1 from a Plasmodium
 RT falciparum isolate collected from Mengpeng Township, Yunnan
 RT Province.";
 RL Chung Kuo Chi Sheng Chung Hsueh Yu Chi Sheng Chung 13:203-208(1995).
 RN [2]
 RC SEQUENCE FROM N.A.
 RC STRAIN=CMPI;
 RX MEDLINE=96379227; PubMed=8784778;
 RA Marchall V.M., Zhang L., Anders R.F., Coppel R.L.;
 RT "Diversity of the vaccine candidate AMA-1 of Plasmodium falciparum.";
 RL Mol. Biochem. Parasitol. 77:109-113(1996).
 DR EMBL: U33275; AAC47105.1; -
 DR InterPro: IPR003298; Apmem_Ag1.
 DR Pfam: PF02430; AMA-1; 1.
 DR PRINTS: PR01361; MEROZOITESA.
 DR NON TER 1 1
 FT SEQUENCE 592 AA; 68412 MW; 5496A73680E7128C CRC64;
 SQ
 Query March 14.8%; Score 432.5; DB 5; Length 592;
 Best Local Similarity 26.7%; Pred. No. 8.3e-29;
 Matches 147; Conservative 77; Mismatches 202; Indels 125; Gaps 23;
 QY 41 GNPFQAVNEMKTFMERFNLTHHOSGIYVDLGODKEVDGTLYRBPAGLCPIWGHIELOQ 100
 DB 95 GNPF-----TEWAKVDIEVHSGIRVDLGEDEAVAGTQRLPSGKCPVFGKGIILEN 148
 QY 101 PDRLPYRNPFLEDPVTEKEYGKSGNPLPGFNLNVTPSGQRISPPME-----LLEKSN 155
 DB 149 SN-----TFLTPATGTEKODLKDGFAPF-----PTNPLMSPTLIDMRLLYKONE 194
 QY 156 NIKASTDLGRCAEFAFKTVAMDKNKATKYRYPVYDSKKRLCHILYVSMQMEGKKYCS 215
 DB 195 DVKULDELTLCSRHAGNM--PDNDKSNYKYPAYVDKDKKCHILYIAQENNGPRYCN 252
 QY 216 VKGEPPDLTWYCFKPKSKVTENHNLIGSAVYGEN-PDAFISKCPNOLRGYRFGYWKGR 274
 DB 253 -KDQSKNSMFCFRPAD-----KLFQNYTYSKNNVDMWEKCPKRNLOAKFGIWDG 306
 QY 275 RCLDYTELDTVIERVESKACQCVKTFENDGVAVDQHTYP--LTSQASNDMP----- 327
 DB 307 NCEDIPIVNEF---SANDLFECKNLVFEIS--ASDQPKQYEQHLDYEKIKEGFKNKVAS 361
 QY 328 -----LHSDQPHSGVGRNNGFYVDITGEGKCALSDQVPCLVSDSAVSYTA 377
 DB 362 MIKSAFLPTGAKADRYKSHGKGMGNVNTET--HKCEIFNVKPTCLINNSYIATTA 418
 QY 378 AGSLSEETNFIIPSN-----PSTPPTPETAL 405
 DB 419 LSHIIEVENNF--PCSLYKDEIMKEIERESKRILKNDNDGKIKLIAPRIEISDDKSL 476
 QY 406 QCTADKFPDSFGACDVQACRQKTSVGGQIQSTSVDTA-----VDCTAD--EQNEGGS 453
 DB 477 KCPDPEWVNSSTCRPFVCK-----CVERRAEVTSSNNEVVVKEBYKDEYADIPHKPTPD 531
 QY 454 NTALI-----AGLVGVLALLLGGCYFAKRLDRNKGVQAAHHEHFEFOSDRGAKKPPS 509
 DB 532 NMKIIIASAANAVALATILM---VYLKRR---KGAKEKYDKMDERODYGSNSR-N 580
 QY 510 DLMQAEPSFW 520
 DB 581 DEMDPEASFV 591
 RESULT 5
 Q967K2

ID 0967K2 PRELIMINARY; PRT; 622 AA.
 AC 0967K2.
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Apical membrane antigen-1 (Fragment).
 GN AMA-1.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 ON NCBI_taxid=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=08-0697;
 RA Escalante A.A., Grebert H.M., Chaiyaraj S.C., Magris M., Biswas S.,
 RA Nahlen B.L., Lal A.A.;
 RT "Polymorphism in the gene encoding the apical membrane antigen-1 (AMA-1) of Plasmodium falciparum. X. Aeombo Bay Cohort Project."
 RL Mol. Biochem. Parasitol. 113:279-287(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=08-0697;
 RA Ananias E.A., Grebert H.M., Chaiyaraj S.C., Magris M., Biswas S.,
 RA Nahlen B.L., Lal A.A.;
 RT Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.
 RL EMBL, AY016413; AAG50120.1;
 DR InterPro; IPR003298; Apmem_Ag1.
 DR Pfam; PF02430; AMA-1; 1.
 DR PRINTS; PR01361; MEROZOITESA.
 DR NON TER 622
 FT SEQUENCE 622 AA; 72038 MW; 918543446A57E30 CRC64;

Query Match 14.8%; Score 431; DB 5; Length 622;
 Best Local Similarity 25.9%; Pred. No. 1.2e-28;
 Matches 147; Conservative 85; Mismatches 216; Indels 120; Gaps 23;

QY 41 GNPFGANVEMKTFMERFNLTHHOSGIYVDLGQDKEVDTLYRBPAGLCPIWGKHIELOQ 100
 DB 107 GNPW-----TEYMAKYDIEVHSGIRVLDGEBAEVAQTLYRLPSGKCPVFGKGIIEEN 160
 QY 101 PDRLPYRNPFLEDPVTEKEYKQSGNPPLPGGFNLNFTVPSGORISPPMB-----LLEKSN 156
 DB 161 SN-----TTFLLPVATENGQYLKD-----GGFAF-----PTEPHMSPTLDMKHFYKDNKY 207
 QY 157 IKASTDLGRCAEFAKTYAMDKNNKATKRYPPVYDSKKRLCHILYVSKQMLEGKKYCSV 216
 DB 208 VGNLDELTLCSRHAGNMII--PDNDKSNYKYPAYVDDKDKCHILYIAOENNGPRYCN- 264
 QY 217 KGEPPDLTMVCPKPKRSVTENHLLYGSAYVGEN--PDAFISCPNOLRGVFGVWKKGR 275
 DB 265 KDQGRNSMFCFRPAKDISFONY-----TYSKNNVVDNMEKVCPRKLNENAKFGLWVDON 319
 QY 276 CLDYTELTDTVIERVESKAQCWVTFENDGVASDOPHTYP--LTSQASWMDWMP----- 327
 DB 330 CEDIDHVNPF--SANDLFECKKLVPFLS--ASDQKQYEQHLTDYEKIKEGFKNNKNSM 374
 QY 338 -----LHOSDQPHSGVGRNNGFYVDTTGGSKCLSDQVPCLVSDSAANSYRA 378
 DB 375 IKSAPFLPTGAFKADRYKSHGKGYMGNVNTET--HKCEIFVWKPKCLINNSYIATTL 431
 QY 379 GSLSETPFIIPSN-----PSVTPTPTETALQ 406
 DB 432 SHPTVENNF--PCSLYKDEIKKEIERESKRITKLANDNEGKKTIAPIFISDDKDSLK 489
 QY 407 CTADKFPDSFGACDVQACRKQKTSVCGQIOGSTVDTCTA-----DEONECGSN----- 454
 DB 490 CPCDEMNVSNTCRFPVCK-----CYERAEVTSNNNEVVVKEEYDEVADIPEHKPTYDK 544
 QY 455 -TALLAGLAVGVLALLGGGCTYFAKRLDRNKGVQAAHNEHFQSDRARKKRPSDLMO 513
 DB 545 MKIIIASAANAVLATILM-----VLYKR-----KGAKEYDKMDEPOHYGKNSNR-NDENL 596
 QY 514 EAEPSPWDAEENIEDGETHVWVEGDY 541

DB 597 DPEASFVGEERK---RASHTPVLMEKEY 621

RESULT 6

Q9GZ05 PRELIMINARY; PRT; 622 AA.

ID 09GZ05
 AC 09GZ05.
 DT 01-MAR-2001 (Tremblrel. 16, Created)
 DT 01-MAR-2001 (Tremblrel. 16, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE Apical membrane antigen 1.
 GN AMA-1.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 ON NCBI_taxid=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FCCL1/HN;
 RA Shan Z.X., Yu X.B., Li X.R., Ma C.L., Fang J.M.;
 RT "Cloning and structure of apical membrane antigen 1 (AMA-1) gene of Plasmodium falciparum isolate FCCL1/HN."
 RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF277003; AAG01325.1;
 DR InterPro; IPR003298; Apmem_Ag1.
 DR Pfam; PF02430; AMA-1; 1.
 DR PRINTS; PR01361; MEROZOITESA.
 DR NON TER 622
 FT SEQUENCE 622 AA; 72045 MW; 69045E66776C3BBB CRC64;

Query Match 14.8%; Score 431; DB 5; Length 622;
 Best Local Similarity 26.4%; Pred. No. 1.2e-28;
 Matches 151; Conservative 83; Mismatches 209; Indels 130; Gaps 25;

QY 41 GNPFGANVEMKTFMERFNLTHHOSGIYVDLGQDKEVDTLYRBPAGLCPIWGKHIELOQ 100
 DB 107 GNPW-----TEYMAKYDIEVHSGIRVLDGEBAEVAQTLYRLPSGKCPVFGKGIIEEN 160
 QY 101 PDRLPYRNPFLEDPVTEKEYKQSGNPPLPGGFNLNFTVPSGORISPPMB-----EKNS 155
 DB 161 S-----KTFLLPVATENGQYLKDGGFAF-----PTEPHMSPTLDMKHFYKDNKY 206
 QY 156 NIKASTDLGRCAEFAKTYAMDKNNKATKRYPPVYDSKKRLCHILYVSKQMLEGKKYCS 215
 DB 207 YVKNLDELTLCSRHAGNMII--PDNDKSNYKYPAYVDDKDKCHILYIAOENNGPRYCN 264
 QY 216 VKGEPPDLTMVCPKPKRSVTENHLLYGSAYVGEN--PDAFISCPNOLRGVFGVWKK 273
 DB 265 -KDESKRNSMFCFRPAKDKLFENY-----TYSKNNVVDNMEVCPKRNLENAKFGLWVD 317
 QY 274 GRCLDYTELTDTVIERVESKAQCWVTFENDGVASDOPHTYP--LTSQASWMDWMP----- 327
 DB 318 GNCEIDIPHVNPF--SANDLFECKKLVPFLS--ASDQKQYEQHLTDYEKIKEGFKNNKNSA 372
 QY 338 -----LHOSDQPHSGVGRNNGFYVDTTGGSKCLSDQVPCLVSDSAANSYR 376
 DB 373 SMISAPFLPTGAFKADRYKSHGKGYMGNVNTET--KCEIFVWKPKCLINNSYIATTL 429
 QY 377 AAGSLSETPFIIPSN-----PSVTPTPTETALQ 404
 DB 430 ALSHNEVENNF--PCSLYKDEIKKEIERESKRITKLANDNEGKKTIAPIFISDDKDS 487
 QY 405 LOCTADKFPDSFGACDVQACRKQKTSVCGQIOGSTVDTCTA-----VDCTAD--EONECG 452
 DB 488 LKCPDDEPVIIVSNTCRFPVCK-----CYERAEVTSNNNEVVVKEEYDEVADIPEHKPTY 542
 QY 453 SNTALI-----AGLAVGVLALLGGGCTYFAKRLDRNKGVQAAHNEHFQSDRARKKR 508
 DB 543 DNMKIIIASAANAVLATILM-----VLYKR-----KGAKEYDKMDEPOHYGKNSNR- 591
 QY 509 SDLMQEAEPSPWDAEENIEDGETHVWVEGDY 541
 DB 592 NDEMIDPEASFVGEERK---RASHTPVLMEKEY 621

RESULT 7
ID 0967K1 PRELIMINARY; PRT; 622 AA.
DB 0967K1
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Apical membrane antigen-1 (Fragment).
GN AMA-1.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=VEN766;
RX MEDLINE=21192561; PubMed=11295182;
RA Escalante A.A., Grebert H.M., Chaiyaraj S.C., Magris M., Biswas S.,
RA Nahlen B.L., Lal A.A.;
RT "Polymorphism in the gene encoding the apical membrane antigen-1 (AMA-1) of Plasmodium falciparum. X. Asambo Bay Cohort Project."
RL Mol. Biochem. Parasitol. 113:279-287(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=VEN766;
RA Ananias E.A., Grebert H.M., Chaiyaraj S.C., Magris M., Biswas S.,
RA Nahlen B.L., Lal A.A.;
RT Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY016414; AAG50121.1;
DR InterPro; IPR003298; Apmem_Ag1.
DR Pfam; PF02430; AMA-1; 1.
DR PRINTS; PRO1361; MERZOITESA.
FT NON TER 622
SQ SEQUENCE 622 AA; 7186 MW; 58A92EA691CD6F21 CRC64;
Query Match 14.8%; Score 431; DB 5; Length 622;
Best Local Similarity 26.2%; Pred. No. 1.2e-28;
Matches 149; Conservative 86; Mismatches 212; Indels 122; Gaps 24;
DB 41 GNPFQAVNEMKTEMERENLTHHOSGIYVDLGDQKXVDGTLTYRPAAGLCPIWGHIELOQ 100
DB 107 GNPF-----TEYAKYDIEKHSGIRVDLGEDAEVAGTQYRLPSGKCVFGKGIIEEN 160
QY 101 PDRLPYNNFLEDPTEKEYKQSGNPLPGGFNLNFTVPSGQRISPPFME-----LLEKNSN 156
DB 161 SN-----TTLTPTATNGQYKID-----GGRAF--PPTBPLMSPTLIDENRHHYKDKY 207
QY 157 IKASTDLGRCAEFKTVAMDKNKATKYRYPFYVDSKRLCHILYVSMQLMGKRYCSV 216
DB 208 VKNLDELTLCSRHAGNM--PDNDKNSNYKYPAYVDDKKCHILYIAQENNGPRYCN- 264
QY 217 KGEPPDLTYCFKPKRKYSTENHLLYGSAYYGEN-PDAFISKCPNOLRGIRFGYWK 275
DB 265 KDESKNMSMFCRPAKDISFGNY-----TYSKNVNVNWEVCPRKNLQNAKFFGLMVDGN 319
QY 276 CLDYTELTD-TVIRVESKAQCWKTFFENDGVAADOPHTYR--LTQASWMDMP----- 327
DB 320 CEDIPHNESALDFE---CNKLVFELS--ASDQPKQYQGHILTYEIKIEGFKNKAS 373
QY 328 -----LHOSDPHSGGVGNRYFYVDTTGEKCALSDQVPCLVSDSAVSYTA 377
DB 374 MIKSAFLPTGAFAKADRYKSHGKGYMGNVNTETQ--KCEIFNVKPTCLINNSYIATTA 430
QY 378 AGSLSETPFIITSN-----PSTPTPTETA 405
DB 431 LSHDIEVNNF--PCSLYKDEIKIEIRSKRIKLNNDDEGNKIIAPRIFISDDKSL 488
QY 406 QCTADKPPDSFGACDVACRKRKTSVGGQISTVDCTA-----DEONECGSN----- 454
DB 489 KCPDPEIVSNSTGNFVCK-----CYEKRAEYVSNNEVVYKRYKDEYADIPHKPT 543
QY 455 --TALLGLAVGVLLALLGGGCGYFAKRLDRNKGVAAAHNHEFQSDRGARKRRPDDL 512

DB 544 KMKIISSAAVAVALTILM---VLYKR----KGNAEKYDKDEPOHYGKNSNR-NDEN 595
QY 513 QEAPSPFWEAEENIEODGETHWVEGDY 541
DB 596 LDPEASFWEK--RASHTPVLMKEPY 621
RESULT 8
ID 0967J3 PRELIMINARY; PRT; 622 AA.
DB 0967J3
DT 01-DEC-2001 (TrEMBLrel. 19, Created)
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Apical membrane antigen-1 (Fragment).
GN AMA-1.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2180;
RX MEDLINE=21192561; PubMed=11295182;
RA Escalante A.A., Grebert H.M., Chaiyaraj S.C., Magris M., Biswas S.,
RA Nahlen B.L., Lal A.A.;
RT "Polymorphism in the gene encoding the apical membrane antigen-1 (AMA-1) of Plasmodium falciparum. X. Asambo Bay Cohort Project."
RL Mol. Biochem. Parasitol. 113:279-287(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=2180;
RA Ananias E.A., Grebert H.M., Chaiyaraj S.C., Magris M., Biswas S.,
RA Nahlen B.L., Lal A.A.;
RT Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AY016438; AAG50145.1;
DR InterPro; IPR003298; Apmem_Ag1.
DR Pfam; PF02430; AMA-1; 1.
DR PRINTS; PRO1361; MERZOITESA.
FT NON TER 622
SQ SEQUENCE 622 AA; 71975 MW; 4B34652F36364455 CRC64;
Query Match 14.6%; Score 426; DB 5; Length 622;
Best Local Similarity 26.5%; Pred. No. 3.3e-28;
Matches 152; Conservative 81; Mismatches 210; Indels 130; Gaps 25;
DB 41 GNPFQAVNEMKTEMERENLTHHOSGIYVDLGDQKXVDGTLTYRPAAGLCPIWGHIELOQ 100
DB 107 GNPF-----TEYAKYDIEKHSGIRVDLGEDAEVAGTQYRLPSGKCVFGKGIIEEN 160
QY 101 PDRLPYNNFLEDPTE--KEYKQSGNPLPGGFNLNFTVPSGQRISPPFME-----LLEKNS 155
DB 161 S-----KTLTPTATNQLKOGFAFP-----PTEPLISPTLQMRHLLYKNE 206
QY 156 NIKASTDLGRCAEFKTVAMDKNKATKYRYPFYVDSKRLCHILYVSMQLMGKRYCS 215
DB 207 YVKNLDELTLCSRHAGN--NPNNDKNSNYKYPAYVDEKCHILYIAQENNGPRYCN 264
QY 216 VKGPPDLTYCFKPKR--SVTENHLLYGSAYYGEN-PDAFISKCPNOLRGIRFGYWK 273
DB 265 -KDESKNMSMFCRPAKDKFENY-----TYSKNVNVNWEVCPRKNLENKAFGLMVD 317
QY 274 GRCLDYTELTDYIERVESKAQCWKTFFENDGVAADOPHTYR--PLTQASWMDMP----- 327
DB 318 GNCEDIPIHNEF--SANDLFECKLVFELS--ASDQPKQYQGHILTYEIKIEGFKNKMA 372
QY 328 -----LHOSDPHSGGVGNRYFYVDTTGEKCALSDQVPCLVSDSAVSYT 376
DB 373 SMKSAFLPTGAFAKADRYKSHGKGYMGNVNTETQ--KCEIFNVKPTCLINNSYIAT 429
QY 377 AAGSLSETPNFIIISN-----PSTPTPTETA 404
DB 430 ALSPHNEVNNF--PCSLYKDEIKIEIRSKRIKLNNDDEGNKIIAPRIFISDDKSL 487

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QY 405 LOCADKPPDSFGACDVQACKROKTSVCGGQIOGSTS-----VDCAD--EQNECG 452
DB 488 LKCCPDEIYVNSGTGNFVCK-----CYEKRAEYTSNNEVVVYKDEYADIEBHRTY 542
QY 453 SNTALI-----AGLAVGVLLALLGGGCFPAKRLDRNKGVAAAHHEHFGSDRGARKRP 508
DB 543 DMKIIIIASSAAVAVLATILV-----YLKR-----KG-NAEKYDKMDQPOHYGKSNR 591
QY 509 SDLMQEAEPFWDAAENIEDGGETHVWEGDY 541
DB 592 NDEMIDPEASFWGEEK--RASHTTPLVIMEXY 621

RESULT 9
Q967KO PRELIMINARY; PRT; 622 AA.
ID Q967KO;
AC Q967KO;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Apical membrane antigen-1 (fragment).
GN AMA-1.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=VEN761;
RX MEDLINE=21192561; PubMed=11295182;
RA Escalante A.A., Grebert H.M., Chaiyaraj S.C., Magris M., Biswas S.,
  Nahlen B.L., Lal A.A.;
  "Polymorphism in the gene encoding the apical membrane antigen-1 (AMA-1) of Plasmodium falciparum. X. Asembo Bay Cohort Project.";
  RT 1) of Plasmodium falciparum.
  RL Mo. Biochem. Parasitol. 113:279-287(2001).
  [2]
  RN SEQUENCE FROM N.A.
  RP STRAIN=VEN761;
  RA Ananias E.A., Grebert H.M., Chaiyaraj S.C., Magris M., Biswas S.,
    Nahlen B.L., Lal A.A.;
    Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
  DR EMBL; AY016415; AAG50122.1;
  DR InterPro; IPR003298; Apmem_Agl.
  DR Pfam; PF02430; AMA-1; 1.
  DR PRINTS; PR01361; MEROZOITESA.
  FT NON_TER 622
  SQ SEQUENCE 622 AA; 71853 MW; F44453994D8013B9 CRC64;

Query Match 14.5%; Score 425; DB 5; Length 622;
Best Local Similarity 26.0%; Pred. No. 4e-28;
Matches 148; Conservative 86; Mismatches 213; Indels 122; Gaps 24;

QY 41 GNPQANVEMKTFMERFNLTHHOSGIYVDLQDKEVDGTLVREPAGLCPIGKHIELQ 100
DB 107 GNPW-----TEYMAKYDIEVHGSGIRVLDGEDAEVAGTQYRLPSGKCPVPGKGIIE 160
QY 101 PDRLRYRNFLLEDVPTKEKYGKSGNPLPGCFNLFTVTPSGQISPPME-----LLEKSN 156
DB 161 SN-----TTFPLTPVATGNQYLK-----GGFAP--PPTPEPLMSPTTLDENHFTYDK 207
QY 157 IKASTDLRCGEFAFKTYAMDKNNKATKYRYPFYVDSKRLCHILYVSMQMEGKKYCSV 216
DB 208 VGNLDELTLCSRHAGMI--PNDKNSNKKYAGYDDKOKKCHILYIAQENNGPRYCN- 264
QY 217 KGEPPDLTWYCFKPKRSTENHLLIYGSAYVGEN-PDAFISKCPNOLRGYFGVKKGR 275
DB 265 KQESKNSWFCFRPAKDISFYNY-----TYSKTVVDNWEKVCPRKILQNAKFGJLVN 319
QY 276 CLDYELND-TYIERESKAQCVKTFENDGVAASDPHTYR--LTSQASWNNMWP----- 327
DB 330 CBDIPHVNEFSALDFE---CNKLVFELS--ASDQPKOYEHHLTDYEIKEGFKKNAS 373
QY 328 -----LHSDQPHSGVGRNYGFYVDTTGGKCALSDQVDCLVSDSAVSYTA 377

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DB 374 MISAFLPTGAFKADRYKSHGKGMGNNTETQ---KCEI FNVKPTCLINNSSYIATTA 430
QY 378 AGSLSEETPPIIPSN-----PSVTPTPTETAL 405
DB 431 LSHPIEVENN--PCSLYKQEIKEIERESEBRLTLNNDDEGNKIIAPRFISDDDSL 488
QY 406 QCTADKPPDSFGACDVQACKROKTSVCGGQIOGSTVDCIA-----DEONECGSN----- 454
DB 489 KCPCDPEIYVNSGTGNFVCK-----CYEKRAEYTSNNEVVVYKDEYADIEBHRTY 543
QY 455 -TALLGLAVGVLLALLGGGCFPAKRLDRNKGVAAAHHEHFGSDRGARKRP 512
DB 544 KMKIIIIASSAAVAVLATILM-----YLKR-----KGNAEKYDKMDQPOHYGKSNR-ND 595
QY 513 QEAEPFWDAAENIEDGGETHVWEGDY 541
DB 596 LDPEASFWGEEK--RASHTTPLVIMEXY 621

RESULT 10
Q25687 PRELIMINARY; PRT; 558 AA.
ID Q25687;
AC Q25687;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
DE Apical membrane antigen 1.
GN AMA-1.
OS Plasmodium chabaudi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5825;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=DS;
RX MEDLINE=96333375; PubMed=8757869;
RA Crewther P.E., Matthew M.L., Flegg R.H., Anders R.F.;
  "Protective immune responses to apical membrane antigen 1 of
  Plasmodium chabaudi involve recognition of strain-specific epitopes.";
  RT Infect. Immun. 64:3310-3317(1996).
  DR EMBL; U49743; AAB36509.1;
  DR InterPro; IPR003298; Apmem_Agl.
  DR Pfam; PF02430; AMA-1; 1.
  DR PRINTS; PR01361; MEROZOITESA.
  SQ SEQUENCE 558 AA; 63996 MW; 1DB43DF0E268DE63 CRC64;

Query Match 14.5%; Score 422.5; DB 5; Length 558;
Best Local Similarity 26.3%; Pred. No. 5.6e-28;
Matches 150; Conservative 94; Mismatches 191; Indels 135; Gaps 24;

QY 42 NPOANVEMKTFMERFNLTHHOSGIYVDLQDKEVDGTLVREPAGLCPIGKHIELQ 101
DB 53 NPWE-----KFMKYDIEKHGSGIRVLDGEDAEVAGTQYRLPSGKCPVPGKGIIE 106
QY 102 DRLPYRNFLLEDVPT-KEKYGKSGNPLPGCFNLFTVTPSGQISPPME-----ELLEKSN 156
DB 107 TK-----SFLPVPVATGDKVREGGLAP-----KADNVISFVLLQNLREMYKHE 152
QY 157 IKASTDLRCGEFAFKTYAMDKNNKATKYRYPFYVDSKRLCHILYVSMQMEGKKYCSV 216
DB 153 IIALNDMSLCAKHA--SFFVGNNSNNSAYRHPAVYDKNNKCYILYVAAQENMGGRYCS- 209
QY 217 KGEPPDLTWYCFKPKRSTENHLLIYGSAYVGENPDAFISKCPNOLRGYFGVKKGR 276
DB 210 NEENNENPFCPTPKK-DEYKNLSYLTKNLRED---METGCPNNSIQNAKFGVVDGVC 265
QY 277 LDY--TELTDYIERESKAQCVKTFENDGVAASDPHTY----- 314
DB 266 SEYCKEYVHDS-----KSLSECNRIYF--DSASDQPKOYEHHLTDYEIKEGFKKNAS 318
QY 315 -----ELTQASWNNMWP-LHSDQPHSGVGRNYGFYVDTTGGKCALSDQVDCLV 367
DB 319 LIGALLPLIGS-----YRADQVSKGKGMGNNTETQ---DKKEKCYIIPNKPTCL 365

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Qy 368 SDSAAVSTAAAGSLSEETPNFIPSN-----PSVTPPT 400
Db 366 NDKRFVATTTALSSL-EEAPSEFPDIIYKKIAEIKVMNVNRNNNGDITKFPRIIFSD 424
Qy 401 PETALQCADKFPDSFGACDVQAC---KROKTSVGOIOGSTVDTCTADEONEGSGS--- 453
Db 425 DKESLKCEPPTQLTQSSCNFPVCNCEVKRQFIS-----ENNEVEIIDEFESEESPIN 478
Qy 454 -NTALLGLAVGVLLALLGGGCFPAKRLDRNKGVQAAHHEHFQSDRGARKRPSDL 511
Db 479 QRMIIITLITAGLALLSLT---FYFK---SNK--PGDDYDKRGQADYTKAKOSRDE 530
Qy 512 MQEAEPSPWDEAENIEQDGETHWVWEGDY 541
Db 531 MLDEPVSFWGEDK---RASHTTPVLMKEPY 557

RESULT 11
ID 061130' PRELIMINARY; PRT; 562 AA.
AC 061130;
DT 01-AUG-1998 (TREMBLrel. 07, Created)
DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
DE 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
GN AMA1.
OS Plasmodium vivax.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5855;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=Sal 1;
RX MEDLINE=99389346; PubMed=10462250;
RA Rogers W.O., Gowda K., Hoffman S.L.;
RT "Construction and immunogenicity of DNA vaccine plasmids encoding four
RL Vaccine 17:3136-3144 (1999).
DR EMBL; AF063138; AAC16731.1; -
DR InterPro; IPR003298; Apmem_Ag1.
DR Pfam; PF02430; AMA-1; 1.
DR PRINTS; PR01361; MEROZOITESA.
KW Merozoite.
SQ SEQUENCE 562 AA; 64477 MW; 51B441344AD807FD CRC64;

Query Match 14.4%; Score 422; DB 5; Length 562;
Best Local Similarity 25.5%; Pred. No. 6.3e-28;
Matches 157; Conservative 90; Mismatches 232; Indels 136; Gaps 28;

Qy 6 VQVLLVAVDCTIFASGL-----SSSTRS-----RESQTLAST-SGNPFOANVEKMT 52
Db 4 IYIIFLSAQCLVHIGKGRNQKPSRLTRSANVLEKGPVTERSTRSNPW-----KA 57
Qy 53 FMERFNLTHHOSGIYVDLGDQKEVDGTLREPAGLCPWGHKIELQOPDLRYNNFLE 112
Db 58 FMEKVDIRHTSSSGRVLDLGEDAEVNAKYRIIPARCEVFGKGIYENS-----VSFLR 112
Qy 113 DVPT-EKEYKOSGNPLPGFNLNFTPSGORISPPM-----ELLEKSNIKASTDLGCA 167
Db 113 PVAAGDQQLKQGGFAFPN-----ANDHISPMTLANLKERYKDYENMKMLNDIALCR 163
Qy 168 EFAFKTV-AMDKNNKATYRYPFYDSSKRLCHILYVSMQMEGKKYCSVKGPEPDLTWY 226
Db 164 THAASFVWAGDQN---SSYRHPAVYDEKCKTCHMLYLSAQENMGGRYCSPPAQNDAY-F 219
Qy 227 CFKPKKSVT-ENHHLIYGSAYGENPDAFISKCPNOLRGYRFGVWKKGRCLDYTELDT 285
Db 220 CFKPKKSNFEN--LVYLSKVRNDW---KKCPKKNLGNKAFGLVWGNCEIEIYVXEV 274
Qy 286 VIERVESAAQCVKTFENDGVASDOPHTYPLTQSASWMDWMLHQ----- 330
Db 275 ---EAEDREKCRIRYF--GASASDOPYOT---EEEMTDYQKIQGGFPQNNEMIKSAFL 325
Qy 331 -----SDPHSGGVGRNYGYVDTTGEKCALSDQVDCIIVSDAAVSTAAAGSLSE- 383

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Db 326 PVGAFNSDNFKSKRGFWMANF---DSYKCKCYIFNTKPTGLINDKNFIATTLASHPEV 382
Qy 384 --ETPNFIIPSN-----PSVTPPTPETALQCADKFPDSFG 417
Db 383 DLEFPCSIYKDEIEREIKOSRNNMLYSVDGERVLPRIIFISNDKESIKCEPERISNS 442
Qy 418 ACYVQACRKRQKTSV--GGQIOGSTVDTCTADEONEGSGN-----TALIAGLAVGV 466
Db 443 TGNFYVC-----NCEKRAELKENNQVYIKPEPRDYENGSEKSNKQMLIITIGI-TCGV 496
Qy 467 LLLALLGGGCFPAKRLDRNKGVQAAHHEHFQSDRGARKRPSDLMQEAEPSPWDEAEN 526
Db 497 CVVA-LASMAFYFRKKANNDK-----YDKMQDAGSGYKPTTRKDEMLDPEASFWEDEK-- 547
Qy 527 IEQDGETHWVWEGDY 541
Db 548 -RASHTTPVLMKEPY 561

RESULT 12
ID 026162 PRELIMINARY; PRT; 555 AA.
AC 026162;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DE 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
GN AMA-1.
OS Plasmodium vivax.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5855;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=PH-84;
RX MEDLINE=95021524; PubMed=7935625;
RA Cheng Q., Saul A.J.;
RT "Sequence analysis of the apical membrane antigen 1 (ama-1) of
RL Plasmodium vivax."
DR Mol. Biochem. Parasitol. 65:183-187 (1994).
DR EMBL; L27503; AAA29479.1; -
DR InterPro; IPR003298; Apmem_Ag1.
DR Pfam; PF02430; AMA-1; 1.
DR PRINTS; PR01361; MEROZOITESA.
DR NON TER 555
SQ SEQUENCE 555 AA; 63420 MW; 432DFC8FB82D9CD5 CRC64;

Query Match 14.4%; Score 420.5; DB 5; Length 555;
Best Local Similarity 25.7%; Pred. No. 8.4e-28;
Matches 154; Conservative 87; Mismatches 218; Indels 141; Gaps 28;

Qy 6 VQVLLVAVDCTIFASGL-----SSSTRS-----RESQTLAST-SGNPFOANVEKMT 52
Db 4 IYIIFLSAQCLVHIGKGRNQKPSRLTRSANVLEKGPVTERSTRSNPW-----KA 57
Qy 53 FMERFNLTHHOSGIYVDLGDQKEVDGTLREPAGLCPWGHKIELQOPDLRYNNFLE 112
Db 58 FMEKVDIRHTSSSGRVLDLGEDAEVNAKYRIIPARCEVFGKGIYENS-----AVSFLT 112
Qy 113 DVPT-EKEYKOSGNPLPGFNLNFTPSGORISPPM-----ELLEKSNIKASTDLGCA 167
Db 113 PVAAGDQQLKQGGFAFPN-----KADHISPMTLANLKERYKDYENMKMLNDIALCR 163
Qy 168 EFAFKTV-AMDKNNKATYRYPFYDSSKRLCHILYVSMQMEGKKYCSVKGPEPDLTWY 226
Db 164 THAASFVWAGDQN---SSYRHPAVYDEKCKTCHMLYLSAQENMGGRYCSPPAQNDAY-F 219
Qy 227 CFKPKKSVT-ENHHLIYGSAYGENPDAFISKCPNOLRGYRFGVWKKGRCLDYTELDT 285
Db 220 CFKPKKSNFEN--LVYLSKVRNDW---KKCRKNLGNKAFGLVWGNCEIEIYVXEV 274
Qy 286 VIERVESK--AQCVKTFENDGVASDOPHTYPLTQSASWMDWMLHQ----- 330

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Db 270 YKVEAKDLRECNRIYF--GASASDQPTQY-----EEMTDYQKIQGFRQNNREMIKSA 323
QY 331 -----SDQPHSGVGRNYGFYYVDTTGCKALSDQVDCIVSDSAVSTYRAGLS 382
Db 324 PLVGAFAISDNFKSGKGFNMANF---DSVKNKCYIFNTKPTCLINDKPFATATLALSHQ 380
QY 383 EETNFIIIPSN-----PSVTPPTETALQCTADKFP 413
Db 381 EVDFEF--PCSYIDETIEREIKKOSRNNMYSVDGERIVLPRIPLFISNDKESIKCPCEPEH 438
QY 414 DSFACDVQACROKTSVCV--GGQIOSTSVDTADEQNECGSN-----TALLIAGIA 462
Db 439 ISNTGNCNYVC-----NCEVRAEIKENNVQVYIKKEFPDYENGEBKSNQMILLITIGI 492
QY 463 VGVLLALLGCGCYFAKRLDRNKGVQAAHHEHFOOSRGARKRPSDLMQEAEPSEFDE 522
Db 493 TGVGVVA--LASMAYFRKKANNDK-----YDKMDQAEAGYGKPTTRKDEMLDPEASFWGE 545

RESULT 13
Q96413 PRELIMINARY; PRT; 563 AA.
AC Q96413;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Apical merozoite antigen 1.
GN AMA1.
OS Plasmodium knowlesi (strain H).
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5851;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=H;
RX MEDLINE=21391817; PubMed=11500430;
RA Rogers W.O., Baird J.K., Kumar A., Tine J.A., Weiss W., Aguilar J.C.,
Gowda K., Gwadz R., Kumar S., Gold M., Hoffman S.L.;
RT "Multistage Malaria Heterologous Prime Boost Vaccine for
RT Plasmodium knowlesi Malaria Provides Partial Protection in Rhesus
RT Macaques";
RL Infect. Immun. 69:5565-5572(2001).
DR EMBL; AF298218; AAC24614.1; -;
DR InterPro: IPR003298; Apmem_Ag1.
DR Pfam; PF02430; AMA-1; 1
DR PRINTS; PRO1361; MERZOITTESA.
KW Merozoite.
SQ SEQUENCE 563 AA; 64694 MW; 9CD4A3C1F019CA2B CRC64;

Query Match 14.4%; Score 420.5; DB 5; Length 563;
Best Local Similarity 24.6%; Pred. No. 8.5e-28;
Matches 148; Conservative 95; Mismatches 251; Indels 107; Gaps 24;

QY 6 VOVLVLVADCTIPASGL---SSSTRSRESQTLASASTSGNPFQANVM---KTEMERN 58
Db 4 IYIILFLSAGCLVHNGKRCERNQKTRTLRSANNASLEKPIIERSIRMSNPWKAEKXD 63
QY 59 LTHHOSGIYVLDGQDKVDTGLYREBAGLCPIWKGHILEQDPDLPIYANNLEVDPT-E 117
Db 64 LERAHNSGIRIDLGDAEAVGNSKRYIPACKCPVFGGIVTENS-----VSFLTPVATCA 118
QY 118 KEYKSGNPLPGGFNLFTPSGGRISPFPM---ELEKNSINIKASTDLGRCAEPAFKT 173
Db 119 ORLKSGGFAFPM-----ADHISPTITIANLKERKENADLMKLDIALCKTHAASF 169
QY 174 VAMDKNKATKRYRPFVYDSKRLCHILYVSMQLEMGKCYCSVKGEPPDLTWYCFKPKS 233
Db 170 VIAEON--TSYRHAIVDEKNTKCMYLSAQENMGPRYCPDSGNKO-AMFCFKPDKN 226
QY 224 VTEHHLLIYGSAYVGENPDATFSKCPNOLRGYRGVWKGRCLDTLTDTLVIERVESK 293
Db 227 -EKFNILVYLSIKVNSD--WENKCPRKVIAGNAKFGELWDGNCSEI-----PYVNEVEAR 277
QY 294 A--QCMVTKFENDGVASDQPHY--PLTSQASNMWMLHQSQPHSG----- 337

Db 278 SLRECNRIYFE--ASASDQPTQYEEELTDYEKIQGFRQNNRMKISAFPLVGAFAISDNF 335
QY 338 -GVRNRYGFYYVDTTGCKALSDQVDCIVSDSAVSTYRAG---SLSEBTPFIIPSN 393
Db 336 KSKRGYMANPDSV--NNKCYIFNTKPTCLINDKPFATATLALSHQEVDFEFPSYKDE 394
QY 394 -----PSVTPPTETALQCTADKFPDSFGACDVQACROKT 429
Db 395 IEREIKKOSRNNMYSVDKERIVLPRIPLFISNDKESIKCPCEPEHISNTGNYVC----- 449
QY 430 SCV--GGQIOSTSV--VDCTADEQNECGSN--TALLIAGVGVLLALLGCGCYFAK 480
Db 450 NCEVRAEIKENNVYIKKEFPDYENGEBKSNQMILLITIGYGAVCVAVASLIFYFRK 509
QY 481 RLDNKNQVQAAHHEHFOOSRGARKRPSDLMQEAEPSEFDEEENIEQDETHVMYEGD 540
Db 510 KAQDDK-----YDKMDQAEAGYKTAATRKDEMLDPEASFWGEDK--RASHTTVLMEKP 561
QY 541 Y 541
Db 562 Y 562

RESULT 14
Q25747 PRELIMINARY; PRT; 604 AA.
AC Q25747;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Apical membrane antigen-1 (Fragment).
GN AMA-1
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=HB3;
RX MEDLINE=96379227; PubMed=8784778;
RA Marshall V.M., Zhang L., Anders R.F., Coppel R.L.;
RT "Diversity of the vaccine candidate AMA-1 of Plasmodium falciparum";
RL Mol. Biochem. Parasitol. 77:109-113(1996).
DR EMBL; U33277; AAC47107.1; -;
DR InterPro: IPR003298; Apmem_Ag1.
DR Pfam; PF02430; AMA-1; 1
DR PRINTS; PRO1361; MERZOITTESA.
DR NON_TER 604
FT 604
SQ SEQUENCE 604 AA; 69886 MW; 791620C3B2AD342B CRC64;

Query Match 14.4%; Score 419.5; DB 5; Length 604;
Best Local Similarity 26.6%; Pred. No. 1.2e-27;
Matches 147; Conservative 78; Mismatches 200; Indels 127; Gaps 24;

QY 41 GNPFOANVEMKTFMERFNLTHHOSGIYVLDGQDKVDTGLYREBAGLCPIWKGHILEQ 100
Db 107 GNPW-----TEYAKVYDIEKVGSGIRVLDGEPAEAVGTGYRLPSGKCPVFGKIIEN 160
QY 101 PDRLPFRNPLEVDPT-E KEYKSGNPLPGGFNLFTPSGGRISPFPM-----LLEKNS 155
Db 161 S-----KTFPLPVATENQDLKDGFAFP-----PTEPLISPTMLDQMRHLKYKNE 206
QY 156 NIKASTDLGRCAEPAFKTVANDKNNKATKRYRPFVYDSKRLCHILYVSMQLEMGKCYCS 215
Db 207 YVKNLDELTLCSRHAGN--MNPDDKNSNYKIPAVYDEKCKHILYIAQENMGPRYCN 264
QY 216 VKGEPPDLTWYCFKPKR--SVTEHHLLIYGSAYVGEN--PDATFSKCPNOLRGYRGVWK 273
Db 265 -KDESKNSMCFRRAKOKLFENY-----TILSNQVVDNMBEVCPFRKVLERAKEAGLWVD 317
QY 274 GRCGLDTLTDTLVIERVESKQCVYKTTENDGVASDQPHY--PLTSQASNMWMLHQSQPHSG 327
Db 318 GNCEDIPIHVNFE--SANDLFEQCNLVPFLS--ASDQPTQYEQHLLTDYEKIQGFRQNNKNA 372

```
OY 338 -----LHSGDPHSGGVGRNYGYVDTTGEKCALSDQVPCLVSDSAVSYT 376
DB 373 SMKSAFLPTGAFKADRYKRGKYNMGVNTETO---KCEIFNVKPTCLINNSYIAT 429
OY 377 AAGSISEEPNFIITSN-----PSTPTPTETA 404
DB 430 ALSHNEVENNF--PCSLYDKBIKEIERESKRILKLNNDGCKKIIAIFRISDDKDS 487
OY 405 LQCTADKPPDSFGACDVQACKRQKTSVCGQIOSTS-----VDCIAD--BONECG 452
DB 488 LKCPDDEPVSSTCNFVCK-----CUEKAEVTSNNEVVYKERYKDEYADIPHKPT 542
OY 453 SNTALI---AGLAVGVLLALLGCGCYFAKRLDRNGVQAHHHEHFEQSDRGARKRP 508
DB 543 DNMKIIIASAAVAVIATILMV-----LYYKR---KG-NAEKTDKMDQPHYKSNR 591
OY 509 SDLMQAEPSFW 520
DB 592 NDEMLDPEASF 603
```

RESULT 15

```
Q26225 PRELIMINARY; PRT; 557 AA.
ID Q26225
AC Q26225;
DT 01-NOV-1996 (TREMBlrel. 01, Created)
DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
DE Apical membrane antigen-1.
OS Plasmodium yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
ON NCBI_TaxID=5861;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=17X;
RX MEDLINE=96408692; PubMed=8813699;
RA Kappe S.H., Adams J.H.;
RT "Sequence analysis of the apical membrane antigen-1 genes (ama-1) of
RL Plasmodium yoelii and Plasmodium berghei."
RL Mol. Biochem. Parasitol. 78:279-283 (1996).
DR EMBL, U45971; AAC47194.1;
DR InterPro, IPR003298; Apmem_Ag1.
DR Pfam, PF02430; AMA-1; 1.
DR PRINTS, PR01361; MEROZOITESA.
SQ SEQUENCE 557 AA; 63531 MW; 34D4EDBCA4A2903F2 CRC64;
```

Query Match 14.3%; Score 419; DB 5; Length 557;
Best Local Similarity 25.3%; Pred. No. 1.1e-27;
Matches 155; Conservative 91; Mismatches 214; Indels 152; Gaps 27;

```
OY 16 CTIFASGSSSTRSRESQTLASSTSGNPFQANVEM-----KTFMERNL 59
DB 11 CSIIYINLSYCS--EGPNQVSDGDN--INVELIPKENTERSIKLINPMDKYMEKDI 64
OY 60 THNHOSGIVYDLDGQKEVDGTLRREPAGLCPIWGHIELOQDRLRYNNFLEVDPTKE 119
DB 65 EKVHSGGIRVLDGEARVENDRIPSGKCPVIGGIIQNS-----VSLFKPATGNE 119
OY 120 YKQSGN-DLPGGFNLNFTPSGORISPPMELLE---KNSNIKASTDLGRCAEPAFTV 174
DB 120 SVRSGLDFPP-----DTDVHISPKSIANLKIWESEHPEILKLNMSICAKHTSPV 170
OY 175 AMDKNKATKRYRPVYDSKRLCHILYVSMQLMGKKYCS---VKSEPDLTTCYCKP 230
DB 171 P-GXDAKST-YRHPVAVDKSDSTCYMLYVAQENMGPPYCSNDANNENQP-----FCPTP 223
OY 231 RKSVTENHLIYSGAYVEN-PDAFISKCPNOLRGVGVWKKGRCLDYTELDTVIER 289
DB 224 EK-IEKYNL-----SYLTKNLRDDWETSCPKNSINAFGIWVDYCTIDYQK---HYVHE 275
OY 290 VESIAQGVKTFPNDGVASDOPHTY-----PLTSQASW 322
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DB 276 SESILACNQLIFNES--ASDPKOYERHLEDATKIROGIVERNGKLGEBALLPICS----- 329
OY 323 NDMMPLHOSDOPHSGGVGRNYGYVDTTGEKCALSDQVPCLVSDSAVSYTAAAGLS 382
DB 330 -----YSGQIKSHGKGYNGNY---DSKNNKCIIFETKPTCLINDKNFIATTLSSSTE 380
OY 383 EETPNF-----IIPSN-----PSVTPPTPTETAQCTADKFPDSF 416
DB 381 EPEENFPCEIYKNKIAEIKVILNQNNTSGNNSIKFPRIFISDKNSLNCPCPEPTKLS 440
OY 417 GACDVQACKRQKTSVCGQ---IOSTSV-----DCTADQNECGSNTALIALAGVGVLL 469
DB 441 STCFPYVC-----SCVEGRQYIAENNVDYIIKEEPIGDYENPNQKLVIIILIGIITVI 495
OY 470 ALLGCGCYFAKRLDRNGVQAHHHEHFEQSDRGARKRPSPDLMOEAPSPFDEAEENTIQ 529
DB 496 LIV--AYYFK-----SGKKGENTDRMQAADDYGSKSRKDEMDPEVSFMGEK---RA 544
OY 530 DGETHVVEG DY 541
DB 545 SHTPVLMKXPY 556
```

RESULT 16

```
Q96712 PRELIMINARY; PRT; 622 AA.
ID Q96712
AC Q96712;
DT 01-DEC-2001 (TREMBlrel. 19, Created)
DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
DE Apical membrane antigen-1 (Fragment).
GN AMA-1.
OS Plasmodium falciparum,
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
ON NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FDL NG;
RX MEDLINE=21192561; PubMed=11295182;
RA Escalante A.A., Grebert H.M., Chaiyaraj S.C., Magris M., Biswas S.,
RL Nahlen B.L., Lal A.A.;
RT "Polymorphism in the gene encoding the apical membrane antigen-1 (AMA-1) of Plasmodium falciparum. X. Asemo Bay Cohort Project."
RL Mol. Biochem. Parasitol. 113:279-287 (2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=FDL NG;
RA Ananias E.A., Grebert H.M., Chaiyaraj S.C., Magris M., Biswas S.,
RL Nahlen B.L., Lal A.A.;
RL Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL, AY016439; AAGS0146.1;
DR InterPro, IPR003298; Apmem_Ag1.
DR Pfam, PF02430; AMA-1; 1.
DR PRINTS, PR01361; MEROZOITESA.
FT NON TER 622
SQ SEQUENCE 622 AA; 71959 MW; CCD62FCC45228065 CRC64;
```

Query Match 14.3%; Score 419; DB 5; Length 622;
Best Local Similarity 26.0%; Pred. No. 1.3e-27;
Matches 148; Conservative 83; Mismatches 215; Indels 124; Gaps 24;

```
OY 41 GNPFQANVEMKTFMERNLTHNHOSGIVYDLDGQKEVDGTLRREPAGLCPIWGHIELOQ 100
DB 107 GNPFN-----TEYNAKTDIEVHSGIRVLDGEBAEVAAGTIRLPSCGKCPVFGKGIITEN 160
OY 101 PDRLPYNNFLEVDPT-EKEYKQSGNPLPGGFNLNFTPSGORISPPM-----ELLEKNS 155
DB 161 SN-----TTFLKPVATNGQDLKQGFAPF-----PTEPLISPTMLDMDRPFYKQNE 206
OY 156 NIKASTDLGRCAEPAFTVAMDKNKATKRYRPVYDSKRLCHILYVSMQLMGKKYCS 215
DB 207 YVKNLDELTECSRAAGNMI--PDNDKNSNYKYPVAVDDKKCKCHILYVAQENNGPRYCN 264
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Qy	216	VKGEPEDLTWCFEKRK-SVTEENHHLIYSAAVYGE--PRAFISKPCGNQALRGVFGWKK	273
Db	265	-KDQSKNSMFCFRPKDKLFEY-----TYSKVVNDWMEKYCFRKNLQNAKFGMLVD	317
Qy	274	GRCLDYTELTDVIERVESKACOWXTFENDVASDQPHYP--LTSQASWMDWP----	323
Db	318	GNCEBII PHVNEP---SANDLFECNKLVFELS--ASDQPMQYBEHLTDYEKIKGFKNKA	372
Qy	328	-----LHQSDDPHSGGAVGNRYGYVDTTGEKCALSDQVBDCLVSDSAAVSYT	376
Db	373	SMIKSAFLPTGAFKADRYKSHGKGMVGNWNTQO---KCEIPIVXKPTCLINNSYIATY	429
Qy	377	AAGSLEETPNIIISN-----PSVPRPPETA	404
Db	430	ALSHPIEVENN--PQSLYKDEIMKEIERESKRIKLNDDNBGNKKI IABRITISDDKDS	487
Qy	405	LOCTRADKPFDSFGACDVQACKROKTSVCGGQIOSTVDCA-----DEONECGSN----	454
Db	488	LKCPDDEPENVSNSTCNFYVC-----CVERRAEVTISNNEVYVAKERYKDEYADLPENKPY	542
Qy	455	---TALLGLAVGAVLLALLGGGCGYFAKRLDENKGVQAANHEHEFOSDGAARKKPSDL	511
Db	543	DKMKIILISSAAVAVLATILM---VYLXKR---KQNAEKYDWDPEQHYGKNSR-NDE	594
Qy	512	MOEAPSPFWDDEBENIEDQGEIHWMEGDI	541
Db	595	MLDPEASFWGEEK---RASHTTPIVLMKEPY	621

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RESULT 17
ID 096734 PRELIMINARY; PRT; 622 AA.
AC 096734;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, last annotation update)
DE Apical membrane antigen-1 (Fragment).
GN AMA-1.
OS Plasmodium falciparum
OC Eukaryote; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_taxid=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=14-0606;
RX MEDLINE=21192561; Pubmed=11295182;
RA Escalante A.A., Grebert H.M., Chaiyaroi S.C., Magris M., Biswas S.,
RA Nahlen B.L., Lal A.A.;
RT "Polymorphism in the gene encoding the apical membrane antigen-1 (AMA-
RT 1) of Plasmodium falciparum. X. Asemo Bay Cohort Project."
RL Mol. Biochem. Parasitol. 113:279-287(2001).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=14-0606;
RA Annatis E.A., Grebert H.M., Chaiyaroi S.C., Magris M., Biswas S.,
RA Nahlen B.L., Lal A.A.;
RL Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AY016423; AAGS0130.1; -;
DR InterPro: IPR003298; Apmem_Agl1.
DR Pfam: PF02430; AMA-1; 1.
DR PRINTS: PR01361; MERZOQITBSA.
SQ NON_TER 622 622
SEQUENCE 622 AA; 72038 MW; D61DAAE60568C45A CRC64;

```

Query Match	14.3%	Score 418;	DB 5;	Length 622;
Best Local Similarity	26.1%;	Pred. No. 1.6e-27;		
Matches 148;	Conservative 81;	Mismatches 219;	Indels 120;	Gaps 23

```

QY 41 GNPFOANVEKTFMERFNTTHHOSGIYVDLGDQKDVDTGLVREBPGLCPIMKHILEQO 100
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 107 GNPM-----TEYMAKYDIEEVHSGSIRYDLGDEDAVAGTQYRLPGSGKVPFGKGIILEN 160
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 101 PDRLEFYRNRFLEDPVEKEYKQSGNLPQGFNINLPVTPBQGRISPPM-----ELLEKN 156
      : : : : : : : : : : : : : : : : : : : : : : : : : : : : : :

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Db 161 SN-----TTFKRPVATGNQYLKD-----GGFAF-----PPTNPILSPMTLDMHMFYKNNEX 2070
Qy 157 IKASIDLRCGAFAFKYAMDKMKNKATKYRYFVYVDSKRLCHILLYVSMQWMBEGKKYCSV 216
Db 208 VKNIDELTLCSHHAN--MNPDDNKSNKYPAVVDYNDKCHILYIAQENNGPRYCN-- 264
Qy 217 KGEPPDLTWYCEPKPKSYTENHLLLYGSAVYGEN--PDAFISKCPNALRGYRFVWKGR 275
Db 265 KDESRRNMFGRPAKDKSFGYU-----TYSKVVDMWEKVCPRKRLNNAKGLWAGN 319
Qy 276 CLDYELIDTYIERESKAQCWVKTFPNDGVASDDQPHYR--LTSASANNMWPR----- 327
Db 330 CEDIPHNEF---SANDLFECKNLVFEYS--ASDPKQOEQHLTDYEKIKEGKKNQASM 374
Qy 328 -----LHOSDQPHSGVGRNRYGFYVDTTGEKCALSDQVPDCLVSDSAVAASYTA 378
Db 375 IKSALPLPGAFADRYKSRGKGYMGNVNRKTQ---KCEIFVWKPRCLINNSYIATTL 431
Qy 379 GSLSEETNPFIIPSN-----PQVTPRPTETALQ 406
Db 432 SHPNVEVHNPF--PCSLYKDEIKKEIERESKRITLNDNDENGMKIIAPRIFISDDIDSLK 469
Qy 407 CHADPEPDSFGACDVQACRQKTSQVGGIOSTVDCFA-----DEQMGCSN----- 454
Db 490 CPDDEIVSNSTGCMFPVCK-----CVERKRAVTSNNVVYKKEZYADEYADIDPHKRTYDK 544
Qy 455 -TALITGLAVGVLLIALLGGCYFAKRLDRNKGYQAAHNEHEFOSDRGAKRRKPSDLMO 513
Db 545 MKIIIASAVALATILM---VLYLKR---KGNAEKYDKMDEPDQYKSNR--NDEMIL 596
Qy 514 EABSPFMDEAENIEODETHVMWGDY 541
Db 597 DPEASFWGBEK---BASHTTPVLMKPY 621

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RESULT 18		
ID	Q26163	PRELIMINARY; PRT; 555 AA.
AC	Q26163;	
DT	01-NOV-1996 (TrEMBLrel. 01, Created)	
DT	01-NOV-1996 (TrEMBLrel. 01, Last sequence update)	
DT	01-MAR-2003 (TrEMBLrel. 23, Last annotation update)	
DE	Apical membrane antigen 1 (Fragment).	
GN	AMA-1.	
OS	Plasmodium vivax.	
OC	Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.	
OX	NCBI_TaxId=5855;	
RN	[1]	
RP	SEQUENCE FROM N.A.	
RC	STRAIN=PVO;	
RY	MEDLINE=95021524; PubMed=7935625;	
RA	Cheng Q., Saul A.J.,	
RT	"Sequence analysis of the apical membrane antigen 1 (ama-1) of Plasmodium vivax."	
RL	Mol. Biochem. Parasitol. 65:183-187(1994).	
DR	EMBL; L27504; AAA29480.1; -	
DR	InterPro; IPR003298; ApMem_Agl.	
DR	Pfam; PF02430; AMA-1; 1.	
DR	PRINTS; PR01351; MEMOZOTESA.	
FT	NON_TER 555	
SQ	SEQUENCE 555 AA; 63575 MW; DC64155A7A1D916 CRC64;	

Query Match	14.3%;	Score 416.5;	DB 5;	Length 555;
Best Local Similarity	25.7%;	Pred. No. 1.9e-27;		
Matches 154;	Conservative 90;	Mismatches 215;	Indels 141;	Gaps 28

```

Qy      6 VQVLLIVADCFIFASGL-----SSSTP-----RSQTSIASR-DSQNPQANBEMKT 52
Db      4 IYIIFLSQCLVHGKCGRNQKPSRLTRISANNVLEKEPTYERSTRMSNPW-----KA 57
Qy
Db
Qy      53 FPERNLTHHSGSYVDIGDKEYVDGTLYREBPAGICPTMGKHTLEQOPDRLPYRNPFLE 112
Db      58 FPEKDYIERHTSSGKRVLDGEDAEVENAKYKRLPAGCCVPFGKGIATVENSQ---VSFLT 112

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Qy 113 DVPT-EKEYKSGNPLPGGFNLNFTVPSGQRIISPPMELL-----EKNSNIKASTDLGRCA 167
Db 113 PVATGDOQLKDGGAFAFP-----KADHISPTTLENLKARYKDVEMKLNLDIALCR 163
Qy 168 EFARFVY-AMDKNNKATKRYRPFYVDSKRLCHILYVMQMEGKKYCSVKGEPDDLTYW 226
Db 164 THAASFVWAGQON--SSYRHPAVYDEKTCYMLYLSAONMGPRYCSPPAONRDVAF 219
Qy 227 CFKPRKSVT-ENHHLIYASVYGENPDPAFISKCPNOLRGYRFGVWKKGRCLDTELDT 285
Db 220 CFKDKKESFEN--LVYLSKAVRNDMD--KKCPKKNLGNKAFGLWVDCNCEBI-----P 269
Qy 286 VIERVESK--AQCWKTFFENDGVASDQPHYPLTSQASWMDWPLHQ----- 330
Db 270 YKVEEADLRECURIVE--GASASDQTOY-----EEMTDYQKIQGFRQNNEMIKSA 323
Qy 331 -----SDQPHSGGVGRNRYGVYVDTTGGKCALSDQVDCLVSDSAVSYTLAGSL 382
Db 324 FLVPGAFNSDNFKSGRGFNWANF--DSVKKKCYIFNTKPTCLINDKPIATTAISHPQ 380
Qy 383 EETNFIIPSN-----PSVTPPTETALQCTADKFP 413
Db 381 EVDKDF--PCSIYKDEIFEREIKOSRNNMLYSVDEGRVLPRIFTSNDKESIKCPEPEH 438
Qy 414 DSFGACDVQACRQKRTSCV--GGQIOSTSVDTADEQNECGSN-----TALLIAGLA 462
Db 439 ISNNTCNFYVC-----NCVEKRAEIKENNOYVYKEPRDYENGEKSNKQMLIIT161 492
Qy 463 VGGVILLALLGGCCFYAFRLRNKGVQAAHHEHESQSRGARKRPSPLMOEAPESFWE 522
Db 493 TGGVCVVA-LASMAVFRKKANNDK-----YDKMDQAGYGGKPTTRKDEMLDPEASFWE 545
```

RESULT 19

```
Q9NFW9 PRELIMINARY; PRT; 605 AA.
ID Q9NFW9
AC Q9NFW9;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE Apical membrane antigen 1 (Fragment).
GN 83/AMA-1.
OS Plasmodium reichenowi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5654;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20416492; PubMed=10960173;
RA Kocken C.H.M., Narum D.L., Massougbodji A., Ayivi B., Dubbeld M.A.,
  van der Weij A., Conway D.J., Sami A., Thomas A.W.;
RT "Molecular characterization of Plasmodium reichenowi apical membrane
  antigen-1 (AMA-1), comparison with P. falciparum AMA-1, and antibody-
  mediated inhibition of red cell invasion."
RL Mol. Biochem. Parasitol. 109:147-156(2000).
DR EMBL; AJ252087; CAB6387.1; -;
DR InterPro; IPR003298; Apmem_Ag1.
DR Pfam; PF02430; AMA-1; 1.
DR PRINTS; PRO1361; MEROZOITESA.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 605 AA; 70072 MW; E4959A99D5C880C6 CRC64;
```

Query Match 14.2%; Score 415.5; DB 5; Length 605;

Best Local Similarity 25.1%; Pred. No. 2.6e-27;

Matches 143; Conservative 80; Mismatches 219; Indels 127; Gaps 21;

```
Qy 30 RESQTLASTS-----GNPQANVEMKTFMERFNLTHHOSGIYVLDGQKXVDGTL 81
Db 80 RHEQNLPSNSNEIYVSNYMGWNP-----TEYMAKYDIEVHSGSIRVLDGEDAEVAGTQ 133
Qy 82 YRPAGLCPIWGKHIELQOQDRLPYRNNFLEDVPT-EKEYKSGNPLPGGFNLNFTVPSG 140
Db 82 YRPAGLCPIWGKHIELQOQDRLPYRNNFLEDVPT-EKEYKSGNPLPGGFNLNFTVPSG 140
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Db 134 YRPSGKCPVFGKCIITENSN-----TFTLTPVATGNODLKDGGAFAFP-----PTN 179
Qy 141 QRISPPME-----LLEKNSNIKASTDLGRCAEFARFVYVDSKRLCHILYVMQMEGKKY 196
Db 180 PLMSFMSLDMMRNRYKNENIKNDELTLCSRHAGNV--PDNKNISNYKPAVYDEQNK 237
Qy 197 LCHILYVMQMEGKKYCSVKGEPDDLTYWCFKPKSVTENHHLIYSAVYGEN-PDAFI 255
Db 238 KCHILYIAQENNNPRYCN-KDQSKRSMCFRPTKDSFQNY-----TYLSKNVVDWE 291
Qy 256 SKCPNOLRGYRFGVWKKGRCLDTELDTVYIEVESKACQWVTFENDGVASDQPHYPL 315
Db 292 KVCPRKNLQNAKFFLWVDCNENIPHYNEF--SANDLFECKLVFELS--ASDQPKQYE 346
Qy 316 --LTSQASWMDWPLHQ-----LHOSDQPHSGGVGRNRYGVYVDTTGGKCAL 358
Db 347 QHLDYQKIQGFRQNNEMIKSAFLPTGAFAKADRYSHGKGYWGNVYOTO--KCEI 403
Qy 359 SDQVDCLVSDSAVSYTLAGSLSEETNFIIPSN----- 393
Db 404 FNVKPTCLINNSYIATTAISHPIEVEHNF--PCSLYKDEIMKEIERESKRILNDND 461
Qy 394 -----PSVTPPTETALQCTADKFPDSFGACDVQACRQKRTSCVGGQIOSTSVDTCA- 445
Db 462 GNKKIIVRIFISDDKESLKCPCDPEWVSNSTCHFVCK-----CVERRTEVTSNNEVYV 516
Qy 446 -----DEONCGSNLTALIAGVGVILLALLGGCCFYAFRLRNKGVQAAH 493
Db 517 KEKYDEYADIPDKPAPYDMMKIIYASSAIAIATILM--VLYKR-----KTNAEKY 568
Qy 494 EHEFQSDRGARKRPSPLMOEAPESFWE 522
Db 569 DKMDQPHYKSGSKSYDEMLEDPEASFWE 597
```

RESULT 20

```
Q9N9G0 PRELIMINARY; PRT; 526 AA.
ID Q9N9G0
AC Q9N9G0;
DT 01-OCT-2000 (TREMblrel. 15, Created)
DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE Apical membrane antigen 1 (Fragment).
GN 83/AMA-1.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=C9-6.1;
RA Kocken C.H.M., Narum D.L., Massougbodji A., Ayivi B., Dubbeld M.A.,
  van der Weij A., Conway D.J., Sami A., Thomas A.W.;
RT "Molecular characterization of Plasmodium reichenowi apical membrane
  antigen-1 (AMA-1), comparison with P. falciparum AMA-1, and antibody-
  mediated inhibition of red cell invasion."
RL Mol. Biochem. Parasitol. 109:147-156(2000).
DR EMBL; AJ271169; CAB97281.1; -;
DR InterPro; IPR003298; Apmem_Ag1.
DR Pfam; PF02430; AMA-1; 1.
DR PRINTS; PRO1361; MEROZOITESA.
FT NON_TER 1
FT NON_TER 1
SQ SEQUENCE 526 AA; 60799 MW; 5654B6461BACF5ED CRC64;
```

Query Match 14.1%; Score 413; DB 5; Length 526;

Best Local Similarity 27.3%; Pred. No. 3.5e-27;

Matches 124; Conservative 72; Mismatches 161; Indels 98; Gaps 18;

```
Qy 41 GNPQANVEMKTFMERFNLTHHOSGIYVLDGQKXVDGTLYRPAGLCPIWGKHIELQO 100
Db 99 GNPW-----TEYMAKYDIEVHSGSIRVLDGEDAEVAGTQYRLPSGKCPVFGKCIITEN 152
```

QY 101 PDRLPYRNNPLEDYPTKEKYKQSGNPLPGCFNLNFTVPSGGRISPFWE-----LLEKSN 156
 DB 153 S-----KTTFLTPATENOYLKD-----GFAF--PPTPLMSPTMLDENRHHFYKDKY 199
 QY 157 IKASTDLCRCFAFAKTVAAMDKNKATKYRYPFYVDSKKRLCHILYVSMQMEGKYCSV 216
 DB 200 VKNDELTCGRHAGNM--PDNDKSNKYKPAYVDDKDKCHILYIAAGNNGPRYCN- 256
 QY 217 KGEPPDLTWYCFKPKSVTENHHLIYGSAYGEN-PDAFISKCPNOLRGYRFGVWKGR 275
 DB 257 KDESKNMSFCFRPAKDISFONY-----TYSKNVVDNMKEYCPKKNLQNNKFGIWDGN 311
 QY 276 CLDYTELTD-TVIERVESKACQWKTENDGVASDQHTYP--LTSQASNDMP----- 327
 DB 312 CEDIPHVEFSALDFE---CNKLVEFLS--ASDQKQYEOHLLTDEYKIKEGFNKNAS 365
 QY 328 -----LHSDQPHSGVGNGYGYVDTTGECALSDQVPCIVSDSAVSYTA 377
 DB 366 MIKSAFLPTGAFKADRYKSHKGVMGNVNETQ--KCEIFNVKPTCLINSSYIATTA 422
 QY 378 AGLSSEETPNFIIPSN-----PSVTPPTPETAL 405
 DB 423 LSHPEVHNPF--PCSLYKNEIMKEIERESKRILKNDNDGKKIAPRIFISDDKSL 480
 QY 406 OCTADKFPDSFGACDVQACRQKTS CVGGQIOTS 440
 DB 481 KCPDPEIVSNSTCNFVCK---CVERKAXVTS 510

RESULT 21

ID 096738 PRELIMINARY; PRT; 622 AA.
 AC 096738;

DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Apical membrane antigen-1 (Fragment).
 GN AMA-1.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VEN764;
 RX MEDLINE=21192561; PubMed=11295182;
 RA Escalante A.A., Grebert H.M., Chaiyaraj S.C., Magris M., Biswas S.,
 RA Nahlen B.L., Lal A.A.;
 RT "Polymorphism in the gene encoding the apical membrane antigen-1 (AMA-1) of Plasmodium falciparum. X. Asembo Bay Cohort Project."
 RL Mol. Biochem. Parasitol. 113:279-287(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VEN764;
 RA Anantia E.A., Grebert H.M., Chaiyaraj S.C., Magris M., Biswas S.,
 RA Nahlen B.L., Lal A.A.;
 RL Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AY016419; AAG50126.1; -;
 DR InterPro; IPR003298; Apmem_Ag1.
 DR Pfam; PF02430; AMA-1; 1.
 DR PRINTS; PR01361; MEROZOITESA.
 DR NON TER 622
 FT SEQUENCE 622 AA; 71943 MW; CB2061BCB14E82 CRC64;

Query Match 14.1%; Score 413; DB 5; Length 622;
 Best Local Similarity 25.8%; Pred. No. 4.4e-27;

Matches 147; Conservative 82; Mismatches 218; Indels 122; Gaps 23;

QY 41 GNPFOANVEMKTFMERFNLTHHSGIYVDLQDKVVDGTLREPAGLCPINGKHELQ 100
 DB 107 GNPW-----TEMACYDIEVHSGIRVDLGEDAVAGTQYRLPGKCPVFGKGIITN 160
 QY 101 PRLPLRNNPLEDPT-EKEYKQSGNPLPGCFNLNFTVPSGGRISPFWE-----ELLEKSN 155

DB 161 SN-----TSFLKPVATGNQDLKDGIAFP-----PTNPILSPMTLDHMRDNYKNE 206
 QY 156 NIKASTDLGCACFAFAKTVAAMDKNKATKYRYPFYVDSKKRLCHILYVSMQMEGKYCS 215
 DB 207 YVKNLDELTLCSRAAG--NMPDNDKSNKYKPAYVDDKDKCHILYIAAGNNGPRYCN 264
 QY 216 VKGEPPDLTWYCFKPKSVTENHHLIYGSAYGEN-PDAFISKCPNOLRGYRFGVWKGR 274
 DB 265 -KDESKNMSFCFRPAKDISFONY-----TYSKNVVDNMKEYCPKKNLEAKAGIWDG 318
 QY 275 RCLDYTELTD-TVIERVESKACQWKTENDGVASDQHTYP--LTSQASNDMP----- 327
 DB 319 NCEDIPHVEF--SANDLFECNKLVEFLS--ASDQKQYEOHLLTDEYKIKEGFNKNAS 373
 QY 328 -----LHSDQPHSGVGNGYGYVDTTGECALSDQVPCIVSDSAVSYTA 377
 DB 374 MIKSAFLPTGAFKADRYKSHKGVMGNVNETQ--KCEIFNVKPTCLINSSYIATTA 430
 QY 378 AGLSSEETPNFIIPSN-----PSVTPPTPETAL 405
 DB 431 LSHPEVHNPF--PCSLYKNEIMKEIERESKRILKNDNDGKKIAPRIFISDDKSL 488
 QY 406 OCTADKFPDSFGACDVQACRQKTS CVGGQIOTSVDCTA-----DEQNECGSN----- 454
 DB 489 KCPDPEIVSNSTCNFVCK---CVERKAXVTSNNEVVKKEYKDEYADIPHKPTTD 543
 QY 455 --TALINGLAVGVLALLLGGCYFAKRLDRNGVQAHAHHEFGSDRGARKKRPDLM 512
 DB 544 KMKIILIASAVALATILM--VLYKR---KGNAEKIDKMBPODYKSNR-NDEN 595
 QY 513 QEAEPFWEAEENIEDGETHWAVEGDY 541
 DB 596 LDPASFWGEK---RASHTTPVMEKPY 621

RESULT 22

ID 096735 PRELIMINARY; PRT; 622 AA.
 AC 096735;

DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE Apical membrane antigen-1 (Fragment).
 GN AMA-1.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VEN759;
 RX MEDLINE=21192561; PubMed=11295182;
 RA Escalante A.A., Grebert H.M., Chaiyaraj S.C., Magris M., Biswas S.,
 RA Nahlen B.L., Lal A.A.;
 RT "Polymorphism in the gene encoding the apical membrane antigen-1 (AMA-1) of Plasmodium falciparum. X. Asembo Bay Cohort Project."
 RL Mol. Biochem. Parasitol. 113:279-287(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VEN759;
 RA Anantia E.A., Grebert H.M., Chaiyaraj S.C., Magris M., Biswas S.,
 RA Nahlen B.L., Lal A.A.;
 RL Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AY016422; AAG50129.1; -;
 DR InterPro; IPR003298; Apmem_Ag1.
 DR Pfam; PF02430; AMA-1; 1.
 DR PRINTS; PR01361; MEROZOITESA.
 DR NON TER 622
 FT SEQUENCE 622 AA; 72010 MW; FA81A1E610F4786B CRC64;

Query Match 14.1%; Score 413; DB 5; Length 622;
 Best Local Similarity 26.1%; Pred. No. 4.4e-27;

Matches 150; Conservative 80; Mismatches 212; Indels 132; Gaps 24;

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Qy 41 GNPFAANVEMKTFMERFNLTHHSGIYVDLGQDKREVDTLYREPAGLCPIWGKHIELQ 100
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 107 GNPW-----TEYMAKYDIEEVHSGIRVDLGEDAEVAGTQYRLPSGKCPVFGKIIEN 160
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 101 PDRLPYRNPLEVDPT-EKEYKQSGNPLPGGFNLNFTVPSGQRISEPFPM----ELLEKNS 155
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 161 SN-----TFLKPYATGQDLKQDGFAPF-----PTNPLISPMTLNMRDYYKNE 206
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 156 NIKASTDLCRCAEAFKTVAMDKNKATKYRPFYDYSKRLCHILYVSMQMEGKYCS 215
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 207 YVKNLDELTLCSRHAGN--NMPDNDKNSNYKPAVYDNDKKCHILYIAQENNGPRCN 264
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 216 VKGEPPDLTWYCFKPKRSVTENHLLYGSAYVGEN-PDAFISKCPNOALRGYRFGWK 274
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 265 -KDESKRSMCFRPAKDKSFQNY-----TFLSKVNVNMEKYCPKRLLENNAKFGMLW 318
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 275 RCLDYTELDTVIEVESKA-----QCMWKTPENDGVASDOPHTP--LTSQASNDMMW 327
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 319 NCEB-----IPRVNEPSANDLFECNKLVEFLS--ASDQKQYEOHLLDYEKIKEGFK 368
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 328 -----LHOSDPHSGVGRNYGFYVDTTGECKALSDQVPDCLVSDSA 372
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 369 NKNASMIKSAFLPTGAFKADRYKSGKGYNMGNYRKTQ--KCEIFNVKPTCLINNSY 425
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 373 VSYTAAGSLSETPNFITPSN-----PSVTPPT 400
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 426 IATFALSHNEVENHF--PCSLYKDEIKKEIERESKRIKLNDDNDEGNKIAPRIFISD 483
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 401 PETALQCTADKFPDSFGACDVQACRKQTSYCGGQIGSTSDCTA-----DEONECCSN 454
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 484 DIDSLKCPDEIYSNSTCFNVCK-----CVERAEVTSNNEVVVKEEYQVADIDIEH 538
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 455 -----TALAGLVGVLLTALLGCGCYFAKRLDRNKGVOAHNEHFEFOSDRGARKR 507
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 539 KPTYDKMIIIIASSAAVAVLATILM---VLYKR---KGAERKTDKDEPDYKSKNSR 591
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 508 PSDLMQEAEPSPWDAEENIEODGETHYVWEGDY 541
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 592 -NDEMLDPEASFWGEEK--RASHTTPVLMKPY 621
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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RESULT 23

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ID Q9TY48 PRELIMINARY; PRT; 621 AA.
AC Q9TY48;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Apical membrane antigen-1 (Fragment).
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=FVO;
RA Aguilar J.C., Hoffman S.L.;
RT "The immunogenicity and protective efficacy of Plasmodium falciparum
  AMA-1 DNA vaccines."
RL Submitted (JAN-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL; U84348; AAD03790.1; -.
DR InterPro; IPR003298; Apmem_Ag1.
DR Pfam; PF02430; AMA-1; 1.
DR PRINTS; PR01361; MEROZOITESA.
DR NON_TER 621
SQ SEQUENCE 621 AA; 71921 MW; 6EA2A8C5142DBA7D CRC64;

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Query Match 14.1%; Score 412.5; DB 5; Length 621;
Best Local Similarity 26.1%; Pred. No. 4.9e-27;
Matches 149; Conservative 80; Mismatches 216; Indels 125; Gaps 25;
Qy 41 GNPFAANVEMKTFMERFNLTHHSGIYVDLGQDKREVDTLYREPAGLCPIWGKHIELQ 100
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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Db 107 GNPW-----TEYMAKYDIEEVHSGIRVDLGEDAEVAGTQYRLPSGKCPVFGKIIEN 160
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 101 PDRLPYRNPLEVDPT-EKEYKQSGNPLPGGFNLNFTVPSGQRISEPFPM----ELLEKNS 155
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 161 SN-----TFLKPYATGQDLKQDGFAPF-----PTNPLISPMTLNMRDYYKNE 206
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 156 NIKASTDLCRCAEAFKTVAMDKNKATKYRPFYDYSKRLCHILYVSMQMEGKYCS 215
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 207 YVKNLDELTLCSRHAGN--NMPDNDKNSNYKPAVYDNDKKCHILYIAQENNGPRCN 264
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 216 VKGEPPDLTWYCFKPKRSVTENHLLYGSAYVGEN-PDAFISKCPNOALRGYRFGWK 273
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 265 -KDSKRSNMFCEFRPAKDKLFENY-----TFLSKVNVNMEEYCPKRLLENNAKFGMLW 317
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 274 GRCLDYTELDTVIEVESKAQCMWKTPENDGVASDOPHTP--LTSQASNDMMW 327
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 318 GNCEDIPIHNEF--SANDLFECNKLVEFLS--ASDQKQYEOHLLDYEKIKEGFK 372
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 328 -----LHOSDPHSGVGRNYGFYVDTTGECKALSDQVPDCLVSDSA 376
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 373 SMKSAFLPTGAFKADRYKSHGKGYNMGNYRKTQ--KCEIFNVKPTCLINNSYIAT 429
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 377 AAGSLSETPNFIT-----PSNPTTP--TETALQ 407
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 430 ALSHPIEVENHPCSLYKDEIKKEIERESKRIKLNDDNDEGNKEIAPRIFISDKSLK 489
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 408 TADKFPDSFGACDVQACRKQTSYCGGQIGSTSDCTA-----VDCPAD--EQNECCSN 455
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 490 PCDEPMVNSTCFRNVCK-----CVERAEVTSNNEVVVKEEYQVADIDIEH 544
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 456 ALI-----AGLAVGVLLTALLGCGCYFAKRLDRNKGVOAHNEHFEFOSDRGARKR 511
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 545 KIITASSAAVAVLATILM-----LYKR---KG-NAEYKDGMDQGHYKSTSRNDE 593
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 512 MQEAEPSPWDAEENIEODGETHYVWEGDY 541
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 594 MLDEASFWGEEK--RASHTTPVLMKPY 620
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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RESULT 24

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ID Q26224 PRELIMINARY; PRT; 557 AA.
AC Q26224;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Apical membrane antigen-1.
OS Plasmodium yoelii.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5861;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=YM;
RX MEDLINE=96408692; PubMed=8813699;
RA Kappe S.H., Adams J.H.;
RT "Sequence analysis of the apical membrane antigen-1 genes (ama-1) of
  P. yoelii yoelii and Plasmodium berghei."
RL Mol. Biochem. Parasitol. 78:219-283(1996).
DR EMBL; U45970; AAC47193.1; -.
DR InterPro; IPR003298; Apmem_Ag1.
DR Pfam; PF02430; AMA-1; 1.
DR PRINTS; PR01361; MEROZOITESA.
DR NON_TER 557
SQ SEQUENCE 557 AA; 63462 MW; 65D407E63D315487 CRC64;

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Query Match 14.1%; Score 412; DB 5; Length 557;
Best Local Similarity 24.3%; Pred. No. 4.6e-27;
Matches 148; Conservative 99; Mismatches 215; Indels 148; Gaps 27;
Qy 16 CTTFASGSSSTRRESQTSASRSGN-----PFOANVEMK-----TFMERFNLTH 61
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 11 CSTYLINLSTYS--EENPVVISDGNINYESIP-KENTERSITLIPMDKRYMEKYIEK 66
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Qy 62 HHOSGIYVDLGQDKREVDTLYREPAGLCPIWGKHIELQDPRLPYRNPLEVDPT-EKEY 120
    |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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Db      67 VHGSGIRVDLGEADARVENDYRIIPSGKCVIIEGITIONSE-----VSLKRVAAIGDKRV 121
Qy      121 KOSGNPLPGGNLNFVTPSGORISPPM-----ELIEKSNISIKASTDLGCAEFKTYAM 176
Db      122 RCGGLAFLP-----ETDVHISPTITNLKTMWKDHODIVNLDMSCAHT--SLVY 170
Qy      177 DKNNAATKRRYPFYVDSKRLCHILYVSOQLMEGKYCS-----VKGEPTDLTWYCKPRK 232
Db      171 PCKDATSAVRHVVVYDKNSSTCYMLVYAAQENMGPRYCSNDANNENQP-----FCTPERK 225
Qy      223 STENHHLIYGSAYGEN--PDAFISKCPNALRGYRFGWKKGRCLDYELTDYLERVE 291
Db      226 --IENIKDL--SYLTKNLRDWETSCKPKSIKNAKFGIWDGYCTDYCK--HYVHSD 277
Qy      292 SKAQCVKTFENDGVAADQPHTY-----PLTSQASWMD 324
Db      278 SLKKNQIIFNES--ASDQPKOYERHLEDATKIAQIVERNKLIIGELLPIGS----- 329
Qy      325 WMPFHOSDOPHSGGVGRNRYGYVDTTGEGKCALSQVDPCLVSDSAVSYTAAGLSFE 384
Db      330 ---YKSGQIKSHGKGYNGNY---DSKNNKCYIFETKPTCLINDKNFIATTALESTEF 382
Qy      385 TENF-----IIPSN-----PSVTPPETALQCTADKFPDSFGA 418
Db      383 EENFPEIYKAKIAEIKYILNANTSGNNSIKFRIFISTDKNSLNCPCDPTKLTST 442
Qy      419 CDVQACKROKTSQVGGQ---IOSTSV---DCTADEONEGNSALTALAGVGLLAL 471
Db      443 CEFYVC-----SCVEQROYIAENNDYIIEKEFIGDYENPKOKLLIIVIGVGIIVILL 497
Qy      472 LGGGCFAPKRLDRNKVOAAHHEFOSDGRGAKRPSDLMQAEESFMDAEENIEQOG 531
Db      498 V---AYYFK-----SGKGENYDRMGQADYKSKSRKDEMDPEVFWGDK--RASH 546
Qy      532 ETHVWVEGDY 541
Db      547 TTPVLMEXKY 556

RESULT 25
095NZ1 PRELIMINARY; PRT; 622 AA.
AC 095NZ1;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Apical membrane antigen-1 (Fragment).
GN AMA-1.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCB1_TaxID=5833;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=VEN767, and VEN762;
RX MEDLINE=21192561; PubMed=11295182;
RA Escalante A.A., Grebert H.M., Chaiyaraj S.C., Magris M., Biswas S.,
  Nahlen B.L., Lal A.A.;
RT "Polymorphism in the gene encoding the apical membrane antigen-1 (AMA-
  1) of Plasmodium falciparum. X. Asemo Bay Cohort Project.";
RL Mol. Biochem. Parasitol. 113:279-287 (2001).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=VEN767, and VEN762;
RA Anantias E.A., Grebert H.M., Chaiyaraj S.C., Magris M., Biswas S.,
  Nahlen B.L., Lal A.A.;
RT Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY016416; AAC50123.1;
DR EMBL; AY016418; AAC50125.1;
DR InterPro; IPR003298; Apmem_Ag1.
DR Pfam; PF02430; AMA-1; 1.
DR PRINTS; PRO1361; MEROZOITESA.
FT NON_TER 622 622

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SQ SEQUENCE 622 AA; 71991 MW; 129C8715D8E29243 CRC64;
Query Match 14.1%; Score 412; DB 5; Length 622;
Beet Local Similarity 25.8%; Pred. No. 5.4e-27;
Matches 147; Conservative 81; Mismatches 219; Indels 122; Gaps 23;

Qy      41 GNPEQANEMKTFMERNFLTHHOGSIYVDIGQDKEVGTLYREBAGLCPIWGIHEDQ 100
Db      107 GNPM-----TEYMAKVIIEVHSGIRVDLGEDEVAAGTQYRLPSGCGPVGKIIEN 160
Qy      101 PDRLPRNNPLEDEVPT-EKEYKQSGNPLPGGNLNFVTPSGORISPPM---ELLEKNS 155
Db      161 SN-----TTFLLKPVATGNQDLKDGGFARP-----PTMPLISPMILDHMRDYYKNE 206
Qy      166 NIKASTDGRCAEPFKVVAADKNNKATKRYRPFYVDSKRLCHILYVSOQLMEGKYCS 215
Db      207 YKKNLDELTLCSRHAGN--KNPDNDKSNRYKPAYDYNDKKCHILYTAQENNPNRCN 264
Qy      216 VKGEPPDLTWYCFKPKSVTENHHLIYGSAYGEN--PDAFISKCPNALRGYRFGWKKG 274
Db      265 -KDESKRSMCFRPAKOKSFQNT-----TYSKVVVNWMEKVCPRKXLENKAPGLWVDG 318
Qy      275 RCLDYTELTDYVIERVESKAQCWKTFFENDGVAADQPHTYP--LTSQASWMDWP----- 327
Db      319 NCEDIPIHYNEF---SANDLFECNKLVEFLS--ASDQPKOYERHLEDYERIKEGFNKQAS 373
Qy      328 -----LHQSOPHSGGVGRNRYGYVDTTGEGKCALSDQVDPCLVSDSAVSYTA 377
Db      374 MIKSAFLPTGAFKARVYKRGKYNWGNVNRKIQ--KCEIFNVKPTCLINDNSIYATTA 430
Qy      378 AGSLSEETPNFIIPSN-----PSVTPPETAL 405
Db      431 LSHPEVEHNF--PCLYKDEIKKEIERESKRIKLNDNDEGNKKIIPRIISDIDBL 488
Qy      406 OCTADKFPDSFGACDVQACKROKTSQVGGQIOSTVDCIA-----DEONEGSGN----- 454
Db      489 KCPDPEIYVNSGTCNPFVCK---CVKRAEVTSNNEVWVEKYEADVPEKPTVD 543
Qy      455 --TALTAGLVGVLLALLGGGCFAPKRLDRNKVOAAHHEFOSDGRGAKRPSDLM 512
Db      544 KMKIITASSAAYAVATITM--VYLTKR---KNAEKYDKMDPEODYGSNSR-NDEN 595

Qy      513 QEAEPSPFMDAEENIEODGETHWVEGDY 541
Db      596 LDPEASFNGEER---RASHTTPVLMEXKY 621

RESULT 26
0967J9 PRELIMINARY; PRT; 622 AA.
AC 0967J9;
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE Apical membrane antigen-1 (Fragment).
GN AMA-1.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCB1_TaxID=5833;
RN (1)
RP SEQUENCE FROM N.A.
RC STRAIN=VEN765;
RX MEDLINE=21192561; PubMed=11295182;
RA Escalante A.A., Grebert H.M., Chaiyaraj S.C., Magris M., Biswas S.,
  Nahlen B.L., Lal A.A.;
RT "Polymorphism in the gene encoding the apical membrane antigen-1 (AMA-
  1) of Plasmodium falciparum. X. Asemo Bay Cohort Project.";
RL Mol. Biochem. Parasitol. 113:279-287 (2001).
RN (2)
RP SEQUENCE FROM N.A.
RC STRAIN=VEN765;
RA Anantias E.A., Grebert H.M., Chaiyaraj S.C., Magris M., Biswas S.,
  Nahlen B.L., Lal A.A.;

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OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCB1_TaxID=5833;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=VEN768;
 RX MEDLINE=21192561; PubMed=11295182;
 RA Escalante A.A., Grebert H.M., Chaiyaraj S.C., Magris M., Biswas S.,
 RA Nahlen B.L., Lal A.A.;
 RT "Polymorphism in the gene encoding the apical membrane antigen-1 (AMA-
 RT 1) of Plasmodium falciparum. X. Aebo Bay Cohort Project."
 RL Mol. Biochem. Parasitol. 113:279-287(2001).
 RN (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=VEN768;
 RA Ananias E.A., Grebert H.M., Chaiyaraj S.C., Magris M., Biswas S.,
 RA Nahlen B.L., Lal A.A.;
 RL Submitted (DEC-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL, AY016421; AAGS0128.1;
 DR InterPro; IPR003298; Apmem_Ag1.
 DR Pfam; PF02430; AMA-1; 1.
 DR PRINTS; PRO1361; MEROZOITESA.
 DR NON_TER 622
 FT 622
 SQ SEQUENCE 622 AA; 71992 MW; F6D2CC94F7CDF041 CRC64;

Query Match 14.0%; Score 410; DB 5; Length 622;
 Best Local Similarity 25.8%; Pred. No. 8.1e-27;
 Matches 147; Conservative 80; Mismatches 220; Indels 122; Gaps 23;

QY 41 GNPFQAVNEMKTFMERFNLTHHOSGIYVDLGODKEVDGTLYRPAAGLCPTWGHIELOQ 100
 DB 107 GNPF-----TEYAKKDIEVHSGIRVDLGEBAEVAAGTYRLPSGKCPVFGGIIEN 160
 QY 101 PDRLPYRNPLEDVPTE-EKEYKSGNPLPGGFNLFTVPSGORISPPME---ELLEKNS 155
 DB 161 SN-----TTFKAPVATGNODLKOGFAFP-----PTNPLISPMTLDKRPDYKNE 206
 QY 156 NIKASTDLGCAEFAFTVAMDKNKATKYRYPVYDSKKRLCHILYVSMQMEGKKYCS 215
 DB 207 YVKMLDELTLCSRHAGNNPPDDKN--SNYKYPAYVDYNDKKCHILYIAQENNGPRYCN 264
 QY 216 VKGPPDLTYCFPRKRSVTENHILYGSAYVGEN-PDAFISKCPNOLRGYRGVWKKG 274
 DB 265 -KDSKNSNMFCEPRADKSFQNY-----TYSNIVVDMNEKVCPRKLNENAKGVLWDG 318
 QY 275 RCLDYTELDTVIRVESKAOQWKTENDGVAASDQPTYP--LTSQASWMDWP----- 327
 DB 319 NCEDIPIVNEF---SANDLFECKNLVFEELS--ASDQPKQYEQHLTDYEKIKEGFKKNKA 373
 QY 328 -----LHOSDQPHSGVGRNYGFYVDTTGEKCALSDQVPDCLVSDSAVSYTA 377
 DB 374 MIKSAFLPTGAFAADRYKSRGKYNMGVNNKTO--KCEIFNVKPTCLINNSYIATTA 430
 QY 378 AGSLSEETPNFIISN-----PSVTPTPTETAL 405
 DB 431 LSHNEVEHNF--PCSLYKDEIKKEIERESKRILKLNDDNDEGNKIIARIFISDDISL 488
 QY 406 OCTADKFPDSFGACDVQACKROKTSYVGGQIOSTSVDTA-----DEQNGCSN----- 454
 DB 489 KCPDDEPVSNSSTCNFVCK-----CCEKRAEVTSSNNEVVYKEKYDADIPHKPTPD 543
 QY 455 --TALLAGLAVGVLLALLAGGCGYFAKRLDRNKGVQAAHNEHFEFOSDRGARKRPSDLM 512
 DB 544 KMKIILYSSAAVAVLATILM---VLYKR-----KGNMEKYDKMBPDQYGSNSR-NDEN 595
 QY 513 QEAPPSFMDAENIENEDGETHVAVEGDY 541
 DB 596 LDPEASFVGEK---RASHTTPTVLMEXKY 621

RESULT 31
 ID Q9N9B4 PRELIMINARY; PRT; 526 AA.
 AC Q9N9B4;

DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE Apical membrane antigen 1 (Fragment).
 GN 83/AMA-1.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCB1_TaxID=5833;
 RN (1)
 RP SEQUENCE FROM N.A.
 RC STRAIN=7-9-1.
 RX MEDLINE=20416492; PubMed=10960173;
 RA Kocken C.H.M., Narum D.L., Massouhoudji A., Ayivi B., Dubbeld M.A.,
 RA van der Wel A., Conway D.J., Sanni A., Thomas A.W.;
 RT "Molecular characterisation of Plasmodium reichenowi apical membrane
 RT antigen-1 (AMA-1), comparison with P. falciparum AMA-1, and antibody-
 RT mediated inhibition of red cell invasion."
 RL Mol. Biochem. Parasitol. 109:147-156(2000).
 DR EMBL; AJ271185; CAB97197.1;
 DR InterPro; IPR003298; Apmem_Ag1.
 DR Pfam; PF02430; AMA-1; 1.
 DR PRINTS; PRO1361; MEROZOITESA.
 DR NON_TER 1
 FT 1
 SQ SEQUENCE 526 AA; 60917 MW; C6522FB072078D2D CRC64;

Query Match 13.9%; Score 407; DB 5; Length 526;
 Best Local Similarity 27.0%; Pred. No. 1.2e-26;
 Matches 123; Conservative 72; Mismatches 161; Indels 100; Gaps 18;

QY 41 GNPFQAVNEMKTFMERFNLTHHOSGIYVDLGODKEVDGTLYRPAAGLCPTWGHIELOQ 100
 DB 99 GNPF-----TEYAKKDIEVHSGIRVDLGEBAEVAAGTYRLPSGKCPVFGGIIEN 152
 QY 101 PDRLPYRNPLEDVPTE-EKEYKSGNPLPGGFNLFTVPSGORISPPME---ELLEKNS 155
 DB 153 S-----KTFELTPVATENODLKOGFAFP-----PTKPLMSPTLDKRPDYKNE 198
 QY 156 NIKASTDLGCAEFAFTVAMDKNKATKYRYPVYDSKKRLCHILYVSMQMEGKKYCS 215
 DB 199 YVKMLDELTLCSRHAGNMT--PDNDKSNYKYPVYDQDKCHILYIAQENNGPRYCN 256
 QY 216 VKGPPDLTYCFPRKRSVTENHILYGSAYVGEN-PDAFISKCPNOLRGYRGVWKKG 274
 DB 257 -KDSKNSNMFCEPRADKSFQNY-----TYSNIVVDMNEKVCPRKLNENAKGVLWDG 310
 QY 275 RCLDYTELDTVIRVESKAOQWKTENDGVAASDQPTYP--LTSQASWMDWP----- 327
 DB 311 NCEDIPIVNEFSAIDLFE---CNKLVFEELS--ASDQPKQYEQHLTDYEKIKEGFKKNKA 364
 QY 328 -----LHOSDQPHSGVGRNYGFYVDTTGEKCALSDQVPDCLVSDSAVSYT 376
 DB 365 SMKSAFLPTGAFAADRYKSRGKYNMGVNNKTO--KCEIFNVKPTCLINNSYIATTA 421
 QY 377 AAGSLSEETPNFIISN-----PSVTPTPTETAL 404
 DB 422 ALSHPIVENNF--PCSLYKDEIKKEIERESKRILKLNDDNDEGNKIIARIFISDDKXS 479
 QY 405 LQCTADKFPDSFGACDVQACKROKTSYVGGQIOSTS 440
 DB 480 LKCPXDPEWVNSGTCRFVCK-----CVERRAEVTSS 510

RESULT 32
 ID Q967J7 PRELIMINARY; PRT; 622 AA.
 AC Q967J7;
 DT 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE Apical membrane antigen-1 (Fragment).
 GN AMA-1.
 OS Plasmodium falciparum.

OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VEN763;
 RX MEDLINE=21193561; PubMed=11295182;
 RA Escalante A.A., Grebert H.M., Chaiyaroj S.C., Magris M., Biewas S.,
 RA Nahlen B., Lal A.A.;
 RT "Polymorphism in the gene encoding the apical membrane antigen-1 (AMA-1) of Plasmodium falciparum. X. Aeombo Bay Cohort Project.";
 RL Mol. Biochem. Parasitol. 113:279-287(2001).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=VEN763;
 RA Ananias E.A., Grebert H.M., Chaiyaroj S.C., Magris M., Biewas S.,
 RA Nahlen B., Lal A.A.;
 RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY016420; AAG50127.1;
 DR InterPro; IPR003298; Apmem_Ag1.
 DR Pfam; PF02430; AMA-1; 1.
 DR PRINTS; PR01361; MEROZOITESA.
 DR NON_TER 622
 FT SEQUENCE 622 AA; 71989 MW; 468816B752CA30D4 CRC64;
 SQ
 Query Match 13.9%; Score 407; DB 5; Length 622;
 Best Local Similarity 25.7%; Pred. No. 1.5e-26;
 Matches 146; Conservative 81; Mismatches 220; Indels 122; Gaps 23;

QY 41 GNPFQANVEMKTEMERENLTHHOSGIYVDLGDKVEDGLTYRPAAGLCPTWGHIELOQ 100
 DB 107 GNPM-----TEYMAKYDIEVHSGIRVLDGEDAEVAGTQYRLPSGKCPVGGKILLEN 160
 QY 101 PRLRYNNLEEDVPT-EKEYKQSGNPLPGGFNLVFTPSGORISPPM-----ELLEKNS 155
 DB 161 SN-----TFLKPVATGNQDLKDGFAFP-----PTNPLISPMTLNMRDIFYKNE 206
 QY 156 NIKASTDLCRCAEPAFTVAMDKNKATKRYRPPVYDSKKRLCHILYVSMQMECKKYCS 215
 DB 207 YKKNDELTLCSRHAGN--MNPNDKNSNYKYPAYVDYNDKCKCHILYIAQENNGPRYCN 264
 QY 216 VGEPPDLTWYCFKPKRK-STENHHLIYGSAYGEN-PDAFISKCPNOLRGYRGVWKKG 274
 DB 265 -KDESKNSMFCRPAKDKSPFY-----TYSKVVVDNWEKVCPRKULENAKFGIWMVG 318
 QY 275 RCLDYTELDTYIERVESKAQCWVKTFENDGVASDOPHTYP--LTSQASNMWMP----- 327
 DB 319 NCEDIPIHNEF---SANDLFECKNLVFEIS--ASDQKQYEGHLDYEXIKKEGFKKNAS 373
 QY 328 -----LHOSDPHSGGVGNRYGFYVDTTGGKCALSDQVPDCLVSDSAANSYTA 377
 DB 374 MIKSAFLPTGAFKADRYKRGKGYNMGNYNRQTQ--KCEIFNVKPTCLINNSSYIATTA 430
 QY 378 AGSLSEETPNFIISN-----PSVTPPTPETA 405
 DB 431 LSHPNVENHF--PCSLYKDEIKKEIERESKRILKLNDDNDEGNKIIAIPRIISDDIDL 488
 QY 406 OCTADKRPDSFGADVQACKRQKTSYVGQO---IGTSYDCTADEONECG----- 452
 DB 489 KCPDDEIYSNNSCNFVCK-----CYEKRAEVISSNNEVVVKEEYKDEYADIPENKPTYD 543
 QY 453 SNTALILAGLAVGVLLALLGGGCTFAKRLDRNKGVQAANHEHEPQSDRGARKRPSDL 512
 DB 544 KMKIIIASAANVAVLATILM-----YLYKR---KGNAEKYDKMDPDQYGSNSR-NDEN 595
 QY 513 QEAEPSEFMDAENINODGETHYMVEDGY 541
 DB 596 LDPEASFWGEEK--RASHTTPVLMKPY 621

DT 01-MAR-2001 (TREMblrel. 16, Created)
 DT 01-MAR-2001 (TREMblrel. 16, Last sequence update)
 DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
 DE Apical membrane antigen 1 (Fragment).
 GN AMA-1.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OX NCBI_TaxID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FVO;
 RA Kocken C.H.M., Dubbeld M.A., Herrera S., Thomas A.W.;
 RT "Diversity of Apical Membrane Antigen 1 sequence in Plasmodium falciparum FVO strain";
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AJ277646; CAC05390.1;
 DR InterPro; IPR003298; Apmem_Ag1.
 DR Pfam; PF02430; AMA-1; 1.
 DR PRINTS; PR01361; MEROZOITESA.
 DR NON_TER 1
 FT SEQUENCE 605 AA; 69897 MW; FED89F02F7690C19 CRC64;
 SQ
 Query Match 13.9%; Score 406.5; DB 5; Length 605;
 Best Local Similarity 26.2%; Pred. No. 1.6e-26;
 Matches 145; Conservative 77; Mismatches 205; Indels 127; Gaps 24;

QY 41 GNPFQANVEMKTEMERENLTHHOSGIYVDLGDKVEDGLTYRPAAGLCPTWGHIELOQ 100
 DB 99 GNPM-----TEYMAKYDIEVHSGIRVLDGEDAEVAGTQYRLPSGKCPVGGKILLEN 152
 QY 101 PRLRYNNLEEDVPT-EKEYKQSGNPLPGGFNLVFTPSGORISPPM-----ELLEKNS 155
 DB 153 SN-----TFLKPVATGNQDLKDGFAFP-----PTNPLISPMTLNMRDIFYKNE 198
 QY 156 NIKASTDLCRCAEPAFTVAMDKNKATKRYRPPVYDSKKRLCHILYVSMQMECKKYCS 215
 DB 199 YKKNDELTLCSRHAGN--MNPNDKNSNYKYPAYVDYNDKCKCHILYIAQENNGPRYCN 256
 QY 216 VGEPPDLTWYCFKPKRK-STENHHLIYGSAYGEN-PDAFISKCPNOLRGYRGVWKKG 273
 DB 257 -KDESKNSMFCRPAKDKLFEFY-----TYSKVVVDNWEKVCPRKULENAKFGIWMVG 309
 QY 274 RCLDYTELDTYIERVESKAQCWVKTFENDGVASDOPHTYP--LTSQASNMWMP----- 327
 DB 310 NCEDIPIHNEF---SANDLFECKNLVFEIS--ASDQKQYEGHLDYEXIKKEGFKKNAS 364
 QY 328 -----LHOSDPHSGGVGNRYGFYVDTTGGKCALSDQVPDCLVSDSAANSYTA 376
 DB 365 MIKSAFLPTGAFKADRYKSHGKGYNMGNYNRQTQ--KCEIFNVKPTCLINNSSYIATTA 421
 QY 377 AGSLSEETPNFIISN-----PSVTPPTPETA 404
 DB 422 ALSHPIEVENHF--PCSLYKDEIKKEIERESKRILKLNDDNDEGNKIIAIPRIISDDIDL 479
 QY 405 LOCTADKRPDSFGADVQACKRQKTSYVGQOIST-----VDCTAD--EONECG 452
 DB 480 LKCPDDEIYSNNSCNFVCK-----CYEKRAEVISSNNEVVVKEEYKDEYADIPENKPTYD 534
 QY 453 SNTALILAGLAVGVLLALLGGGCTFAKRLDRNKGVQAANHEHEPQSDRGARKRPSDL 508
 DB 535 DMKIIIASAANVAVLATILM-----YLYKR---KGNAEKYDKMDPDQYGSNSR-NDEN 593
 QY 509 SDLMQAEPSFWDE 522
 DB 584 NDEMLDPEASFWGE 597

RESULT 33
 ID 096V78 PRELIMINARY; PRT; 605 AA.
 AC 096V78;
 AC 096V78;

RESULT 34
 ID 096718 PRELIMINARY; PRT; 622 AA.
 AC 096718;
 DT 01-DEC-2001 (TREMblrel. 19, Created)

DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, last annotation update)
 GN Apical membrane antigen-1 (Fragment).
 OS AMA-1.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 NCBI_TaxID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Fas 30-6-7;
 RX MEDLINE=21192561; PubMed=11295182;
 RA Escalante A.A., Grebert H.M., Chalyaraj S.C., Magris M., Biswas S.,
 RA Nahlen B.L., Lal A.A.;
 RT "Polymorphism in the gene encoding the apical membrane antigen-1 (AMA-1) of Plasmodium falciparum. X. Assemb Bay Cohort Project.";
 RL Mol. Biochem. Parasitol. 113:279-287(2001).
 (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Fas 30-6-7;
 RX MEDLINE=20416492; PubMed=10960173;
 RA Kocken C.H.M., Narm D.L., Maesoujodji A., Ayivi B., Dubbeld M.A.,
 RA van der Weij A., Conway D.J., Sami A., Thomas A.W.;
 RT "Molecular characterisation of Plasmodium reichenowi apical membrane antigen-1 (AMA-1), comparison with P. falciparum AMA-1, and antibody-mediated inhibition of red cell invasion.";
 RL Mol. Biochem. Parasitol. 109:147-156(2000).
 DR EMBL; AJ271175; CAB97187.1;
 DR InterPro; IPR003298; Apmem_Ag1.
 DR Pfam; PF02430; AMA-1; 1.
 DR PRINTS; PRO1361; MEROZOITESA.
 FT NON_TER 1 526
 FT TER 526
 SQ SEQUENCE 526 AA; 60779 MW; 790A5FCBA7FBB68C CRC64;

Query Match 13.8%; Score 404; DB 5; Length 526;
 Best Local Similarity 27.0%; Pred. No. 2.1e-26;
 Matches 123; Conservative 68; Mismatches 166; Indels 98; Gaps 17;

DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, last annotation update)
 GN Apical membrane antigen-1 (Fragment).
 OS AMA-1.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 NCBI_TaxID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Fas 30-6-7;
 RX MEDLINE=21192561; PubMed=11295182;
 RA Escalante A.A., Grebert H.M., Chalyaraj S.C., Magris M., Biswas S.,
 RA Nahlen B.L., Lal A.A.;
 RT "Polymorphism in the gene encoding the apical membrane antigen-1 (AMA-1) of Plasmodium falciparum. X. Assemb Bay Cohort Project.";
 RL Mol. Biochem. Parasitol. 113:279-287(2001).
 (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Fas 30-6-7;
 RX MEDLINE=20416492; PubMed=10960173;
 RA Kocken C.H.M., Narm D.L., Maesoujodji A., Ayivi B., Dubbeld M.A.,
 RA van der Weij A., Conway D.J., Sami A., Thomas A.W.;
 RT "Molecular characterisation of Plasmodium reichenowi apical membrane antigen-1 (AMA-1), comparison with P. falciparum AMA-1, and antibody-mediated inhibition of red cell invasion.";
 RL Mol. Biochem. Parasitol. 109:147-156(2000).
 DR EMBL; AJ271175; CAB97187.1;
 DR InterPro; IPR003298; Apmem_Ag1.
 DR Pfam; PF02430; AMA-1; 1.
 DR PRINTS; PRO1361; MEROZOITESA.
 FT NON_TER 1 526
 FT TER 526
 SQ SEQUENCE 526 AA; 60779 MW; 790A5FCBA7FBB68C CRC64;

Query Match 13.9%; Score 405; DB 5; Length 622;
 Best Local Similarity 26.0%; Pred. No. 2.2e-26;
 Matches 149; Conservative 78; Mismatches 217; Indels 128; Gaps 24;

DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, last annotation update)
 GN Apical membrane antigen-1 (Fragment).
 OS AMA-1.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 NCBI_TaxID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Fas 30-6-7;
 RX MEDLINE=21192561; PubMed=11295182;
 RA Escalante A.A., Grebert H.M., Chalyaraj S.C., Magris M., Biswas S.,
 RA Nahlen B.L., Lal A.A.;
 RT "Polymorphism in the gene encoding the apical membrane antigen-1 (AMA-1) of Plasmodium falciparum. X. Assemb Bay Cohort Project.";
 RL Mol. Biochem. Parasitol. 113:279-287(2001).
 (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Fas 30-6-7;
 RX MEDLINE=20416492; PubMed=10960173;
 RA Kocken C.H.M., Narm D.L., Maesoujodji A., Ayivi B., Dubbeld M.A.,
 RA van der Weij A., Conway D.J., Sami A., Thomas A.W.;
 RT "Molecular characterisation of Plasmodium reichenowi apical membrane antigen-1 (AMA-1), comparison with P. falciparum AMA-1, and antibody-mediated inhibition of red cell invasion.";
 RL Mol. Biochem. Parasitol. 109:147-156(2000).
 DR EMBL; AJ271175; CAB97187.1;
 DR InterPro; IPR003298; Apmem_Ag1.
 DR Pfam; PF02430; AMA-1; 1.
 DR PRINTS; PRO1361; MEROZOITESA.
 FT NON_TER 1 526
 FT TER 526
 SQ SEQUENCE 526 AA; 60779 MW; 790A5FCBA7FBB68C CRC64;

RESULT 37
 Q9N9F4 PRELIMINARY; PRT; 526 AA.
 AC Q9N9F4;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE Apical membrane antigen 1 (Fragment).
 GN 83/AMA-1.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 NCBI_TaxID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=30-2.1.
 RX MEDLINE=20416492; PubMed=10960173;
 RA Kocken C.H.M., Narm D.L., Maesoujodji A., Ayivi B., Dubbeld M.A.,
 RA van der Weij A., Conway D.J., Sami A., Thomas A.W.;
 RT "Molecular characterisation of Plasmodium reichenowi apical membrane antigen-1 (AMA-1), comparison with P. falciparum AMA-1, and antibody-mediated inhibition of red cell invasion.";
 RL Mol. Biochem. Parasitol. 109:147-156(2000).
 DR EMBL; AJ271175; CAB97187.1;
 DR InterPro; IPR003298; Apmem_Ag1.
 DR Pfam; PF02430; AMA-1; 1.
 DR PRINTS; PRO1361; MEROZOITESA.
 FT NON_TER 1 526
 FT TER 526
 SQ SEQUENCE 526 AA; 60779 MW; 790A5FCBA7FBB68C CRC64;

Query Match 13.8%; Score 404; DB 5; Length 526;
 Best Local Similarity 27.0%; Pred. No. 2.1e-26;
 Matches 123; Conservative 68; Mismatches 166; Indels 98; Gaps 17;

DT 01-DEC-2001 (Tremblrel. 19, last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, last annotation update)
 GN Apical membrane antigen-1 (Fragment).
 OS AMA-1.
 OS Plasmodium falciparum.
 OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 NCBI_TaxID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Fas 30-6-7;
 RX MEDLINE=21192561; PubMed=11295182;
 RA Escalante A.A., Grebert H.M., Chalyaraj S.C., Magris M., Biswas S.,
 RA Nahlen B.L., Lal A.A.;
 RT "Polymorphism in the gene encoding the apical membrane antigen-1 (AMA-1) of Plasmodium falciparum. X. Assemb Bay Cohort Project.";
 RL Mol. Biochem. Parasitol. 113:279-287(2001).
 (2)
 RP SEQUENCE FROM N.A.
 RC STRAIN=Fas 30-6-7;
 RX MEDLINE=20416492; PubMed=10960173;
 RA Kocken C.H.M., Narm D.L., Maesoujodji A., Ayivi B., Dubbeld M.A.,
 RA van der Weij A., Conway D.J., Sami A., Thomas A.W.;
 RT "Molecular characterisation of Plasmodium reichenowi apical membrane antigen-1 (AMA-1), comparison with P. falciparum AMA-1, and antibody-mediated inhibition of red cell invasion.";
 RL Mol. Biochem. Parasitol. 109:147-156(2000).
 DR EMBL; AJ271175; CAB97187.1;
 DR InterPro; IPR003298; Apmem_Ag1.
 DR Pfam; PF02430; AMA-1; 1.
 DR PRINTS; PRO1361; MEROZOITESA.
 FT NON_TER 1 526
 FT TER 526
 SQ SEQUENCE 526 AA; 60779 MW; 790A5FCBA7FBB68C CRC64;

Query Match 13.9%; Score 405; DB 5; Length 622;
 Best Local Similarity 26.0%; Pred. No. 2.2e-26;
 Matches 149; Conservative 78; Mismatches 217; Indels 128; Gaps 24;

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DT 01-NOV-1996 (TREMblrel. 01, last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, last annotation update)
DE Apical membrane antigen 1 precursor (Fragment).
GN AMA-1.
OS Plasmodium cynomolgi.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
CX NCBI_TaxID=5827;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=96123401; PubMed=8577338;
RA Dutta S., Malhotra P., Chahan S.;
RT "Sequence analysis of apical membrane antigen 1 (AMA-1) of Plasmodium
RT cynomolgi baetiellii."
RL Mol. Biochem. Parasitol. 73:267-270(1995).
DR EMBL; X86099; CA60053.1;
DR InterPro; IPR003298; Apmem_Agl.
DR Pfam; PF02430; AMA-1; 1
DR PRINTS; PRO1361; MEROZOITESA.
KW Signal.
FT SIGNAL.
FT NON TER.
SQ SEQUENCE 562 AA; 64606 MW; 84E78359ABF49B42 CRC64;

Query Match 13.8%; Score 404; DB 5; Length 562;
Best Local Similarity 24.6%; Pred. No. 2.3e-26;
Matches 150; Conservative 97; Mismatches 238; Indels 124; Gaps 26;

OY 6 VQVLLVADCTIFASGL-----SSSTRRESQTL-----ASTSGNPFQANVEKKT 52
DB 4 IYVLFSAQCLVHIGKCGDEKPSRLTRKSNVLEKGPVERSTRNSFW-----KA 57
OY 53 FMERFNLTHHOSGIYVDLGODKEVDGTLVREPAGLCPIMGKHIELQPDRLPYRNPLE 112
DB 58 FMEKYDVERTSSGIRVDLGDAEVENSKYRIPOGKCVFPGKIVIEHSN-----VSFLK 112
OY 113 DVPT-EKYEKOSGNPLPGGFNLNFTVPSGQRIISPPM-----ELLEKSNITASTDLGRCA 167
DB 113 PVAQGDQCLKDGGAFAFP-----ADHISPTINLLEKRYESVEMKLNIDIALCR 163
OY 168 EFARFVY-AMDKNNKATKYRPFYVYDSKKRLCHILYVSMOLMEGKYCVSGEPDLTWY 226
DB 164 THAASFVWAGDON--SYRHPAVYDEKCKTCHMLYSAQENVGGRYSRDAENRD-AMF 219
OY 227 CFKPRKSVTENHNLVYSAVYGENPDAFISCPNOALRGVFGVWKGRCLDYTELDTV 286
DB 220 CFNVDK-IIDPENLVYLSKVVRND--WEKCPKRLGNAKFGILWVGNCEIIFYVKEV- 274
OY 287 IERVESKAQCVKTFENDGVAADQPHY--DLTSQASWMDW-----PLHQ 331
DB 275 --EAEDLRKCRIVFE--ASASDQPTQYEELTDYOKIQEGYRQNNRMKISAFLPVGA 330
OY 332 DQPHSGGVGRNYGYVDTTGEKCALSDQVPCLVSAASVSTAAG--SLSEETPNF 388
DB 331 NSDFFKSGKGFNANFDSVNR-RCYIINSKPTCLINDKNFVATTAISHPOEVNEPFC 389
OY 389 IIPSN-----PSVTPPTETALQCTADKPPDSFGACDVQAC 424
DB 390 IYKOEIEREIKOSRNNQLVNDKARIVLPRIIFISNDMDIKCCEPHINSNCFNYVC 449
OY 425 KRQKTSYV--GGQIGSTG---VDCTADEQNECG--SNVTLINGLAVGVLLALLGGG 475
DB 450 -----NCVEKRAEIKENNEVVIKEEFKEDYQNEDEKSNKMLIILIGTVGCVVLA 504
OY 476 CYFAKRLDRNKGVAAHHEHFGQDRGARKRPS---DLMOEAPSPFDEAEENIEDGE 532
DB 505 FYFPRK-----EHNDKYDKMDQAEQYKPTARKDEMULDPEASFGEDK---RASHT 552
OY 533 THVWVEGDY 541
DB 553 TPVLMKPY 561

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O96719
ID ID O96719 PRELIMINARY; PRT; 622 AA.
AC O96718;
DT 01-DEC-2001 (TREMblrel. 19, Created)
DT 01-DEC-2001 (TREMblrel. 19, last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, last annotation update)
DE Apical membrane antigen-1 (Fragment).
GN AMA-1.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
CX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=395-94;
RC STRAIN=395-94;
RX MEDLINE=21192561; PubMed=11295182;
RA Escalante A.A., Grebert H.M., Chaiyaroj S.C., Magris M., Biswas S.,
RA Nahlen B.L., Lal A.A.;
RT "Polymorphism in the gene encoding the apical membrane antigen-1 (AMA-1) of Plasmodium falciparum. X. Asembo Bay Cohort Project."
RL Mol. Biochem. Parasitol. 113:279-287(2001).
DR InterPro; IPR003298; Apmem_Agl.
DR Pfam; PF02430; AMA-1; 1.
DR PRINTS; PRO1361; MEROZOITESA.
FT NON TER.
SQ SEQUENCE 622 AA; 71954 MW; 6A6A2FD25F6E59 CRC64;

Query Match 13.8%; Score 404; DB 5; Length 622;
Best Local Similarity 25.5%; Pred. No. 2.7e-26;
Matches 145; Conservative 85; Mismatches 217; Indels 122; Gaps 23;

OY 41 GNPFQANVEKTFMERFNLTHHOSGIYVDLGODKEVDGTLVREPAGLCPIMGKHIELQ 100
DB 107 GNPF-----TEYAKYDIEVHOSGIRVDLGDAEVAAGTOYRLPSKCPVFGIGIIE 160
OY 101 PDRLPYRNPLEDVPTE--KEYKOSGNPLPGGFNLNFTVPSGQRIISPPMELL-----EK 155
DB 161 SN-----TTFLPVAATENQCLKDGGAFAFP-----PKRLISPTLTDQMRDFYK 206
OY 156 NIKASTDLGCAEAFATVAMDKNKATKYRPFYVYDSKKRLCHILYVSMOLMEGKYCV 215
DB 207 YVKNLDELTLCSRAAGN--MNPNDENSNTKYPAVYDYKCKCHILYIAAQENNGPRYCN 264
OY 216 VKGEPDLTWYCFKPRKSVTENHNLVYSAVYGEN--PDAFISCPNOALRGVFGVWK 274
DB 265 -KDSKNSWFCFRPAKDKSFQNY-----TYSKVVDNMEKCPKRLGNAKFGILWVDG 318
OY 275 RCLDYTELDTVIERVESKAQCVKTFENDGVAADQPHY--DLTSQASWMDW----- 327
DB 319 NCEDIPVHNF-----SANDLPECNKLIVFELS--ASDQKQYEQHLTDYEXIKCKGN 373
OY 328 -----LHSGDQHSQGVGRNYGYVDTTGEKCALSDQVPCLVSAASVSTAAG 377
DB 374 MIKSAFLPTGAFAKADRYKSHGKGMGNVYTERO--KCEIFVNYKPTCLINNSYIA 430
OY 378 AGSLSEETPNFIIIPSN-----PSVTPPTETAL 405
DB 431 LSHNVEVHNF--PCSLYKOEIKKEIERESKRITKLNNDDEGNKKTIAPIFISDQ 488
OY 406 QCTADKPPDSFGACDVQACRKQKTSYVGGQIGSTVDTCTA-----DEQNECGSN 454
DB 489 KCPCAPEIVNSNCFNYVC-----CYEKAQAVTSNNEVVYKKEVYADIPENKPT 543
OY 455 --TALLINGLAVGVLLALLGGGCTPAKRLDRNKGVAAHHEHFGQDRGARKRPS 512
DB 544 KMKIIIASAIVAVLATITLM--VLYLKR-----KGAQEKYDKMDEPHQYKSN 595

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Job time : 110 secs

QY 513 OEAPSPFWDABENIEODGFTHWJEGDY 541
DB 596 LDPEASFVWGEER--RASHTPVLMEKPY 621

RESULT 40

Q9N9E6 PRELIMINARY; PRT; 526 AA.
AC Q9N9E6;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, last sequence update)
DE 01-JUN-2001 (TREMBlrel. 17, last annotation update)
DE Apical membrane antigen 1 (Fragment).
GN 83/AMA-1.
OS Plasmodium falciparum.
OC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
OX NCBI_TaxID=5833;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C1-4.1;
RX MEDLINE=20416492; PubMed=10960173;
RA Kocken C.H.M., Narum D.L., Massouhodi A., Ayivi B., Dubbeld M.A.,
van der Wel A., Conway D.J., Sanni A., Thomas A.W.;
"Molecular characterisation of Plasmodium reichenowi apical membrane
antigen-1 (AMA-1), comparison with P. falciparum AMA-1, and antibody-
mediated inhibition of red cell invasion."
RT MOL. Biochem. Parasitol. 109:147-156 (2000).
RL EMBL; AJ271183; CAB97195.1; -
DR InterPro; IPR003298; Apmem_Agl.
DR Pfam; PF02430; AMA-1; 1.
DR PRINTS; PR01361; MEROZOITESA.
FT NON_TER 1
FT TER 526
SQ SEQUENCE 526 AA; 60834 MW; FB9F569E4DE8BD1 CRC64;

Query Match 13.8%; Score 403; DB 5; Length 526;
Best Local Similarity 27.4%; Pred. No. 2.6e-26;

Matches 125; Conservative 70; Mismatches 160; Indels 102; Gaps 19;

QY 41 GNPFOANVEMKTFMERFNLTHHQSIGIYVDLGQDKEVDGTLVREPAGLCPWKGHLELQ 100
DB 99 GNPW-----TEYMAKDIIEVHSGIRVDLGEDAEVAGTQYRLPSGKCPVFGKIIEN 152
QY 101 PDRLPFRNNFLEVPTE-KEYKOSGNPLDGGFNLNFTVPSGORISFPWELL---EKNS 155
DB 153 SN-----TFTLPVATENDLKDGFAPF-----PTNPMSPTLDQMRHFYKDK 198
QY 156 NIKASTDLGRCAFRTVAMDKNKATKYRYPFYVDSKKRLCHILYVSMQMEGKKYCS 215
DB 199 YVKNLDELTLCSRHAGN--MNPNDKSNKYKPAVYDDKDKCHILYIAAQNNGPRYCN 256
QY 216 VKGEPDDLTYWCFKPRK-SVTENHLLYGSAYVGEN-PDAFISKCPNALRGYRFGWKK 273
DB 257 -KDESKRNSMFCRPAKDKLFENY-----TYSKIVVDXWEKVCPRKNLQNAKFGMLWD 309
QY 274 GRCLDYTELTD-TVIERVESKAQCWKTFFNDGVAASDQHTYR--LTSQASWMDWMP--- 327
DB 310 GNCEDIPHVNEFPALIDFE---CNKLVPFLS--ASDQKQYEOHLTYEKIKEGFKKN 363
QY 328 -----LHSDQPHSGGVRNYGFYVDTTGEKALSDQVPCDCLVSDSAVSY 375
DB 364 ASNIKAFLPTGAFKADRYKSHGKIWMGNVNTETO--KCEIFNVKFTCLINNSSYIAT 420
QY 376 TAAAGLSSEETPNFIIPSN-----PSVTPTPET 403
DB 421 TALSHPIEVENN--PXSLYKNEIMKEIERESKRILKLNDDGNNKKLIAPRIFISDDK 478
QY 404 ALQCTADKFPDSFGACDVQACKROKISCVGQIOSTS 440
DB 479 SLKPCPCDPEIIVNSTCNFVCK---CVKRAEVTS 510

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